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UTILITY PATENT APPLICATION TRANSMITTAL

(for new nonprovisional applications under 37 CFR 1.53(b))

Attorney Docket No.	04983.0169.US01/38-21(15786)B
First Named Inventor or Application Identifier	BYRUM
Title	Nucleic Acid Molecules and Other Molecules Associated with Plants
Express Mail Label No.	

APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents

ADDRESS TO: Assistant Commissioner for Patents
Box Patent Application
Washington, DC 20231

1. ☐ *Fee Transmittal Form (Form PTO-1082)
(Submit an original and a duplicate for fee processing)

2. ☒ Specification [*Total Pages* 913]
(preferred arrangement set forth below)
- Descriptive title of the Invention
- Cross References to Related Applications
- Statement Regarding Fed sponsored R&D
- Reference to Microfiche Appendix
- Background of the Invention
- Brief Summary of the Invention
- Brief Description of the Drawings (if filed)
- Detailed Description
- Claims
- Abstract of the Disclosure

3. ☐ Drawing(s) *(35 USC 113)* [*Total Sheets*]

4. ☐ Oath or Declaration [*Total Pages*]
a. ☐ Newly executed (original or copy)
b. ☐ Copy from a prior application (37 CFR 1.63(d))
(for continuation/divisional with Box 17 completed)
[Note Box 5 below]
i. ☐ DELETION OF INVENTOR(S)
Signed statement attached deleting inventor(s) named in the prior application, see 37 CFR 1.63(d)(2) and 1.33(b).

5. ☐ Incorporation By Reference *(useable if Box 4b is checked)*
The entire disclosure of the prior application, from which a copy of the oath or declaration is supplied under Box 4b, is considered as being part of the disclosure of the accompanying application and is hereby incorporated by reference therein.

6. ☐ Microfiche Computer Program *(Appendix)*

7. Nucleotide and/or Amino Acid Sequence Submission
(if applicable, all necessary)
a. ☒ Computer Readable Copy
b. ☒ Paper Copy (identical to computer copy)
c. ☒ Statement verifying identity of above copies

ACCOMPANYING APPLICATION PARTS

8. ☐ Assignment Papers (cover sheet & document(s))
9. ☐ 37 CFR 3.73(b) Statement *(when there is an assignee)* ☐ Power of Attorney
10. ☐ English Translation Document *(if applicable)*
11. ☐ Information Disclosure Statement (IDS)/PTO-1449 ☐ Copies of IDS Citations
12. ☐ Preliminary Amendment
13. ☒ Return Receipt Postcard (MPEP 503) (Two)
(should be specifically itemized)
14. ☐ *Small Entity Statement(s) ☐ Statement filed in prior application, Status still proper and desired
15. ☐ Certified Copy of Priority Document(s)
(if foreign priority is claimed)
16. ☐ Other:

*NOTE FOR ITEMS 1 & 14 IN ORDER TO BE ENTITLED TO PAY SMALL ENTITY FEES, A SMALL ENTITY STATEMENT IS REQUIRED (37 C F R § 1 27), EXCEPT IF ONE FILED IN A PRIOR APPLICATION IS RELIED UPON (37 C F.R § 1 28)

17. **If a CONTINUING APPLICATION**, *check appropriate box and supply the requisite information:*
☐ Continuation ☐ Divisional ☐ Continuation-in-part (CIP) of prior application No: /
Prior Application Information: Examiner: Group/Art Unit:

18. CORRESPONDENCE ADDRESS

☒ *Customer Number or Bar Code Label* 22930 *or* ☐ *Correspondence address below*
(Insert Customer No. or Attach bar code label here)

NAME	David R. Marsh HOWREY SIMON ARNOLD & WHITE, LLP				
ADDRESS	Box No. 34 1299 Pennsylvania Avenue, N.W.				
CITY	Washington	STATE	DC	ZIP CODE	20004-2402
COUNTRY	US	TELEPHONE	202-783-0800	FAX	202-383-7195

Name (Print/Type)	David R. Marsh/Timothy W. Riffe	Registration No. (Attorney/Agent)	41,408/43,881
Signature	Timothy W. Riffe	Date	April 21, 2000

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HOWREY SIMON ARNOLD & WHITE
HOWREY LLP
ATTORNEYS AT LAW

1299 PENNSYLVANIA AVE., NW
WASHINGTON, DC 20004-2402
PHONE 202.783.0800
FAX 202.383.6610
A LIMITED LIABILITY PARTNERSHIP

jc696 U.S. PTO
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jc525 U.S. PTO
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April 21, 2000

Box Patent Application

Assistant Commissioner for Patents
Washington, D.C. 20231

Re: U.S. Non-Provisional Utility Patent Application
Application No.: To Be Assigned
Filed: Herewith
For: Nucleic Acid Molecules and Other Molecules Associated with Plants
Inventors: Joseph R. BYRUM *et al.*
Atty. Docket: 04983.0169.US01/38-21(15786)B

Sir:

The following documents are forwarded herewith for appropriate action by the U.S. Patent and Trademark Office:

1. Utility Patent Application Transmittal (PTO/SB/05);

2. U.S. Utility Patent Application entitled:

Nucleic Acid Molecules and Other Molecules Associated with Plants

and naming as inventors:

Joseph R. BYRUM and David K. KOVALIC,

the application consisting of:

a. A specification containing:

(i) 910 pages of a description prior to the claims;

(ii) 2 pages of claims (11 claims);

(iii) a one (1) page abstract; and

(iv) 8,451 pages of a sequence listing;

3. A CD-ROM containing the sequence listing;

4. Statement Regarding Sequence Submission; and

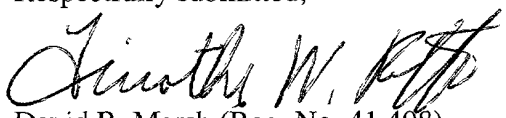
5. Two (2) return postcards.

This application is being filed without an executed Declaration, and without payment of official fees.

In accordance with 37 C.F.R. § 1.821(f), the paper copy of the sequence listing and the computer readable copy of the sequence listing submitted herewith in the above application are the same.

It is respectfully requested that, of the two attached postcards, one be stamped with the filing date of these documents and returned to our courier, and the other, prepaid postcard, be stamped with the filing date and unofficial application number and returned as soon as possible.

Respectfully submitted,



David R. Marsh (Reg. No. 41,408)
Timothy W. Riffe (Reg. No. 43,881)

Enclosures

NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH PLANTS

Field of the Invention

The present invention is in the field of plant genetics. More specifically the invention relates to nucleic acid molecules and nucleic acid molecules that contain markers, in particular, single nucleotide polymorphism (SNP) and repetitive element markers. In addition, the present invention provides nucleic acid molecules having regulatory elements or encoding proteins or fragments thereof and nucleic acid molecules present in non-coding regions.. The invention also relates to proteins and fragments of proteins so encoded and antibodies capable of binding the proteins. The invention also relates to methods of using the nucleic acid molecules, for example, for gene identification and analysis, markers, repetitive elements and fragments of repetitive elements, regulatory elements, proteins and fragments of proteins.

Background of the Invention

I. SEQUENCE TAGGED CONNECTOR NUCLEIC ACID MOLECULES AND THE BACTERIAL ARTIFICIAL CHROMOSOMES (BACS) CONTAINING THESE SEQUENCES.

Sequence tagged connectors, or STCs, are sequences of insert data generated from both ends (at the vector-insert point) of a BAC clone in a genomic library. These sequences, and BACs containing these STC sequences, can be used, for example, for marker development, genetic mapping or linkage analysis, marker assisted breeding, and physical genome mapping (Venter, *et al., Nature, 381:*364-366 (1996), the entirety of which is herein incorporated by reference; Choi and Wing, http://www.genome.clemson.edu/protocols2-nj.html July, 1998). STCs can represent a copy of up to a full length of a mRNA transcript, a promoter element or

part of a promoter, can contain simple sequence repeats (also called microsatellites) repetitive elements or fragments of repetitive elements, other DNA markers, or any combination thereof.

Markers have been used in genetic mapping which can be a step in isolating a gene. Genetic mapping or linkage analysis is based on the level at which markers and genes are co-inherited (Rothwell, *Understanding Genetics. 4th Ed.,* Oxford University Press, New York, p. 703 (1988). Statistical tests like chi-square analysis can be used to test the randomness of segregation or linkage (Kochert, *The Rockefeller Foundation International Program on Rice Biotechnology*, University of Georgia, Athens, GA, pp 1-14 (1989), the entirety of which is herein incorporated by reference. In linkage mapping, the proportion of recombinant individuals out of the total mapping population provides the information for determining the genetic distance between the loci (Young, *Encyclopedia of Agricultural Science*, Vol. 3, pp 275-282 (1994), the entirety of which is herein incorporated by reference).

Classical mapping studies utilize easily observable, visible traits instead of molecular markers. These visible traits are also known as naked eye polymorphisms. These traits can be morphological like plant height, fruit size, shape and color or physiological like disease response, photoperiod sensitivity or crop maturity. Visible traits are useful and are still in use because they represent actual phenotypes and are easy to score without any specialized lab equipment. By contrast, the other types of genetic markers are arbitrary loci for use in linkage mapping and often not associated to specific plant phenotypes (Young, *Encyclopedia of Agricultural Science,* Vol. 3, pp. 275-282 (1994). Many morphological markers cause such large effects on phenotype that they are undesirable in breeding programs. Many other visible traits have the disadvantage of being developmentally regulated (i.e., expressed only at certain stages; or in specific tissues and organs). Often times, visible traits mask the effects of linked minor genes making it nearly

impossible to identify desirable linkages for selection (Tanksely, *et al., Biotech. 7*:257-264 (1989), the entirety of which is herein incorporated by reference).

Although a number of important agronomic characters are controlled by loci having major effects on phenotype, many economically important traits, such as yield and some forms of disease resistance, are quantitative in nature. This type of phenotypic variation in a trait is characterized by continuous, normal distribution of phenotypic values in a particular population (Beckmann and Soller, *Oxford Surveys of Plant Molecular Biology, Miffen.* (ed.), Vol. 3, Oxford University Press, UK., pp. 196-250 (1986), the entirety of which is herein incorporated by reference). Such traits are governed by a large number of loci, Quantitative Trait Loci (QTL), each of which can make a small positive or negative effect to the final phenotype value of the trait (Beckmann and Soller, *Oxford Surveys of Plant Molecular Biology, Miffen.* (ed.), Vol. 3, Oxford University Press, U.K., pp. 196-250 (1986). Loci contributing to such genetic variation are often termed minor genes as opposed to major genes with large effects that follow a Mendelian pattern of inheritance. Polygenic traits are also predicted to follow a Mendelian type of inheritance, however the contribution of each locus is expressed as an increase or decrease in the final trait value.

Markers have been used in physical mapping studies with BAC libraries made from plant genomes. Such mapping studies have been carried out in rice (Kim *et al., Genomics 34*:213-218 (1996), herein incorporated by reference; Hang, *Plant Mol. Biol. 35:*129-133 (1997), herein incorporated by reference; Zhang and Wing., *Plant Mol. Bio. 35:*115-127 (1997) herein incorporated by reference; Chen *et al., Proc. Acad. Sci. (U.S.A.) 94:*3431-3435 (1997) herein incorporated by reference; Wang *et al., Plant J. 7:*525-533 (1995) herein incorporated by reference) sorghum (Zwick *et al., Genetics 148:*1983-1992 (1998) herein incorporated by

reference; Zhang, *et al., Molecular Breeding 2:*11-24 (1996) the entirety of which is herein incorporated by reference) maize, (Chen, *et al., Proc. Acad. Sci. (U.S.A.) 94:*3431-3435 (1997), and *Arabidopsis* (Kim, *et al., Genomics 34:*213-218 (1996) the entirety of which is herein incorporated by reference.

Repetitive elements have been used in physical mapping in cereals (Ananiev, *et al., Proc. Acad. Sci. (U.S.A.) 95*:13073-8 (1998), the entirety of which is herein incorporated by reference; McLean *et al., Mol Gen Genet 253*:687-694 (1997), the entirety of which is herein incorporated by reference).

II. SEQUENCE COMPARISONS

STCs and sequenced BACs can be compared, for example, to sequences that encode promoters or proteins. These homologies can be determined by similarity searches (Adams, *et al., Science 252*:1651-1656 (1991), herein incorporated by reference).

A characteristic feature of a DNA sequence is that it can be compared with other DNA sequences. Sequence comparisons can be undertaken by determining the similarity of the test or query sequence with sequences in publicly available or propriety databases ("similarity analysis") or by searching for certain motifs ("intrinsic sequence analysis")(e.g., *cis* elements)(Coulson, *Trends in Biotechnology, 12:*76-80 (1994), the entirety of which is herein incorporated by reference; Birren, *et al., Genome Analysis, 1*:543-559 (1997), the entirety of which is herein incorporated by reference).

Similarity analysis includes database search and alignment. Examples of public databases include the DNA Database of Japan (DDBJ)(http://www.ddbj.nig.ac.jp/); Genebank (http://www.ncbi.nlm.nih.gov/web/Genbank/Index.htlm); and the European Molecular Biology

Laboratory Nucleic Acid Sequence Database (EMBL) (http://www.ebi.ac.uk/ebi_docs/embl_db.html). A number of different search algorithms have been developed, one example of which are the suite of programs referred to as BLAST programs. There are five implementations of BLAST, three designed for nucleotide sequences queries (BLASTN, BLASTX, and TBLASTX) and two designed for protein sequence queries (BLASTP and TBLASTN) (Coulson, *Trends in Biotechnology, 12:*76-80 (1994); Birren, *et al., Genome Analysis, 1:*543-559 (1997)).

BLASTN takes a nucleotide sequence (the query sequence) and its reverse complement and searches them against a nucleotide sequence database. BLASTN was designed for speed, not maximum sensitivity, and may not find distantly related coding sequences. BLASTX takes a nucleotide sequence, translates it in three forward reading frames and three reverse complement reading frames, and then compares the six translations against a protein sequence database. BLASTX is useful for sensitive analysis of preliminary (single-pass) sequence data and is tolerant of sequencing errors (Gish and States, *Nature Genetics, 3:*266-272 (1993), the entirety of which is herein incorporated by reference). BLASTN and BLASTX may be used in concert for analyzing STC data (Coulson, *Trends in Biotechnology, 12:*76-80 (1994); Birren, *et al., Genome Analysis, 1:*543-559 (1997).

Given a coding nucleotide sequence and the protein it encodes, it is often preferable to use the protein as the query sequence to search a database because of the greatly increased sensitivity to detect more subtle relationships. This is due to the larger alphabet of proteins (20 amino acids) compared with the alphabet of nucleic acid sequences (4 bases), where it is far easier to obtain a match by chance. In addition, with nucleotide alignments, only a match (positive score) or a mismatch (negative score) is obtained, but with proteins, the presence of

conservative amino acid substitutions can be taken into account. Here, a mismatch may yield a positive score if the non-identical residue has physical/chemical properties similar to the one it replaced. Various scoring matrices are used to supply the substitution scores of all possible amino acid pairs. A general purpose scoring system is the BLOSUM62 matrix (Henikoff and Henikoff, *Proteins, 17:*49-61 (1993), the entirety of which is herein incorporated by reference), which is currently the default choice for BLAST programs. BLOSUM62 is tailored for alignments of moderately diverged sequences and thus may not yield the best results under all conditions. Altschul, *J. Mol. Biol. 36:*290-300 (1993), the entirety of which is herein incorporated by reference, uses a combination of three matrices to cover all contingencies. This may improve sensitivity, but at the expense of slower searches. In practice, a single BLOSUM62 matrix is often used but others (PAM40 and PAM250) may be attempted when additional analysis is necessary. Low PAM matrices are directed at detecting very strong but localized sequence similarities, whereas high PAM matrices are directed at detecting long but weak alignments between very distantly related sequences.

Homologues in other organisms are available that can be used for comparative sequence analysis. Multiple alignments are performed to study similarities and differences in a group of related sequences. CLUSTAL W is a multiple sequence alignment package available that performs progressive multiple sequence alignments based on the method of Feng and Doolittle, *J. Mol. Evol.* 25:351-360 (1987), the entirety of which is herein incorporated by reference. Each pair of sequences is aligned and the distance between each pair is calculated; from this distance matrix, a guide tree is calculated, and all of the sequences are progressively aligned based on this tree. A feature of the program is its sensitivity to the effect of gaps on the alignment; gap penalties are varied to encourage the insertion of gaps in probable loop regions instead of in the

middle of structured regions. Users can specify gap penalties, choose between a number of scoring matrices, or supply their own scoring matrix for both the pairwise alignments and the multiple alignments. CLUSTAL W for UNIX and VMS systems is available at: ftp.ebi.ac.uk. Another program is MACAW (Schuler *et al.*, *Proteins, Struct. Func. Genet, 9:*180-190 (1991), the entirety of which is herein incorporated by reference, for which both Macintosh and Microsoft Windows versions are available. MACAW uses a graphical interface, provides a choice of several alignment algorithms, and is available by anonymous ftp at: ncbi.nlm.nih.gov (directory/pub/macaw).

Sequence motifs are derived from multiple alignments and can be used to examine individual sequences or an entire database for subtle patterns. With motifs, it is sometimes possible to detect distant relationships that may not be demonstrable based on comparisons of primary sequences alone. Currently, the largest collection of sequence motifs in the world is PROSITE (Bairoch and Bucher, *Nucleic Acid Research, 22:*3583-3589 (1994), the entirety of which is herein incorporated by reference). PROSITE may be accessed via either the ExPASy server on the World Wide Web or anonymous ftp site. Many commercial sequence analysis packages also provide search programs that use PROSITE data.

A resource for searching protein motifs is the BLOCKS E-mail server developed by S. Henikoff, *Trends Biochem Sci., 18:*267-268 (1993), the entirety of which is herein incorporated by reference; Henikoff and Henikoff, *Nucleic Acid Research, 19:*6565-6572 (1991), the entirety of which is herein incorporated by reference; Henikoff and Henikoff, *Proteins, 17:*49-61 (1993). BLOCKS searches a protein or nucleotide sequence against a database of protein motifs or "blocks." Blocks are defined as short, ungapped multiple alignments that represent highly conserved protein patterns. The blocks themselves are derived from entries in PROSITE as well

as other sources. Either a protein or nucleotide query can be submitted to the BLOCKS server; if a nucleotide sequence is submitted, the sequence is translated in all six reading frames and motifs are sought in these conceptual translations. Once the search is completed, the server will return a ranked list of significant matches, along with an alignment of the query sequence to the matched BLOCKS entries.

Conserved protein domains can be represented by two-dimensional matrices, which measure either the frequency or probability of the occurrences of each amino acid residue and deletions or insertions in each position of the domain. This type of model, when used to search against protein databases, is sensitive and usually yields more accurate results than simple motif searches. Two popular implementations of this approach are profile searches (such as GCG program ProfileSearch) and Hidden Markov Models (HMMs) (Krough, *et al., J. Mol. Biol. 235*:1501-1531 (1994); Eddy, *Current Opinion in Structural Biology 6*:361-365 (1996), both of which are herein incorporated by reference in their entirety). In both cases, a large number of common protein domains have been converted into profiles, as present in the PROSITE library, or HHM models, as in the Pfam protein domain library (Sonnhammer, *et al., Proteins 28*:405-420 (1997), the entirety of which is herein incorporated by reference). Pfam contains more than 500 HMM models for enzymes, transcription factors, signal transduction molecules, and structural proteins. Protein databases can be queried with these profiles or HMM models, which will identify proteins containing the domain of interest. For example, HMMSW or HMMFS, two programs in a public domain package called HMMER (Sonnhammer, *et al., Proteins 28*:405-420 (1997)) can be used.

PROSITE and BLOCKS represent collected families of protein motifs. Thus, searching these databases entails submitting a single sequence to determine whether or not that sequence is

similar to the members of an established family. Programs working in the opposite direction compare a collection of sequences with individual entries in the protein databases. An example of such a program is the Motif Search Tool, or MoST (Tatusov, *et al., Proc. Natl. Acad. Sci. 91:*12091-12095 (1994), the entirety of which is herein incorporated by reference). On the basis of an aligned set of input sequences, a weight matrix is calculated by using one of four methods (selected by the user); a weight matrix is simply a representation, position by position in an alignment, of how likely a particular amino acid will appear. The calculated weight matrix is then used to search the databases. To increase sensitivity, newly found sequences are added to the original data set, the weight matrix is recalculated, and the search is performed again. This procedure continues until no new sequences are found.

Summary of the Invention

The present invention provides a substantially purified nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof.

The present invention also provides a substantially purified nucleic acid molecule, the nucleic acid molecule capable of specifically hybridizing to a second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof.

The present invention also provides a substantially purified nucleic acid molecule encoding a protein or fragment thereof, wherein the protein or fragment thereof is selected from the group consisting a *Glycine max* protein or fragment thereof from Table 1.

The present invention also provides a substantially purified nucleic acid molecule encoding a *Glycine max* protein or fragment thereof, wherein the *Glycine max* protein or

fragment thereof is encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof or fragments of either.

The present invention also provides a substantially purified protein or fragment thereof encoded by a nucleic acid sequence selected from the group that encodes a *Glyciine max* protein or fragment thereof from Table 1.

The present invention also provides a substantially purified protein or fragment thereof encoded by a first nucleic acid molecule which specifically hybridizes to a second nucleic acid molecule, the second nucleic acid molecule selected from the group that encodes a *Glycine max* protein or fragments thereof from Table 1.

The present invention also provides a substantially purified protein or fragment thereof encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof or fragments of either.

The present invention also provides a transformed cell having a nucleic acid molecule which comprises: (A) an exogenous promoter region which functions in the cell to cause the production of a mRNA molecule; which is linked to (B) a structural nucleic acid molecule, wherein the structural nucleic acid molecule encodes a protein or fragment thereof selected from the group consisting of a *Glycine max* protein or fragment thereof in Table 1; which is linked to (C) a 3' non-translated sequence that functions in the cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of the mRNA molecule.

The present invention also provides a plant cell, a mammalian cell, a bacterial cell, an insect cell and a fungal cell transformed with a nucleic acid molecule of the present invention.

The present invention also provides a computer readable medium having recorded thereon one or more of the nucleotide sequences depicted in SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof.

The present invention also provides a computer readable medium having recorded thereon one or more of the nucleotide sequences encoding a protein or fragment thereof, wherein the protein or fragment thereof is selected from the group consisting of a *Glycine max* protein or fragment thereof in Table 1.

The present invention provides a computer readable medium having recorded thereon one or more of the nucleotide sequences depicted in SEQ ID NO:1 through SEQ ID NO: 20082.

The present invention provides a method of introgressing a trait into a plant comprising using a nucleic acid marker for marker assisted selection of the plant, the nucleic acid marker complementary to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof, and introgressing the trait into a plant.

The present invention provides a method for screening for a trait comprising interrogating genomic DNA for the presence or absence of a marker molecule that is genetically linked to a nucleic acid sequence complementary to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof; and detecting the presence or absence of the marker.

The present invention provides a method for determining the likelihood of the level, presence or absence of a trait in a plant comprising the steps of: (A) obtaining genomic DNA from the plant; (B) detecting a marker nucleic acid molecule; the marker nucleic acid molecule wherein the marker nucleic acid molecule specifically hybridizes with a nucleic acid sequence that is genetically linked to a nucleic acid sequence complementary to a nucleic acid sequence

selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof; (C) and determining the level, presence or absence of the marker nucleic acid molecule, wherein the level, presence or absence of the marker nucleic acid molecule is indicative of the likely presence in the plant of the trait.

The present invention provides a method for determining a genomic polymorphism in a plant that is predictive of a trait comprising the steps: (A) incubating a marker nucleic acid molecule, under conditions permitting nucleic acid hybridization, and a complementary nucleic acid molecule obtained from the plant, the marker nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof; (B) permitting hybridization between the marker nucleic acid molecule and the complementary nucleic acid molecule obtained from the plant; and (C) detecting the presence of the polymorphism.

The present invention provides a method of determining an association between a polymorphism and a plant trait comprising: (A) hybridizing a nucleic acid molecule specific for the polymorphism to genetic material of a plant, wherein the nucleic acid molecule comprises a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof; and (B) calculating the degree of association between the polymorphism and the plant trait.

Detailed Description of the Invention

Agents of the invention:

(a) Nucleic Acid Molecules

Agents of the present invention include nucleic acid molecules and more specifically BACs and STC nucleic acid molecules or nucleic acid fragment molecules thereof.

A subset of the nucleic acid molecules of the present invention includes nucleic acid molecules that are marker molecules. Another subset of the nucleic molecules of the present invention include nucleic acid molecules that are promoters and/or regulatory elements. Another subset of the nucleic acid molecules of the present invention include nucleic acid molecules that encode proteins or fragments of proteins. In a preferred embodiment the nucleic acid molecules of the present invention are derived from *Glycine max* (soybean) and more preferably *Glycine max,* genotype A3244 (Asgrow, Des Moines, Iowa).

Fragment STC nucleic acid molecules and fragments of BACs may encode significant portion(s) of, or indeed most of, the STC or BAC nucleic acid molecule. In addition, a fragment nucleic acid molecule can encode a *Glycine max* protein or fragment thereof. Alternatively, the fragments may comprise smaller oligonucleotides (having from about 15 to about 250 nucleotide residues, and more preferably, about 15 to about 30 nucleotide residues).

The term "substantially purified", as used herein, refers to a molecule separated from substantially all other molecules normally associated with it in its native state. More preferably a substantially purified molecule is the predominant species present in a preparation. A substantially purified molecule may be greater than 60% free, preferably 75% free, more preferably 90% free, and most preferably 95% free from the other molecules (exclusive of

solvent) present in the natural mixture. The term "substantially purified" is not intended to encompass molecules present in their native state.

The agents of the present invention will preferably be "biologically active" with respect to either a structural attribute, such as the capacity of a nucleic acid to hybridize to another nucleic acid molecule, or the ability of a protein to be bound by an antibody (or to compete with another molecule for such binding). Alternatively, such an attribute may be catalytic, and thus involve the capacity of the agent to mediate a chemical reaction or response.

The agents of the present invention may also be recombinant. As used herein, the term recombinant means any agent (e.g., DNA, peptide etc.), that is, or results, however indirect, from human manipulation of a nucleic acid molecule.

It is understood that the agents of the present invention may be labeled with reagents that facilitate detection of the agent (e.g., fluorescent labels (Prober, *et al., Science 238*:336-340 (1987); Albarella *et al.,* EP 144914, chemical labels (Sheldon *et al.,* U.S. Patent 4,582,789; Albarella *et al.,* U.S. Patent 4,563,417, modified bases (Miyoshi *et al.,* EP 119448, all of which are hereby incorporated by reference in their entirety).

It is further understood, that the present invention provides bacterial, viral, microbial, insect, fungal and plant cells comprising the agents of the present invention.

The genetic variability resulting from transposable elements ranges from changes in the size and arrangement of whole genomes to changes in single nucleotides. They may produce major effects on phenotypic traits or small silent changes detectable only at the DNA sequence level. Transposable elements may also produce variation when they excise, leaving small footprints of their previous presence (Kidwell and Lisch, *Proc. Natl. Acad. Sci. (U.S.A.) 94*:7704-7711 (1997)).

In addition, other markers such as AFLP markers, RFLP markers, RAPD markers, phenotypic markers or isozyme markers can be utilized (Walton, Seed World 22-29 (July, 1993), the entirety of which is herein incorporated by reference; Burow and Blake, *Molecular Dissection of Complex Traits*, 13-29, Eds. Paterson, CRC Press, New York (1988), the entirety of which is herein incorporated by reference). DNA markers can be developed from nucleic acid molecules using restriction endonucleases, the PCR and/or DNA sequence information. RFLP markers result from single base changes or insertions/deletions. These codominant markers are highly abundant in plant genomes, have a medium level of polymorphism and are developed by a combination of restriction endonuclease digestion and Southern blotting hybridization. CAPS are similarly developed from restriction nuclease digestion but only of specific PCR products. These markers are also codominant, have a medium level of polymorphism and are highly abundant in the genome. The CAPS result from single base changes and insertions/deletions. Another marker type, RAPDs, are developed from DNA amplification with random primers and result from single base changes and insertions/deletions in plant genomes. They are dominant markers with a medium level of polymorphisms and are highly abundant. AFLP markers require using the PCR on a subset of restriction fragments from extended adapter primers. These markers are both dominant and codominant, are highly abundant in genomes and exhibit a medium level of polymorphism. SSRs require DNA sequence information. These codominant markers result from repeat length changes, are highly polymorphic, and do not exhibit as high a degree of abundance in the genome as CAPS, AFLPs and RAPDs. SNPs also require DNA sequence information. These codominant markers result from single base substitutions. They are highly abundant and exhibit a medium of polymorphism (Rafalski, *et al.*, In: *Nonmammalian Genomic Analysis*, ed. Birren and Lai, Academic Press, San Diego, CA, pp. 75-134 (1996), the

entirety of which is herein incorporated by reference). Methods to isolate such markers are known in the art.

Long Terminal repeat retrotransposons and *MITEs* have been found to be associated with the genes of many plants where some of the transposable elements contribute regulatory sequences. *MITEs* such as the *Tourist* element in maize and the *Stowaway* element in Sorghum are found frequently in the 5' and 3' noncoding regions of genes and are frequently associated with the regulatory regions of genes of diverse flowering plants (Kidwell and Lisch, *Proc. Natl. Acad. Sci. (U.S.A.) 94*:7704-7711 (1997)). It is understood that one or more of the Long Terminal repeat retrotransposons and/or MITES may be a marker, and even more preferably a marker for a gene.

(ii) Nucleic Acid Molecules Comprising Regulatory Elements

Another class of agents of the present invention are nucleic acid molecules having promoter regions or partial promoter regions, including those located within SEQ ID NO: 1 through SEQ ID NO:20082. Such promoter regions are typically found upstream of the trinucleotide ATG sequence at the start site of a protein coding region.

As used herein, a promoter region is a region of a nucleic acid molecule that is capable, when located in *cis* to a nucleic acid sequence that encodes for a protein or fragment thereof to function in a way that directs expression of one or more mRNA molecules that encodes for the protein or fragment thereof.

Promoters of the present invention can include between about 300bp upstream and about 10kb upstream of the trinucleotide ATG sequence at the start site of a protein coding region. Promoters of the present invention can preferably include between about 300bp upstream and about 5kb upstream of the trinucleotide ATG sequence at the start site of a protein coding region.

Promoters of the present invention can more preferably include between about 300bp upstream and about 2kb upstream of the trinucleotide ATG sequence at the start site of a protein coding region. Promoters of the present invention can include between about 300bp upstream and about 1kb upstream of the trinucleotide ATG sequence at the start site of a protein coding region. While in many circumstances a 300bp promoter may be sufficient for expression, additional sequences may act to further regulate expression, for example, in response to biochemical, developmental or environmental signals.

It is also preferred that the promoters of the present invention contain a CAAT and a TATA *cis* element. Moreover, the promoters of the present invention can contain one or more *cis* elements in addition to a CAAT and a TATA box.

By "regulatory element" it is intended a series of nucleotides that determines if, when, and at what level a particular gene is expressed. The regulatory DNA sequences specifically interact with regulatory or other proteins. Many regulatory elements act in *cis* ("*cis* elements") and are believed to affect DNA topology, producing local conformations that selectively allow or restrict access of RNA polymerase to the DNA template or that facilitate selective opening of the double helix at the site of transcriptional initiation. *Cis* elements occur within, but are not limited to promoters, and promoter modulating sequences (inducible elements). *Cis* elements can be identified using known *cis* elements as a target sequence or target motif in the BLAST programs of the present invention.

Promoters of the present invention include homologues of *cis* elements known to effect gene regulation that show homology with the nucleic acid molecules of the present invention. These *cis* elements include, but are not limited to, oxygen responsive *cis* elements (Cowen, *et al.*, *J Biol. Chem. 268(36):*26904-26910 (1993) the entirety of which is herein incorporated by

reference), light regulatory elements (Bruce and Quaill, *Plant Cell 2 (11):*1081-1089 (1990) the entirety of which is herein incorporated by reference; Bruce, *et al., EMBO J. 10:*3015-3024 (1991), the entirety of which is herein incorporated by reference; Rocholl, *et al., Plant Sci. 97:*189-198 (1994), the entirety of which is herein incorporated by reference; Block, *et al., Proc. Natl. Acad. Sci. (U.S.A.) 87:*5387-5391 (1990), the entirety of which is herein incorporated by reference; Giuliano, *et al., Proc. Natl. Acad. Sci. (U.S.A.) 85:*7089-7093 (1988), the entirety of which is herein incorporated by reference; Staiger, *et al., Proc. Natl. Acad. Sci. (U.S.A.) 86:*6930-6934 (1989), the entirety of which is herein incorporated by reference; Izawa, *et al., Plant Cell 6:*1277-1287 (1994), the entirety of which is herein incorporated by reference; Menkens, *et al., Trends in Biochemistry 20:*506-510 (1995), the entirety of which is herein incorporated by reference; Foster, *et al., FASEB J. 8:*192-200 (1994), the entirety of which is herein incorporated by reference; Plesse, *et al., Mol Gen Gene 254:*258-266 (1997), the entirety of which is herein incorporated by reference; Green, *et al., EMBO J. 6:*2543-2549 (1987), the entirety of which is herein incorporated by reference; Kuhlemeier *et al., Ann. Rev Plant Physiol. 38:*221-257 (1987), the entirety of which is herein incorporated by reference; Villain *et al., J. Biol. Chem. 271:*32593-32598 (1996), the entirety of which is herein incorporated by reference; Lam *et al., Plant Cell 2:*857-866 (1990), the entirety of which is herein incorporated by reference; Gilmartin, *et al., Plant Cell 2:*369-378 (1990), the entirety of which is herein incorporated by reference; Datta, *et al., Plant Cell 1:*1069-1077 (1989) the entirety of which is herein incorporated by reference; Gilmartin, *et al., Plant Cell 2:*369-378 (1990), the entirety of which is herein incorporated by reference; Castresana, *et al., EMBO J.* 7:1929-1936 (1988), the entirety of which is herein incorporated by reference; Ueda, *et al., Plant Cell 1:*217-227 (1989), the entirety of which is herein incorporated by reference; Terzaghi, *et al., Annu. Rev. Plant Physiol. Plant Mol.*

*Biol. 46:*445-474 (1995), the entirety of which is herein incorporated by reference; Green *et al., EMBO J.* 6:2543-2549 (1987), the entirety of which is herein incorporated by reference; Villain, *et al., J. Biol. Chem. 271:*32593-32598 (1996), the entirety of which is herein incorporated by reference; Tjaden, *et al., Plant Cell 6:*107-118 (1994), the entirety of which is herein incorporated by reference; Tjaden, *et al., Plant Physiol. 108:*1109-1117 (1995), the entirety of which is herein incorporated by reference; Ngai, *et al., Plant J. 12:*1021-1234 (1997), the entirety of which is herein incorporated by reference; Bruce, *et al., EMBO J. 10:*3015-3024 (1991), the entirety of which is herein incorporated by reference; Ngai, *et al., Plant J. 12:*1021-1034 (1997), the entirety of which is herein incorporated by reference), elements responsive to gibberellin, (Muller, *et al., J. Plant Physiol. 145:*606-613 (1995), the entirety of which is herein incorporated by reference; Croissant, *et al., Plant Science 116:*27-35 (1996), the entirety of which is herein incorporated by reference; Lohmer, *et al., EMBO J. 10:*617-624 (1991), the entirety of which is herein incorporated by reference; Rogers, *et al., Plant Cell 4:*1443-1451 (1992), the entirety of which is herein incorporated by reference; Lanahan *et al., Plant Cell* 4:203-211 (1992) the entirety of which is herein incorporated by reference; Skriver *et al., Proc. Natl. Acad. Sci. (U.S.A.) 88:*7266-7270 (1991) the entirety of which is herein incorporated by reference; Gilmartin, *et al., Plant Cell 2:*369-378 (1990), the entirety of which is herein incorporated by reference; Huang, *et al., Plant Mol. Biol. 14:*655-668 (1990), the entirety of which is herein incorporated by reference, Gubler, *et al., Plant Cell 7:*1879-1891 (1995), the entirety of which is herein incorporated by reference), elements responsive to abscisic acid, (Busk, *et al., Plant Cell 9:*2261-2270 (1997), the entirety of which is herein incorporated by reference; Guiltinan, *et al., Science 250:*267-270 (1990), the entirety of which is herein incorporated by reference; Shen, *et al., Plant Cell 7:*295-307 (1995) the entirety of which is herein incorporated by reference; Shen

*et al., Plant Cell 8:*1107-1119 (1996), the entirety of which is herein incorporated by reference; Seo *et al., Plant Mol. Biol. 27:*1119-1131 (1995), the entirety of which is herein incorporated by reference; Marcotte *et al., Plant Cell* 1:969-976 (1989) the entirety of which is herein incorporated by reference; Shen *et al., Plant Cell* 7:295-307 (1995), the entirety of which is herein incorporated by reference; Iwasaki *et al., Mol Gen Genet* 247:391-398 (1995), the entirety of which is herein incorporated by reference; Hattori *et al., Genes Dev.* 6:609-618 (1992), the entirety of which is herein incorporated by reference; Thomas *et al., Plant Cell* 5:1401-1410 (1993), the entirety of which is herein incorporated by reference), elements similar to abscisic acid responsive elements, (Ellerstrom *et al., Plant Mol. Biol. 32:*1019-1027 (1996), the entirety of which is herein incorporated by reference), auxin responsive elements (Liu *et al., Plant Cell 6:*645-657 (1994) the entirety of which is herein incorporated by reference; Liu *et al., Plant Physiol.* 115:397-407 (1997), the entirety of which is herein incorporated by reference; Kosugi *et al., Plant J.* 7:877-886 (1995), the entirety of which is herein incorporated by reference; Kosugi *et al., Plant Cell* 9:1607-1619 (1997), the entirety of which is herein incorporated by reference; Ballas *et al., J. Mol. Biol. 233:*580-596 (1993), the entirety of which is herein incorporated by reference), a *cis* element responsive to methyl jasmonate treatment (Beaudoin and Rothstein, *Plant Mol. Biol. 33:*835-846 (1997), the entirety of which is herein incorporated by reference), a *cis* element responsive to abscisic acid and stress response (Straub *et al., Plant Mol. Biol.* 26:617-630 (1994), the entirety of which is herein incorporated by reference), ethylene responsive *cis* elements (Itzhaki *et al., Proc. Natl. Acad. Sci. (U.S.A.)* 91:8925-8929 (1994), the entirety of which is herein incorporated by reference; Montgomery *et al., Proc. Acad. Sci. (U.S.A.) 90:*5939-5943 (1993), the entirety of which is herein incorporated by reference; Sessa *et al., Plant Mol. Biol.* 28:145-153 (1995), the entirety of which is herein

incorporated by reference; Shinshi *et al., Plant Mol. Biol.* 27:923-932 (1995), the entirety of which is herein incorporated by reference), salicylic acid *cis* responsive elements, (Strange *et al., Plant J.* 11:1315-1324 (1997), the entirety of which is herein incorporated by reference; Qin *et al., Plant Cell* 6:863-874 (1994), the entirety of which is herein incorporated by reference), a *cis* element that responds to water stress and abscisic acid (Lam *et al., J. Biol. Chem.* 266:17131-17135 (1991), the entirety of which is herein incorporated by reference; Thomas *et al., Plant Cell* 5:1401-1410 (1993), the entirety of which is herein incorporated by reference; Pla *et al., Plant Mol Biol* 21:259-266 (1993), the entirety of which is herein incorporated by reference), a *cis* element essential for M phase-specific expression (Ito *et al., Plant Cell* 10:331-341 (1998), the entirety of which is herein incorporated by reference), sucrose responsive elements (Huang *et al., Plant Mol. Biol.* 14:655-668 (1990), the entirety of which is herein incorporated by reference; Hwang *et al., Plant Mol Biol* 36:331-341 (1998), the entirety of which is herein incorporated by reference; Grierson *et al., Plant J.* 5:815-826 (1994), the entirety of which is herein incorporated by reference), heat shock response elements (Pelham *et al., Trends Genet.* 1:31-35 (1985), the entirety of which is herein incorporated by reference), elements responsive to auxin and/or salicylic acid and also reported for light regulation (Lam *et al., Proc. Natl. Acad. Sci. (U.S.A.)* 86:7890-7897 (1989), the entirety of which is herein incorporated by reference; Benfey *et al., Science* 250:959-966 (1990), the entirety of which is herein incorporated by reference), elements responsive to ethylene and salicylic acid (Ohme-Takagi *et al., Plant Mol. Biol.* 15:941-946 (1990), the entirety of which is herein incorporated by reference), elements responsive to wounding and abiotic stress (Loake *et al., Proc. Natl. Acad. Sci. (U.S.A.)* 89:9230-9234 (1992), the entirety of which is herein incorporated by reference; Mhiri *et al., Plant Mol. Biol.* 33:257-266 (1997), the entirety of which is herein incorporated by reference), antoxidant response

elements (Rushmore *et al., J. Biol. Chem.* 266:11632-11639, the entirety of which is herein incorporated by reference; Dalton *et al., Nucleic Acids Res.* 22:5016-5023 (1994), the entirety of which is herein incorporated by reference), Sph elements (Suzuki *et al., Plant Cell 9:*799-807 1997), the entirety of which is herein incorporated reference), Elicitor responsive elements, (Fukuda *et al., Plant Mol. Biol.* 34:81-87 (1997), the entirety of which is herein incorporated by reference; Rushton *et al., EMBO J.* 15:5690-5700 (1996), the entirety of which is herein incorporated by reference), metal responsive elements (Stuart *et al., Nature* 317:828-831 (1985), the entirety of which is herein incorporated by reference; Westin *et al., EMBO J.* 7:3763-3770 (1988), the entirety of which is herein incorporated by reference; Thiele *et al., Nucleic Acids Res.* 20:1183-1191 (1992), the entirety of which is herein incorporated by reference; Faisst *et al., Nucleic Acids Res.* 20:3-26 (1992), the entirety of which is herein incorporated by reference), low temperature responsive elements, (Baker *et al., Plant Mol. Biol.* 24:701-713 (1994), the entirety of which is herein incorporated by reference; Jiang *et al., Plant Mol. Biol.* 30:679-684 (1996), the entirety of which is herein incorporated by reference; Nordin *et al., Plant Mol. Biol.* 21:641-653 (1993), the entirety of which is herein incorporated by reference; Zhou *et al., J. Biol. Chem.* 267:23515-23519 (1992), the entirety of which is herein incorporated by reference), drought responsive elements, (Yamaguchi *et al., Plant Cell* 6:251-264 (1994), the entirety of which is herein incorporated by reference; Wang et al., *Plant Mol. Biol.* 28:605-617 (1995), the entirety of which is herein incorporated by reference; Bray EA, *Trends in Plant Science* 2:48-54 (1997), the entirety of which is herein incorporated by reference) enhancer elements for glutenin, (Colot *et al., EMBO J.* 6:3559-3564 (1987), the entirety of which is herein incorporated by reference; Thomas *et al., Plant Cell* 2:1171-1180 (1990), the entirety of which is incorporated by reference; Kreis *et al., Philos. Trans. R. Soc. Lond.,* B314:355-365 (1986), the entirety of which is herein

incorporated by reference), light-independent regulatory elements, (Lagrange *et al., Plant Cell* 9:1469-1479 (1997), the entirety of which is herein incorporated by reference; Villain *et al., J. Biol. Chem.* 271:32593-32598 (1996), the entirety of which is herein incorporated by reference), OCS enhancer elements, (Bouchez *et al., EMBO J.* 8:4197-4204 (1989), the entirety of which is herein incorporated by reference; Foley *et al., Plant J.* 3:669-679 (1993), the entirety of which is herein incorporated by reference), ACGT elements, (Foster *et al., FASEB J.* 8:192-200 (1994), the entirety of which is herein incorporated by reference; Izawa *et al., Plant Cell* 6:1277-1287 (1994), the entirety of which is herein incorporated by reference; Izawa *et al., J. Mol. Biol.* 230:1131-1144 (1993) the entirety of which is herein incorporated by reference), negative *cis* elements in plastid related genes, (Zhou *et al., J. Biol. Chem.* 267:23515-23519 (1992), the entirety of which is herein incorporated by reference; Lagrange *et al., Mol. Cell Biol.* 13:2614-2622 (1993), the entirety of which is herein incorporated by reference; Lagrange *et al., Plant Cell* 9:1469-1479 (1997), the entirety of which is herein incorporated by reference; Zhou *et al., J. Biol. Chem.* 267:23515-23519 (1992), the entirety of which is herein incorporated by reference), prolamin box elements, (Forde *et al., Nucleic Acids Res.* 13:7327-7339 (1985), the entirety of which is herein incorporated by reference; Colot *et al., EMBO J.* 6:3559-3564 (1987), the entirety of which is herein incorporated by reference; Thomas *et al., Plant Cell* 2:1171-1180 (1990), the entirety of which is herein incorporated by reference; Thompson *et al., Plant Mol. Biol.* 15:755-764 (1990), the entirety of which is herein incorporated by reference; Vicente *et al., Proc. Natl. Acad. Sci. (U.S.A.)* 94:7685-7690 (1997), the entirety of which is herein incorporated by reference), elements in enhancers from the IgM heavy chain gene (Gillies *et al., Cell* 33:717-728 (1983), the entirety of which is herein incorporated by reference; Whittier *et al., Nucleic Acids Res.* 15:2515-2535 (1987), the entirety of which is herein incorporated by reference.

(iii) Nucleic Acid Molecules Comprising Genes or Fragments Thereof

Nucleic acid molecules of the present invention can comprise one or more genes or fragments thereof. Such genes or fragments thereof include homologues of known genes or protein coding regions in other organisms or genes or fragments thereof that elicit only limited or no matches with known genes or protein coding regions. Table 1 sets forth a list of nucleic acid molecules that encode *Glycine max* proteins or fragments thereof which are homologues of known proteins.

Genomic sequences can be screened for the presence of proteins or genes utilizing one or a number of different search algorithms have that been developed, one example of which are the suite of programs referred to as BLAST programs. Other examples of suitable programs that can be utilized are known in the art, several of which are described above in the Background and under the section titled "Uses of the Agents of the Invention." In addition, unidentified reading frames may be screened for protein coding regions by prediction software such as GenScan, which is located at http://gnomic.standford.edu/GENSCANW.html.

In a preferred embodiment of the present invention, the *Glycine max* protein or fragment thereof of the present invention is a homologue of another plant protein. In another preferred embodiment of the present invention, the *Glycine max* protein or fragment thereof of the present invention is a homologue of a fungal protein. In another preferred embodiment of the present invention, the *Glycine max* protein or fragment thereof of the present invention is a homologue of a mammalian protein. In another preferred embodiment of the present invention, the *Glycine max* protein or fragment thereof of the present invention is a homologue of a bacterial protein.

In a preferred embodiment of the present invention, the *Glycine max* protein or fragments thereof or nucleic acid molecule or fragment thereof has a BLAST score of more than 200,

preferably a BLAST score of more than 300, even more preferably a BLAST score of more than 400.

In another preferred embodiment of the present invention, the nucleic acid molecule encoding the *Glycine max* protein or fragment thereof and/or nucleic acid molecule or fragment thereof exhibits a % identity with its homologue of between about 25% and about 40%, more preferably of between about 40 and about 70%, even more preferably of between about 70% and about 90%, and even more preferably between about 90% and 99%. In another preferred embodiment, of the present invention, the *Glycine max* the nucleic acid molecule encoding the Glycine max protein or fragment thereof exhibits a % identity with its homologue of 100%.

In a preferred embodiment of the present invention, the *Glycine max* protein or fragment thereof or nucleic acid molecule or fragment thereof exhibits a % coverage of between about 0 % and about 33%, more preferably of between about 34% and about 66%, and even more preferably of between about 67% and about 100%.

Genomic sequences can be screened for the presence of proteins utilizing one or a number of different search algorithms have that been developed, one example of which are the suite of programs referred to as BLAST programs. Other examples of suitable programs that can be utilized are known in the art, several of which are described above in the Background. Nucleic acid molecules of the present invention also include non-*Glycine max* homologues. Preferred non-*Glycine max* homologues are selected from the group consisting of alfalfa, *Arabidopsis* barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, an ornamental plant, maize, pea, peanut, pepper, potato, rice, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eucalyptus, apple, lettuce, lentils, grape, banana, tea, turf grasses, sunflower, oil palm, and *Phaseolus*.

In a preferred embodiment, nucleic acid molecules having SEQ ID NO: 1 through SEQ ID NO: 20082 or complements and fragments of either can be utilized to obtain such homologues.

The degeneracy of the genetic code, which allows different nucleic acid sequences to code for the same protein or peptide, is known in the literature. (U.S. Patent No. 4,757,006, the entirety of which is herein incorporated by reference).

In an aspect of the present invention, one or more of the nucleic acid molecules of the present invention differ in nucleic acid sequence from those encoding a soybean protein or fragment thereof in SEQ ID NO: 1 through SEQ ID NO: 20082 due to the degeneracy in the genetic code in that they encode the same protein but differ in nucleic acid sequence.

In another further aspect of the present invention, one or more of the nucleic acid molecules of the present invention differ in nucleic acid sequence from those encoding a soybean protein or fragment thereof in SEQ ID NO: 1 through SEQ ID NO:20082 due to the fact that the different nucleic acid sequences encode a protein having one or more conservative amino acid residues.

It is understood that codons capable of coding for such conservative amino acid substitutions are known in the art.

It is well known in the art that one or more amino acids in a native sequence can be substituted with another amino acid(s), the charge and polarity of which are similar to that of the native amino acid, *i.e.*, a conservative amino acid substitution, resulting in a silent change. Conserved substitutes for an amino acid within the native polypeptide sequence can be selected from other members of the class to which the naturally occurring amino acid belongs. Amino acids can be divided into the following four groups: (1) acidic amino acids, (2) basic amino

acids, (3) neutral polar amino acids, and (4) neutral nonpolar amino acids. Representative amino acids within these various groups include, but are not limited to, (1) acidic (negatively charged) amino acids such as aspartic acid and glutamic acid; (2) basic (positively charged) amino acids such as arginine, histidine, and lysine; (3) neutral polar amino acids such as glycine, serine, threonine, cysteine, cystine, tyrosine, asparagine, and glutamine; and (4) neutral nonpolar (hydrophobic) amino acids such as alanine, leucine, isoleucine, valine, proline, phenylalanine, tryptophan, and methionine.

Conservative amino acid changes within the native polypeptides sequence can be made by substituting one amino acid within one of these groups with another amino acid within the same group. Biologically functional equivalents of the proteins or fragments thereof of the present invention can have 10 or fewer conservative amino acid changes, more preferably seven or fewer conservative amino acid changes, and most preferably five or fewer conservative amino acid changes. The encoding nucleotide sequence will thus have corresponding base substitutions, permitting it to encode biologically functional equivalent forms of the proteins or fragments of the present invention.

It is understood that certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigent-binding regions of antibodies or binding sites on substrate molecules. Because it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence and, of course, its underlying DNA coding sequence and, nevertheless, obtain a protein with like properties. It is thus contemplated by the inventors that various changes may be made in the peptide sequences of the proteins or fragments of the present invention, or corresponding DNA

sequences that encode said peptides, without appreciable loss of their biological utility or activity. It is understood that codons capable of coding for such amino acid changes are known in the art.

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biological function on a protein is generally understood in the art (Kyte and Doolittle, *J. Mol. Biol. 157*, 105-132 (1982), herein incorporated by reference in its entirety). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like.

Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics (Kyte and Doolittle, 1982); these are isoleucine (+4.5), valine (+4.2), leucine (+3.8), phenylalanine (+2.8), cysteine/cystine (+2.5), methionine (+1.9), alanine (+1.8), glycine (-0.4), threonine (-0.7), serine (-0.8), tryptophan (-0.9), tyrosine (-1.3), proline (-1.6), histidine (-3.2), glutamate (-3.5), glutamine (-3.5), aspartate (-3.5), asparagine (-3.5), lysine (-3.9), and arginine (-4.5).

In making such changes, the substitution of amino acids whose hydropathic indices are within ±2 is preferred, those which are within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U.S. Patent 4,554,101, incorporated herein by reference in its entirety, states that the greatest local average hydrophilicity of a protein, as govern by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein

As detailed in U.S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0), lysine (+3.0), aspartate (+3.0±1), glutamate (+3.0±1), serine (+0.3), asparagine (+0.2), glutamine (+0.2), glycine (0), threonine (-0.4), proline (-0.5±1), alanine (-0.5), histidine (-0.5), cysteine (-1.0), methionine (-1.3), valine (-1.5), leucine (-1.8), isoleucine (-1.8), tyrosine (-2.3), phenylalanine (-2.5), and tryptophan (-3.4). In making such changes, the substitution of amino acids whose hydrophilicity values are within ±2 is preferred, those which are within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

In a further aspect of the present invention, one or more of the nucleic acid molecules of the present invention differ in nucleic acid sequence from those encoding a protein or fragment thereof set forth in SEQ ID NO: 1 through SEQ ID NO: 20082 or fragment thereof due to the fact that one or more codons encoding an amino acid has been substituted for a codon that encodes a nonessential substitution of the amino acid originally encoded.

(iv) Nucleic Acid Molecules Comprising Introns and/or Intron/Exon Junctions

Nucleic acid molecules of the present invention can comprise an intron and/or one or more intron/exon junction. Sequences of the present invention can be screened for introns and intron/exon junctions utilizing one or a number of different search algorithms that have that been developed, one example of which are the suite of programs referred to as BLAST programs. Other examples of suitable programs that can be utilized are known in the art, several of which are described above in the Background and in the section entitled "Uses of the Agents of the Present Invention".

(b) Protein and Peptide Molecules

A class of agents comprises one or more of the protein or peptide molecules encoded by SEQ ID NO: 1 through SEQ ID NO:20082, fragments thereof or complements thereof or one or more of the proteins encoded by a nucleic acid molecule or fragment thereof or peptide molecules encoded by other nucleic acid agents of the present invention. Protein and peptide molecules can be identified using known protein or peptide molecules as a target sequence or target motif in the BLAST programs of the present invention. In a preferred embodiment, the protein or peptide molecules of the present invention are derived from *Glycine max* (soybean) and more preferably *Glycine max,* genotype A3244.

As used herein, the term "protein molecule" or "peptide molecule" includes any molecule that comprises five or more amino acids. It is well known in the art that proteins or peptides may undergo modification, including post-translational modifications, such as, but not limited to, disulfide bond formation, glycosylation, phosphorylation, or oligomerization. Thus, as used herein, the term "protein molecule" or "peptide molecule" includes any protein molecule that is modified by any biological or non-biological process. The terms "amino acid" and "amino acids" refer to all naturally occurring L-amino acids. This definition is meant to include norleucine, ornithine, homocysteine, and homoserine.

One or more of the protein or fragments of peptide molecules may be produced via chemical synthesis, or more preferably, by expression in a suitable bacterial or eukaryotic host. Suitable methods for expression are described by Sambrook, *et al.*, *Molecular Cloning, A Laboratory Manual, 2nd Edition,* Cold Spring Harbor Press, Cold Spring Harbor, New York (1989), or similar texts.

A "protein fragment" is a peptide or polypeptide molecule whose amino acid sequence comprises a subset of the amino acid sequence of that protein. A protein or fragment thereof that comprises one or more additional peptide regions not derived from that protein is a "fusion" protein. Such molecules may be derivatized to contain carbohydrate or other moieties (such as keyhole limpet hemocyanin, etc.). Fusion protein or peptide molecules of the present invention are preferably produced via recombinant means.

Another class of agents comprises protein or peptide molecules encoded by SEQ ID NO: 1 through SEQ ID NO:20082 or complements thereof or, fragments or fusions thereof in which conservative, non-essential, or not relevant, amino acid residues have been added, replaced, or deleted. An example of such a homologue is the homologue protein of all non-*Glycine max* plant species, including but not limited to alfalfa, barley, *Brassica*, broccoli, cabbage, citrus, cotton, garlic, oat, oilseed rape, onion, canola, flax, maize, an ornamental plant, pea, peanut, pepper, potato, rice, rye, sorghum, strawberry, sugarcane, sugarbeet, tomato, wheat, poplar, pine, fir, eukalyptus, apple, lettuce, peas, lentils, grape, banana, tea, turf grasses, etc. Particularly preferred non-*Glycine max* plants to utilize for the isolation of homologues would include alfalfa, barley, cotton, corn, oat, oilseed rape, rice, corn, canola, ornamentals, sugarcane, sugarbeet, tomato, potato, wheat, and turf grasses. Such a homologue can be obtained by any of a variety of methods. Most preferably, as indicated above, one or more of the disclosed sequences (SEQ ID NO: 1 through SEQ ID NO:20082 or complements thereof) will be used to define a pair of primers that may be used to isolate the homologue-encoding nucleic acid molecules from any desired species. Such molecules can be expressed to yield homologues by recombinant means.

(c) Antibodies

One aspect of the present invention concerns antibodies, single-chain antigen binding molecules, or other proteins that specifically bind to one or more of the protein or peptide molecules of the present invention and their homologues, fusions or fragments. Such antibodies may be used to quantitatively or qualitatively detect the protein or peptide molecules of the present invention. As used herein, an antibody or peptide is said to "specifically bind" to a protein or peptide molecule of the present invention if such binding is not competitively inhibited by the presence of non-related molecules. In a preferred embodiment the antibodies of the present invention bind to proteins derived from *Glycine max* (soybean) and more preferably bind to proteins or fragments thereof of *Glycine max,* genotype A3244.

Nucleic acid molecules that encode all or part of the protein of the present invention can be expressed, via recombinant means, to yield protein or peptides that can in turn be used to elicit antibodies that are capable of binding the expressed protein or peptide. Such antibodies may be used in immunoassays for that protein. Such protein-encoding molecules, or their fragments may be a "fusion" molecule (i.e., a part of a larger nucleic acid molecule) such that, upon expression, a fusion protein is produced. It is understood that any of the nucleic acid molecules of the present invention may be expressed, via recombinant means, to yield proteins or peptides encoded by these nucleic acid molecules.

The antibodies that specifically bind proteins and protein fragments of the present invention may be polyclonal or monoclonal, and may comprise intact immunoglobulins, or antigen binding portions of immunoglobulins (such as (F(ab'), $F(ab')_2$ fragments), or single-chain immunoglobulins producible, for example, via recombinant means). It is understood that practitioners are familiar with the standard resource materials which describe specific conditions

and procedures for the construction, manipulation and isolation of antibodies (see, for example, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Press, Cold Spring Harbor, New York (1988), the entirety of which is herein incorporated by reference).

Murine monoclonal antibodies are particularly preferred. BALB/c mice are preferred for this purpose, however, equivalent strains may also be used. The animals are preferably immunized with approximately 25 μg of purified protein (or fragment thereof) that has been emulsified in a suitable adjuvant (such as TiterMax adjuvant (Vaxcel, Norcross, GA)). Immunization is preferably conducted at two intramuscular sites, one intraperitoneal site, and one subcutaneous site at the base of the tail. An additional i.v. injection of approximately 25 μg of antigen is preferably given in normal saline three weeks later. After approximately 11 days following the second injection, the mice may be bled and the blood screened for the presence of anti-protein or peptide antibodies. Preferably, a direct binding Enzyme-Linked Immunoassay (ELISA) is employed for this purpose.

More preferably, the mouse having the highest antibody titer is given a third i.v. injection of approximately 25 μg of the same protein or fragment. The splenic leukocytes from this animal may be recovered 3 days later, and are then permitted to fuse, most preferably, using polyethylene glycol, with cells of a suitable myeloma cell line (such as, for example, the P3X63Ag8.653 myeloma cell line). Hybridoma cells are selected by culturing the cells under "HAT" (hypoxanthine-aminopterin-thymine) selection for about one week. The resulting clones may then be screened for their capacity to produce monoclonal antibodies ("mAbs"), preferably by direct ELISA.

In one embodiment, anti-protein or peptide monoclonal antibodies are isolated using a fusion of a protein, protein fragment, or peptide of the present invention, or conjugate of a

protein, protein fragment, or peptide of the present invention, as immunogens. Thus, for example, a group of mice can be immunized using a fusion protein emulsified in Freund's complete adjuvant (e.g., approximately 50 μg of antigen per immunization). At three week intervals, an identical amount of antigen is emulsified in Freund's incomplete adjuvant and used to immunize the animals. Ten days following the third immunization, serum samples are taken and evaluated for the presence of antibody. If antibody titers are too low, a fourth booster can be employed. Polysera capable of binding the protein or peptide can also be obtained using this method.

In a preferred procedure for obtaining monoclonal antibodies, the spleens of the above-described immunized mice are removed, disrupted, and immune splenocytes are isolated over a ficoll gradient. The isolated splenocytes are fused, using polyethylene glycol with BALB/c-derived HGPRT (hypoxanthine guanine phosphoribosyl transferase) deficient P3x63xAg8.653 plasmacytoma cells. The fused cells are plated into 96-well microtiter plates and screened for hybridoma fusion cells by their capacity to grow in culture medium supplemented with hypothanthine, aminopterin and thymidine for approximately 2-3 weeks.

Hybridoma cells that arise from such incubation are preferably screened for their capacity to produce an immunoglobulin that binds to a protein of interest. An indirect ELISA may be used for this purpose. In brief, the supernatants of hybridomas are incubated in microtiter wells that contain immobilized protein. After washing, the titer of bound immunoglobulin can be determined using, for example, a goat anti-mouse antibody conjugated to horseradish peroxidase. After additional washing, the amount of immobilized enzyme is determined (for example through the use of a chromogenic substrate). Such screening is performed as quickly as possible after the identification of the hybridoma in order to ensure that a desired clone is not overgrown

by non-secreting neighbors. Desirably, the fusion plates are screened several times since the rates of hybridoma growth vary. In a preferred sub-embodiment, a different antigenic form of immunogen may be used to screen the hybridoma. Thus, for example, the splenocytes may be immunized with one immunogen, but the resulting hybridomas can be screened using a different immunogen. It is understood that any of the protein or peptide molecules of the present invention may be used to raise antibodies.

As discussed below, such antibody molecules or their fragments may be used for diagnostic purposes. Where the antibodies are intended for diagnostic purposes, it may be desirable to derivatize them, for example with a ligand group (such as biotin) or a detectable marker group (such as a fluorescent group, a radioisotope or an enzyme).

The ability to produce antibodies that bind the protein or peptide molecules of the present invention permits the identification of mimetic compounds of those molecules. A "mimetic compound" is a compound that is not that compound, or a fragment of that compound, but which nonetheless exhibits an ability to specifically bind to antibodies directed against that compound.

It is understood that any of the agents of the present invention can be substantially purified and/or be biologically active and/or recombinant.

Uses of the Agents of the Invention

Nucleic acid molecules and fragments thereof of the present invention may be employed for genetic mapping studies using linkage analysis (genetic markers). A genetic linkage map shows the relative locations of specific DNA markers along a chromosome. Maps are used for the identification of genes associated with genetic diseases or phenotypic traits, comparative genomics, and as a guide for physical mapping. Through genetic mapping, a fine scale linkage map can be developed using DNA markers, and, then, a genomic DNA library of large-sized

fragments can be screened with molecular markers linked to the desired trait. In a preferred embodiment of the present invention, the genomic library screened with the nucleic acid molecules of the present invention is a genomic library of *Glycine max.*

Mapping marker locations is based on the observation that two markers located near each other on the same chromosome will tend to be passed together from parent to offspring. During gamete production, DNA strands occasionally break and rejoin in different places on the same chromosome or on the homologous chromosome. The closer the markers are to each other, the more tightly linked and the less likely a recombination event will fall between and separate them. Recombination frequency thus provides an estimate of the distance between two markers.

In segregating populations, target genes have been reported to have been placed within an interval of 5-10 cM with a high degree of certainty (Tanksley *et al., Trends in Genetics 11(2):*63-68 (1995), the entirety of which is herein incorporated by reference). The markers defining this interval are used to screen a larger segregating population to identify individuals derived from one or more gametes containing a crossover in the given interval. Such individuals are useful in orienting other markers closer to the target gene. Once identified, these individuals can be analyzed in relation to all molecular markers within the region to identify those closest to the target.

Markers of the present invention can be employed to construct linkage maps and to locate genes with qualitative and quantitative effects. The genetic linkage of additional marker molecules can be established by a genetic mapping model such as, without limitation, the flanking marker model reported by Lander and Botstein, *Genetics, 121*:185-199 (1989), and the interval mapping, based on maximum likelihood methods described by Lander and Botstein, *Genetics, 121*:185-199 (1989), the entirety of which is herein incorporated by reference and

implemented in the software package MAPMAKER/QTL (Lincoln and Lander, *Mapping Genes Controlling Quantitative Traits Using MAPMAKER/QTL,* Whitehead Institute for Biomedical Research, Massachusetts, (1990)). Additional software includes Qgene, Version 2.23 (1996), Department of Plant Breeding and Biometry, 266 Emerson Hall, Cornell University, Ithaca, NY, the manual of which is herein incorporated by reference in its entirety). Use of the Qgene software is a particularly preferred approach.

A maximum likelihood estimate (MLE) for the presence of a marker is calculated, together with an MLE assuming no QTL effect, to avoid false positives. A $\log_{10}$ of an odds ratio (LOD) is then calculated as: LOD = $\log_{10}$ (MLE for the presence of a QTL/MLE given no linked QTL).

The LOD score essentially indicates how much more likely the data are to have arisen assuming the presence of a QTL than in its absence. The LOD threshold value for avoiding a false positive with a given confidence, say 95%, depends on the number of markers and the length of the genome. Graphs indicating LOD thresholds are set forth in Lander and Botstein, *Genetics, 121*:185-199 (1989), the entirety of which is herein incorporated by reference and further described by Arús and Moreno-González, *Plant Breeding*, Hayward, Bosemark, Romagosa (eds.) Chapman & Hall, London, pp. 314-331 (1993).

Additional models can be used. Many modifications and alternative approaches to interval mapping have been reported, including the use of non-parametric methods (Kruglyak and Lander, *Genetics, 139:*1421-1428 (1995), the entirety of which is herein incorporated by reference). Multiple regression methods or models can be also be used, in which the trait is regressed on a large number of markers (Jansen, *Biometrics in Plant Breed*, van Oijen, Jansen (eds.) Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding,

The Netherlands, pp. 116-124 (1994); Weber and Wricke, *Advances in Plant Breeding,* Blackwell, Berlin, 16 (1994). Procedures combining interval mapping with regression analysis, whereby the phenotype is regressed onto a single putative QTL at a given marker interval, and at the same time onto a number of markers that serve as 'cofactors,' have been reported by Jansen and Stam, *Genetics, 136*:1447-1455 (1994) and Zeng, *Genetics, 136*:1457-1468 (1994). Generally, the use of cofactors reduces the bias and sampling error of the estimated QTL positions (Utz and Melchinger, *Biometrics in Plant Breeding,* van Oijen, Jansen (eds.) Proceedings of the Ninth Meeting of the Eucarpia Section Biometrics in Plant Breeding, The Netherlands, pp.195-204 (1994), thereby improving the precision and efficiency of QTL mapping (Zeng, *Genetics, 136*:1457-1468 (1994). These models can be extended to multi-environment experiments to analysis genotype-environment interactions (Jansen *et al., Theo. Appl. Genet. 91:*33-37 (1995).

Selection of an appropriate mapping population is important to map construction. The choice of appropriate mapping population depends on the type of marker systems employed (Tanksley *et al., J.P. Gustafson and R. Appels* (eds.), Plenum Press, New York, pp. 157-173 (1988), the entirety of which is herein incorporated by reference). Consideration must be given to the source of parents (adapted vs. exotic) used in the mapping population. Chromosome pairing and recombination rates can be severely disturbed (suppressed) in wide crosses (adapted x exotic) and generally yield greatly reduced linkage distances. Wide crosses will usually provide segregating populations with a relatively large array of polymorphisms when compared to progeny in a narrow cross (adapted x adapted).

An F_2 population is the first generation of selfing after the hybrid seed is produced. Usually a single F_1 plant is selfed to generate a population segregating for all the genes in

Mendelian (1:2:1) fashion. Maximum genetic information is obtained from a completely classified F_2 population using a codominant marker system (Mather, Measurement of Linkage in Heredity: Methuen and Co., (1938), the entirety of which is herein incorporated by reference). In the case of dominant markers, progeny tests (e.g., F_3, BCF_2) are required to identify the heterozygotes, thus making it equivalent to a completely classified F_2 population. However, this procedure is often prohibitive because of the cost and time involved in progeny testing. Progeny testing of F_2 individuals is often used in map construction where phenotypes do not consistently reflect genotype (e.g., disease resistance) or where trait expression is controlled by a QTL. Segregation data from progeny test populations (e.g., F_3 or BCF_2) can be used in map construction. Marker-assisted selection can then be applied to cross progeny based on marker-trait map associations (F_2, F_3), where linkage groups have not been completely disassociated by recombination events (i.e., maximum disequilibrium).

Recombinant inbred lines (RIL) (genetically related lines; usually $>F_5$, developed from continuously selfing F_2 lines towards homozygosity) can be used as a mapping population. Information obtained from dominant markers can be maximized by using RIL because all loci are homozygous or nearly so. Under conditions of tight linkage (i.e., about <10% recombination), dominant and co-dominant markers evaluated in RIL populations provide more information per individual than either marker type in backcross populations (Reiter, *Proc. Natl. Acad. Sci. (U.S.A.) 89*:1477-1481 (1992). However, as the distance between markers becomes larger (i.e., loci become more independent), the information in RIL populations decreases dramatically when compared to codominant markers.

Backcross populations (e.g., generated from a cross between a successful variety (recurrent parent) and another variety (donor parent) carrying a trait not present in the former)

can be utilized as a mapping population. A series of backcrosses to the recurrent parent can be made to recover most of its desirable traits. Thus a population is created consisting of individuals nearly like the recurrent parent but each individual carries varying amounts or mosaic of genomic regions from the donor parent. Backcross populations can be useful for mapping dominant markers if all loci in the recurrent parent are homozygous and the donor and recurrent parent have contrasting polymorphic marker alleles (Reiter *et al., Proc. Natl. Acad. Sci. (U.S.A.) 89*:1477-1481 (1992). Information obtained from backcross populations using either codominant or dominant makers is less than that obtained from F_2 populations because one, rather than two, recombinant gametes are sampled per plant. Backcross populations, however, are more informative (at low marker saturation) when compared to RILs as the distance between linked loci increases in RIL populations (i.e., about 0.15% recombination). Increased recombination can be beneficial for resolution of tight linkages, but may be undesirable in the construction of maps with low marker saturation.

Near-isogenic lines (NIL)(created by many backcrosses to produce an array of individuals that are nearly identical in genetic composition except for the trait or genomic region under interrogation) can be used as a mapping population. In mapping with NILs, only a portion of the polymorphic loci are expected to map to a selected region.

Bulk segregant analysis (BSA) is a method developed for the rapid identification of linkage between markers and traits of interest (Michelmore, *et al., Proc. Natl. Acad. Sci. (U.S.A.) 88*:9828-9832 (1991). In BSA, two bulked DNA samples are drawn from a segregating population originating from a single cross. These bulks contain individuals that are identical for a particular trait (resistant or susceptible to particular disease) or genomic region but arbitrary at

unlinked regions (i.e., heterozygous). Regions unlinked to the target region will not differ between the bulked samples of many individuals in BSA.

Applications for markers in plant breeding include: Quantitative Trait Loci (QTL) mapping (Edwards *et al, Genetics* 116:113-115 (1987), the entirety of which is herein incorporated by reference); Nienhuis *et al, Crop Sci.* 27:797-803 (1987); Osborn *et al, Theor. Appl. Genet.* 73:350-356 (1987); Romero-Severson *et al, Use of RFLPs In Analysis of Quantitative Trait Loci In* Maize, In Helentjaris and Burr (eds.) pp. 97-102 (1989), the entirety of which is herein incorporated by reference; Young *et al, Genetics* 120:570-585 (1988), the entirety of which is herein incorporated by reference; Martin *et al, Science* 243:1725-1728 (1989), the entirety of which is herein incorporated by reference): Sarfatti *et al., Theor. Appl Genet.* 78:22-26 (1989), the entirety of which is herein incorporated by reference; Tanksley , *et al., Biotech. 7*:257-264 (1989); Barone *et al, Mol. Gen. Genet.* 224:177-182 (1990), the entirety of which is herein incorporated by reference); Jung *et al, Theor, Appl. Genet.* 79:663-672 (1990), the entirety of which is herein incorporated by reference; Keim *et al, Genetics* 126:735-742 (1990), the entirety of which is herein incorporated by reference, *Theor. Appl. Genet.* 79:465-369 (1990), the entirety of which is herein incorporated by reference; Paterson *et al., Genetics* 124:735-742 (1990), the entirety of which is herein incorporated by reference; Martin *et al, Proc. Natl. Acad. Sci. (U.S.A.)* 88:2336-2340 (1991), the entirety of which is herein incorporated by reference; Messeguer *et al, Theor. Appl. Genet.* 82:529-536 (1991), the entirety of which is herein incorporated by reference; Michelmore *et al, Proc Natl. Acad. Sci. (U.S.A.)* 88:9828-9832 (1991), the entirety of which is herein incorporated by reference; Ottaviano *et al, Theor. Appl. Genet.* 81:713-719 (1991), the entirety of which is herein incorporated by reference; Yu *et al, Theor. Appl. Genet.* 81:471-476 (1991), the entirety of which is herein incorporated by

reference; Diers *et al, Crop Sci.* 32:77-383 (1992), the entirety of which is herein incorporated by reference, *Theor. Appl. Genet.* 83:608-612 (1992), the entirety of which is herein incorporated by reference, *J. Plant Nut.* 15:2127-2136 (1992), the entirety of which is herein incorporated by reference; Doebley *et al, Proc. Natl. Acad. Sci. (U.S.A.)* 87:9888-9892 (1990), the entirety of which is herein incorporated by reference), screening genetic resource strains for useful quantitative trait alleles and introgression of these alleles into commercial varieties (Beckmann and Soller, *Theor. Appl. Genet.* 67:35-43 (1983), the entirety of which is herein incorporated by reference; Tanksley *et al*, (1989) the entirety of which is incorporated by reference), or the mapping of mutations (Rafalski, *et al.*, In: *Nonmammalian Genomic Analysis*, ed. Birren and Lai, Academic Press, San Diego, CA, pp. 75-134 (1996). Additionally, markers can be used to characterize transformants or germplasm, as a genetic diagnostic test for plant breeding or to identify individuals or varieties (Soller and Beckmann, *Theor. Appl. Genet.* 67:25-33 (1983), the entirety of which is herein incorporated by reference; Tanksley *et al,* 1989). Markers also can be used to obtain information about: (1) the number, effect, and chromosomal location of each gene affecting a trait; (2) effects of multiple copies of individual genes (gene dosage); (3) interaction between/among genes controlling a trait (epistasis); (4) whether individual genes affect more than one trait (pleiotropy); and (5) stability of gene function across environments (G x E interactions).

It is understood that one or more of the nucleic acid molecules of the present invention may in one embodiment be used as markers in genetic mapping. In a preferred embodiment, nucleic acid molecules of the present invention may in one embodiment be used as markers with *Glycine max.*

The nucleic acid molecules of the present invention may be used for physical mapping. Physical mapping, in conjunction with linkage analysis, can enable the isolation of genes. Physical mapping has been reported to identify the markers closest in terms of genetic recombination to a gene target for cloning. Once a DNA marker is linked to a gene of interest, the chromosome walking technique can be used to find the genes via overlapping clones. For chromosome walking, random molecular markers or established molecular linkage maps are used to conduct a search to localize the gene adjacent to one or more markers. A chromosome walk (Bukanov and Berg, *Mo. Microbiol, 11:*509-523 (1994), the entirety of which is herein incorporated by reference; Birkenbihl and Vielmetter *Nucleic Acids Res. 17:*5057-5069 (1989), the entirety of which is herein incorporated by reference; Wenzel and Herrmann, *Nucleic Acids Res. 16:*8323-8336, (1988), the entirety of which is herein incorporated by reference) is then initiated from the closest linked marker. Starting from the selected clones, labeled probes specific for the ends of the insert DNA are synthesized and used as probes in hybridizations against a representative library. Clones hybridizing with one of the probes are picked and serve as templates for the synthesis of new probes; by subsequent analysis, contigs are produced.

The degree of overlap of the hybridizing clones used to produce a contig can be determined by comparative restriction analysis. Comparative restriction analysis can be carried out in different ways all of which exploit the same principle; two clones of a library are very likely to overlap if they contain a limited number of restriction sites for one or more restriction endonucleases located at the same distance from each other. The most frequently used procedures are, fingerprinting (Coulson *et al, Proc. Natl. Acad. Sci. (U.S.A.)* 83:7821-7821, (1986), the entirety of which is herein incorporated by reference); Knott *et al., Nucleic Acids Res.* 16:2601-2612 (1988), the entirety of which is herein incorporated by reference; Eiglmeier *et al.*,

Mol. Microbiol. 7(2)::197-206 (1993), the entirety of which is herein incorporated by reference, 1993), restriction fragment mapping (Smith and Birnstiel, *Nucleic Acids Res.* 3:2387-2398 (1976), the entirety of which is herein incorporated by reference, or the "landmarking" technique (Charlebois *et al.*, *J. Mol. Biol.* 222:509-524 (1991), the entirety of which is herein incorporated by reference

To generate a physical map of a genome with BACs using the fingerprinting technique, a BAC library containing a number of clones equivalent to 4X-20X haploid genome can be used. (Zhang and Wing ., *Plant Mol. Bio.* 35:115-127 (1997)). For example, BAC DNA can be purified with the conventional alkaline lysis procedure as used for plasmid DNA purification, digested with the restriction enzyme used for construction of the BAC libraries and end-labeled with ^{32}P-dATP, digested with Sau3AI and fractionated on a denaturing polyacrylamide gel. The gel is dried to chromatography paper and exposed to X-ray film. Fingerprints are scanned and then converted into database records, according to the positions of each band relative to the bands of the closest molecular-weight marker on a gel. The incoming database of fingerprints are first compared against each other to assemble contigs if overlapped, and then compared against all existing databases to place the incoming BACs and BAC contigs in established contigs if overlapped. The physical length of a contig in kb is estimated according to the number of restriction sites of the enzyme used for the first digestion prior to fragment end labeling

Restriction analysis of a certain clone can be carried out, for example, according to a method originally described by Smith and Berstiel, *Nucleic Acids Res.* 3:2387-2398 (1976), First, the number and size of cloned restriction fragments to be mapped are determined by complete digestion and agarose gel electrophoresis. Then, the clone is linearized at a unique restriction site outside of the cloned DNA. Aliquots of the linearized molecules are digested to

different extents with the enzyme selected for mapping. These partially cut samples are separated on agarose gels, blotted, and hybridized to a labeled fragment of vector DNA. This probe is derived entirely from one side or the other of the unique site used to linearize the clone.

The results show a ladder of DNA fragments that have the same unique end. By repeating these analyses in pairs with all the neighboring intermediate DNA fragments, the correct order of restriction fragments as well as the orientation of the cloned insert can be deduced. The order of restriction fragments produced by restriction enzymes other than the cloning enzyme can be determined similarly. Fragment data from different enzymes are then combined by a computer program and compared with the alignments of other clones of the library (Kohara *et al., Cell 50:*495-508 (1987), the entirety of which is herein incorporated by reference).

The landmarking technique can be carried out without any labeling and relies on agarose gel analysis. Clones are first digested preferably with a 6 bp specific endonuclease A, if possible with the original clone enzyme. Clones are then digested with a second endonuclease B. Endonuclease B is chosen based on its ability to cut rarely in the genome, for example, on average only once in 30 kbp. Of the fragments generated by digestion of one clone with enzyme A, statistically only a small number (between zero and three fragments) will also be cut by enzyme B. The very specific pattern of those fragments which are produced by double digestion are easily recognized. Any of these fragments which have a restriction site for the rarely cutting endonuclease is called a "landmark" Generally one common landmark is sufficient for defining two overlapping clones.

Alternatively to chromosome walking and the associated comparative restriction analyses methods, chromosome landing also has been reported to be used to locate a gene of interest

(Tanksley *et al., Trends in Genetics 11(2):*63-68 (1995), the entirety of which is herein incorporated by reference. For chromosome landing, a DNA marker is isolated at a physical distance from the targeted gene. High resolution linkage analysis is used to identify such a marker that cosegregates with the gene. The marker is isolated at a distance that is less than the average insert size of the genomic library used for clone isolation. The DNA marker is then used to screen the library and isolate (or "land" on) the clone containing the gene without chromosome walking. Genome coverage of a library can also be determined by cross-hybridization of individual large insert clones by screening a BAC library with single copy RFLP markers distributed randomly across the genome by hybridization. To assure accuracy of the physical map, the markers should be single-copy or of single-locus origin, if multiple-copy.

Chromosome landing of large-insert clones using chromosome-specific DNA markers such as STSs microsatellites, RFLPs, or other markers can correlate physical and genetic maps (Zwick *et al., Genetics* 148:1983-1992 (1998), the entirety of which is herein incorporated by reference in its entirety). These strategies include chromosome landing of BACs containing markers or BAC contigs by BAC-FISH (Fluorescent *In Situ* Hybridization), a technique that involves tagging the DNA marker with an observable label. BAC clones giving positive hybridization signals are individually analyzed by FISH to metaphase chromosome spreads. The location of the labeled probe can be detected after it binds to its complementary DNA strand in an intact chromosome. The FISH of a BAC selected from a BAC contig will directly place the BAC contig to a specific chromosome region and establish a linkage relationships of the BAC contig to another BAC contig .

Likewise, BACs and STCs of the present invention can be used for contig mapping (Venter, *et al., Nature, 381:*364-366 (1996), the entirety of which is herein incorporated by

reference). A "seed" BAC insert can be sequenced and then STCs and the corresponding BAC of each STC can be placed on the sequenced insert using the BLASTN program. Marker or gene containing STCs can be determined by the BLASTN program and their corresponding BACs can be hybridized to specific chromosomes using BAC-FISH (Zwick *et al., Genetics* 148:1983-1992 (1998)).

STCs can be used to identify a minimum tiling path of BACs by computational procedures. Any nucleation sequence (the sequence of an entire BAC, for example) can be electronically compared to a database of STCs to identify the next clones to be sequenced to maximally extend a contig. Chosen STCs need to occupy correct positions in the tiling path. Several factors can contribute to errors in the positioning and selection of these clones. An STC that contains all or part of a repetitive element can appear to align at any part of the growing mosaic which contains that element. One method of selecting the appropriate BAC is to mask out all sections of DNA sequence which are known to be repetitive elements. The sequence symbols of these section are replaced with Ns. These sections of DNA are not used to align the STC. STCs which are completely comprised of Ns are discarded. In this way, the unmasked sections of DNA may be aligned against the growing mosaic without misplacing them due to redundant sequence. A program publicly available, PowerBLAST includes a number of options for masking repetitive elements and low complexity subsequences (Zhang and Madden, *Genome Res.* 7:649-56 (1997), the entirety of which is herein incorporated by reference. cDNA and genomic libraries also can be used as probe sources, thus directly combining the ordering of the genomic DNA with the localization of transcribed sequences. By a simultaneous hybridization to the genomic and back to the transcriptional libraries, results are produced on sequence homologies between transcribed sequences.

It is understood that the nucleic acid molecules of the present invention may in one embodiment be used in physical mapping. In a preferred embodiment, nucleic acid molecules of the present invention may in one embodiment be used in the physical mapping of *Glycine max.*

Nucleic acid molecules of the present invention can be used in comparative mapping (physical and genetic). Comparative mapping within families provides a method to the degree of sequence conservation, gene order, ploidy of species, ancestral relationships and the rates at which individual genomes are evolving. Comparative mapping has been carried out by cross-hybridizing molecular markers across species within a given family. As in genetic mapping, molecular markers are needed but instead of direct hybridization to mapping filters, the markers are used to select large insert clones from a total genomic DNA library of a related species. The selected clones, each a representative of a single marker, can then be used to physically map the region in the target species. The advantage of this method for comparative mapping is that no mapping population or linkage map of the target species is needed and the clones may also be used in other closely related species. By comparing the results obtained by genetic mapping in model plants, with those from other species, similarities of genomic structure among plants species can be established. Cross-hybridization of RFLP markers have been reported and conserved gene order has been established in many studies. Such macroscopic synteny is utilized for the estimation of correspondence of loci among these crops. These loci include not only Mendelian genes but also Quantitative Trait Loci (QTL) (Mohan *et al., Molecular Breeding* 3:87-103 (1997), the entirety of which is herein incorporated by reference.

It is understood that markers of the present invention may in another embodiment be used in comparative mapping. In a preferred embodiment the markers of present invention may be

used in the comparative mapping of *Glycine clandestina*, *Glycine gracilis*, *Glycine soja*, *Glycine tomentella*, and *Glycine tabaina*

The nucleic acid molecules of the present invention can be used to identify polymorphisms. In one embodiment, one or more of the STC nucleic acid molecules or a BAC nucleic acid molecule (or a sub-fragment of either) may be employed as a marker nucleic acid molecule to identify such polymorphism(s). Alternatively, such polymorphisms can be detected through the use of a marker nucleic acid molecule or a marker protein that is genetically linked to (i.e., a polynucleotide that co-segregates with) such polymorphism(s).

In an alternative embodiment, such polymorphisms can be detected through the use of a marker nucleic acid molecule that is physically linked to such polymorphism(s). For this purpose, marker nucleic acid molecules comprising a nucleotide sequence of a polynucleotide located within 1 mb of the polymorphism(s), and more preferably within 100 kb of the polymorphism(s), and most preferably within 10 kb of the polymorphism(s) can be employed.

The genomes of animals and plants naturally undergo spontaneous mutation in the course of their continuing evolution (Gusella, *Ann. Rev. Biochem. 55*:831-854 (1986)). A "polymorphism" is a variation or difference in the sequence of the gene or its flanking regions that arises in some of the members of a species. The variant sequence and the "original" sequence co-exist in the species' population. In some instances, such co-existence is in stable or quasi-stable equilibrium.

A polymorphism is thus said to be "allelic," in that, due to the existence of the polymorphism, some members of a species may have the original sequence (i.e., the original "allele") whereas other members may have the variant sequence (i.e., the variant "allele"). In the simplest case, only one variant sequence may exist, and the polymorphism is thus said to be di-

allelic. In other cases, the species' population may contain multiple alleles, and the polymorphism is termed tri-allelic, etc. A single gene may have multiple different unrelated polymorphisms. For example, it may have a di-allelic polymorphism at one site, and a multi-allelic polymorphism at another site.

The variation that defines the polymorphism may range from a single nucleotide variation to the insertion or deletion of extended regions within a gene. In some cases, the DNA sequence variations are in regions of the genome that are characterized by short tandem repeats (STRs) that include tandem di- or tri-nucleotide repeated motifs of nucleotides. Polymorphisms characterized by such tandem repeats are referred to as "variable number tandem repeat" ("VNTR") polymorphisms. VNTRs have been used in identity analysis (Weber, U.S. Patent 5,075,217; Armour, *et al.*, *FEBS Lett. 307*:113-115 (1992); Jones, *et al.*, *Eur. J. Haematol. 39*:144-147 (1987); Horn, *et al.*, PCT Application WO91/14003; Jeffreys, European Patent Application 370,719; Jeffreys, U.S. Patent 5,175,082; Jeffreys *et al.*, *Amer. J. Hum. Genet. 39*:11-24 (1986); Jeffreys *et al.*, *Nature 316*:76-79 (1985); Gray, *et al.*, *Proc. R. Acad. Soc. Lond. 243*:241-253 (1991); Moore, *et al.*, *Genomics 10*:654-660 (1991); Jeffreys, *et al.*, *Anim. Genet. 18*:1-15 (1987); Hillel, *et al.*, *Anim. Genet. 20*:145-155 (1989); Hillel, *et al.*, *Genet. 124*:783-789 (1990), all of which are herein incorporated by reference in their entirety).

The detection of polymorphic sites in a sample of DNA may be facilitated through the use of nucleic acid amplification methods. Such methods specifically increase the concentration of polynucleotides that span the polymorphic site, or include that site and sequences located either distal or proximal to it. Such amplified molecules can be readily detected by gel electrophoresis or other means.

The most preferred method of achieving such amplification employs the polymerase chain reaction ("PCR") (Mullis, *et al.*, *Cold Spring Harbor Symp. Quant. Biol. 51*:263-273 (1986); Erlich, *et al.*, European Patent Appln. 50,424; European Patent Appln. 84,796, European Patent Application 258,017, European Patent Appln. 237,362; Mullis, European Patent Appln. 201,184; Mullis, *et al.*, U.S. Patent No. 4,683,202; Erlich., U.S. Patent No. 4,582,788; and Saiki, *et al.*, U.S. Patent No. 4,683,194, all of which are herein incorporated by reference), using primer pairs that are capable of hybridizing to the proximal sequences that define a polymorphism in its double-stranded form.

In lieu of PCR, alternative methods, such as the "Ligase Chain Reaction" ("LCR") may be used (Barany, *Proc. Natl. Acad. Sci.(U.S.A.) 88*:189-193 (1991), the entirety of which is herein incorporated by reference. LCR uses two pairs of oligonucleotide probes to exponentially amplify a specific target. The sequences of each pair of oligonucleotides is selected to permit the pair to hybridize to abutting sequences of the same strand of the target. Such hybridization forms a substrate for a template-dependent ligase. As with PCR, the resulting products thus serve as a template in subsequent cycles and an exponential amplification of the desired sequence is obtained.

LCR can be performed with oligonucleotides having the proximal and distal sequences of the same strand of a polymorphic site. In one embodiment, either oligonucleotide will be designed to include the actual polymorphic site of the polymorphism. In such an embodiment, the reaction conditions are selected such that the oligonucleotides can be ligated together only if the target molecule either contains or lacks the specific nucleotide that is complementary to the polymorphic site present on the oligonucleotide. Alternatively, the oligonucleotides may be

selected such that they do not include the polymorphic site (see, Segev, PCT Application WO 90/01069, the entirety of which is herein incorporated by reference).

The "Oligonucleotide Ligation Assay" ("OLA") may alternatively be employed (Landegren, *et al.*, *Science 241*:1077-1080 (1988), the entirety of which is herein incorporated by reference). The OLA protocol uses two oligonucleotides which are designed to be capable of hybridizing to abutting sequences of a single strand of a target. OLA, like LCR, is particularly suited for the detection of point mutations. Unlike LCR, however, OLA results in "linear" rather than exponential amplification of the target sequence.

Nickerson, *et al.* have described a nucleic acid detection assay that combines attributes of PCR and OLA (Nickerson, *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 87*:8923-8927 (1990), the entirety of which is herein incorporated by reference). In this method, PCR is used to achieve the exponential amplification of target DNA, which is then detected using OLA. In addition to requiring multiple, and separate, processing steps, one problem associated with such combinations is that they inherit all of the problems associated with PCR and OLA.

Schemes based on ligation of two (or more) oligonucleotides in the presence of nucleic acid having the sequence of the resulting "di-oligonucleotide", thereby amplifying the di-oligonucleotide, are also known (Wu, *et al.*, *Genomics 4*:560 (1989), the entirety of which is herein incorporated by reference), and may be readily adapted to the purposes of the present invention.

Other known nucleic acid amplification procedures, such as allele-specific oligomers, branched DNA technology, transcription-based amplification systems, or isothermal amplification methods may also be used to amplify and analyze such polymorphisms (Malek, *et al.*, U.S. Patent 5,130,238; Davey, *et al.*, European Patent Application 329,822; Schuster *et al.*,

U.S. Patent 5,169,766; Miller, *et al.*, PCT Application WO 89/06700; Kwoh, *et al.*, *Proc. Natl. Acad. Sci.* (U.S.A.) *86*:1173-1177 (1989); Gingeras, *et al.*, PCT Application WO 88/10315; Walker, *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 89*:392-396 (1992), all of which are herein incorporated by reference in their entirety).

The identification of a polymorphism can be determined in a variety of ways. By correlating the presence or absence of it in an plant with the presence or absence of a phenotype, it is possible to predict the phenotype of that plant. If a polymorphism creates or destroys a restriction endonuclease cleavage site, or if it results in the loss or insertion of DNA (e.g., a VNTR polymorphism), it will alter the size or profile of the DNA fragments that are generated by digestion with that restriction endonuclease. As such, individuals that possess a variant sequence can be distinguished from those having the original sequence by restriction fragment analysis. Polymorphisms that can be identified in this manner are termed "restriction fragment length polymorphisms" ("RFLPs"). RFLPs have been widely used in human and plant genetic analyses (Glassberg, UK Patent Application 2135774; Skolnick, *et al.*, *Cytogen. Cell Genet. 32*:58-67 (1982); Botstein, *et al.*, *Ann. J. Hum. Genet. 32*:314-331 (1980); Fischer, *et al.* (PCT Application WO90/13668); Uhlen, PCT Application WO90/11369).

Polymorphisms can also be identified by Single Strand Conformation Polymorphism (SSCP) analysis. The SSCP technique is a method capable of identifying most sequence variations in a single strand of DNA, typically between 150 and 250 nucleotides in length (Elles, *Methods in Molecular Medicine: Molecular Diagnosis of Genetic Diseases*, Humana Press (1996), the entirety of which is herein incorporated by reference); Orita *et al., Genomics 5:*874-879 (1989), the entirety of which is herein incorporated by reference). Under denaturing conditions a single strand of DNA will adopt a conformation that is uniquely dependent on its

sequence conformation. This conformation usually will be different, even if only a single base is changed. Most conformations have been reported to alter the physical configuration or size sufficiently to be detectable by electrophoresis. A number of protocols have been described for SSCP including, but not limited to Lee *et al., Anal. Biochem. 205:*289-293 (1992), the entirety of which is herein incorporated by reference; Suzuki *et al., Anal. Biochem. 192:*82-84 (1991), the entirety of which is herein incorporated by reference; Lo *et al., Nucleic Acids Research 20:*1005-1009 (1992), the entirety of which is herein incorporated by reference; Sarkar *et al., Genomics 13:*441-443 (1992), the entirety of which is herein incorporated by reference). It is understood that one or more of the nucleic acids of the present invention, may be utilized as markers or probes to detect polymorphisms by SSCP analysis.

Polymorphisms may also be found using a DNA fingerprinting technique called amplified fragment length polymorphism (AFLP), which is based on the selective PCR amplification of restriction fragments from a total digest of genomic DNA to profile that DNA. Vos, *et al.*, *Nucleic Acids Res. 23:*4407-4414 (1995), the entirety of which is herein incorporated by reference. This method allows for the specific co-amplification of high numbers of restriction fragments, which can be visualized by PCR without knowledge of the nucleic acid sequence.

AFLP employs basically three steps. Initially, a sample of genomic DNA is cut with restriction enzymes and oligonucleotide adapters are ligated to the restriction fragments of the DNA. The restriction fragments are then amplified using PCR by using the adapter and restriction sequence as target sites for primer annealing. The selective amplification is achieved by the use of primers that extend into the restriction fragments, amplifying only those fragments in which the primer extensions match the nucleotide flanking the restriction sites. These amplified fragments are then visualized on a denaturing polyacrylamide gel.

AFLP analysis has been performed on *Salix* (Beismann, *et al.*, *Mol. Ecol. 6*:989-993 (1997), the entirety of which is herein incorporated by reference); *Acinetobacter* (Janssen, *et al.*, *Int. J. Syst. Bacteriol 47*:1179-1187 (1997), the entirety of which is herein incorporated by reference), *Aeromonas popoffi* (Huys, *et al.*, *Int. J. Syst. Bacteriol. 47*:1165-1171 (1997), the entirety of which is herein incorporated by reference), rice (McCouch, *et al.*, *Plant Mol. Biol. 35*:89-99 (1997), the entirety of which is herein incorporated by reference); Nandi, *et al.*, *Mol. Gen. Genet. 255*:1-8 (1997); Cho, *et al.*, *Genome 39*:373-378 (1996), herein incorporated by reference), barley (*Hordeum vulgare*) (Simons, *et al.*, *Genomics 44*:61-70 (1997), the entirety of which is herein incorporated by reference; Waugh, *et al.*, *Mol. Gen. Genet. 255*:311-321 (1997), the entirety of which is herein incorporated by reference; Qi, *et al.*, *Mol. Gen. Genet. 254*:330-336 (1997), the entirety of which is herein incorporated by reference; Becker, *et al.*, *Mol. Gen. Genet. 249*:65-73 (1995), the entirety of which is herein incorporated by reference), potato (Van der Voort, *et al.*, *Mol. Gen. Genet. 255*:438-447 (1997), the entirety of which is herein incorporated by reference; Meksem, *et al.*, *Mol. Gen. Genet. 249*:74-81 (1995), the entirety of which is herein incorporated by reference), *Phytophthora infestans* (Van der Lee, *et al.*, *Fungal Genet. Biol. 21*:278-291 (1997), the entirety of which is herein incorporated by reference), *Bacillus anthracis* (Keim, *et al.*, *J. Bacteriol. 179*:818-824 (1997)), *Astragalus cremnophylax* (Travis, *et al.*, *Mol. Ecol. 5*:735-745 (1996), the entirety of which is herein incorporated by reference), *Arabidopsis* (Cnops, *et al.*, *Mol. Gen. Genet. 253*:32-41 (1996), the entirety of which is herein incorporated by reference), *Escherichia coli* (Lin, *et al.*, *Nucleic Acids Res. 24*:3649-3650 (1996), the entirety of which is herein incorporated by reference), *Aeromonas* (Huys, *et al.*, *Int. J. Syst. Bacteriol. 46*:572-580 (1996), the entirety of which is herein incorporated by reference), nematode (Folkertsma, *et al.*, *Mol. Plant Microbe Interact. 9*:47-54 (1996), the

entirety of which is herein incorporated by reference), tomato (Thomas, *et al.*, *Plant J. 8*:785-794 (1995), the entirety of which is herein incorporated by reference), and human (Latorra, *et al.*, *PCR Methods Appl. 3*:351-358 (1994) the entirety of which is herein incorporated by reference). AFLP analysis has also been used for fingerprinting mRNA (Money, *et al.*, *Nucleic Acids Res. 24*:2616-2617 (1996), the entirety of which is herein incorporated by reference; Bachem, *et al.*, *Plant J. 9*:745-753 (1996), the entirety of which is herein incorporated by reference). It is understood that one or more of the nucleic acid molecules of the present invention, may be utilized as markers or probes to detect polymorphisms by AFLP analysis for fingerprinting mRNA.

Polymorphisms may also be found using random amplified polymorphic DNA (RAPD) (Williams *et al., Nucl. Acids Res. 18*:6531-6535 (1990), the entirety of which is herein incorporated by reference) and cleavable amplified polymorphic sequences (CAPS) (Lyamichev *et al.*, *Science 260*:778-783 (1993), the entirety of which is herein incorporated by reference). It is understood that one or more of the nucleic acid molecules of the present invention, may be utilized as markers or probes to detect polymorphisms by RAPD or CAPS analysis.

Nucleic acid molecules of the present invention can be used to monitor expression. A microarray-based method for high-throughput monitoring of plant gene expression may be utilized to measure gene-specific hybridization targets. This 'chip'-based approach involves using microarrays of nucleic acid molecules as gene-specific hybridization targets to quantitatively measure expression of the corresponding plant genes (Schena *et al.*, *Science 270*:467-470 (1995), the entirety of which is herein incorporated by reference; Shalon, Ph.D. Thesis. Stanford University (1996), the entirety of which is herein incorporated by reference).

Every nucleotide in a large sequence can be queried at the same time. Hybridization can be used to efficiently analyze nucleotide sequences.

Several microarray methods have been described. One method compares the sequences to be analyzed by hybridization to a set of oligonucleotides or cDNA molecules representing all possible subsequences (Bains and Smith, *J. Theor. Biol.* 135:303 (1989), the entirety of which is herein incorporated by reference). A second method hybridizes the sample to an array of oligonucleotide or cDNA probes. An array consisting of oligonucleotides or cDNA molecules complementary to subsequences of a target sequence can be used to determine the identity of a target sequence, measure its amount, and detect differences between the target and a reference sequence. Nucleic acid molecule microarrays may also be screened with protein molecules or fragments thereof to determine nucleic acid molecules that specifically bind protein molecules or fragments thereof.

Additionally, microarrays of BACs may be prepared to sufficiently cover 3X of an entire genome. Such microarrays can be used in a variety of genomics experiments including gene mapping, DNA fingerprinting and promoter identification. Microarrays of genomic DNA can also be used for parallel analysis of genomes at single gene resolution (Lemieux *et al., Molecular Breeding* 277-289 (1988), the entirety of which is herein incorporated by reference). It is understood that one or more of the molecules of the present invention, preferably one or more of the nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a genomic microarray based method. In a preferred embodiment of the present invention, one or more of the *Glycine max* nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a genomic microarray based method. For example, Genomic Mismatch Scanning (GMS), a hybridization-based method of

linkage analysis that allows rapid identification of regions of identity-by-descent between two related individuals, can be carried out with microarrays. GMS is reported to have been used to identify genetically common chromosomal segments based on the ability of these DNA sequences to form extensive regions of mismatch-free heteroduplexes. A series of enzymatic steps, coupled with filter binding, is used to selectively remove heteroduplexes that contain mismatches (i.e., chromosomal regions that do not share identity-by descent.). Fragments of chromosomal DNA representing inherited regions are hybridized to a microarray of ordered genomic clones and positive hybridization signals pinpoint regions of identity-by-descent at high resolution (Lemieux *et al., Molecular Breeding* 277-289 (1988))

It is understood that one or more of the molecules of the present invention, preferably one or more of the nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method to locate regions of identity-by-descent between related individuals. In a preferred embodiment of the present invention, one or more of the *Glycine max* nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method to locate regions of identity-by-descent between related individuals. The GMS microarray approach can also be used as a tool to map mutigenic traits. For example, in yeast, the entire genomic sequence is known and it has been reported that the genes responsible for growth at elevated temperature, a trait required for the pathogenicity of certain yeast strains, may be determined using GMS (Lemieux *et al*, *Molecular Breeding* 277-289 (1988)). By analyzing the inheritance of large numbers of tetrads derived from crosses of pathogenic and wild type strains, all the genes responsible for a yeast strain's ability to grow at 42°C, for example, could be identified.

It is understood that one or more of the molecules of the present invention, preferably one or more of the nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method to map multigenic traits. In a preferred embodiment of the present invention, one or more of the *Glycine max* nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method to map multigenic traits.

Plant repeat elements may be used with GMS microarraying to identify species specific chromosomes in another species background. For example, the maize genome contains moderately repetitive DNA sequences (ZLRS) representing about 2500 copies per haploid genome; these sequences are present in the genus *Zea* and absent in other graminaceous species. Ananiev *et al.*, *(Proc. Natl. Acad. Sci. (U.S.A.) 94*:3526-3529 (1997), all of which are herein incorporated by reference in their entirety) have reported unusual plants with individual maize chromosomes added to a complete oat genome generated by embryo rescue from oat (*Avena sativa*) x *Zea mays* crosses. By using highly repetitive maize-specific sequences as probes, Ananiev *et al.* (1997) were able to selectively isolate cosmid clones containing maize genomic DNA.

It is understood that one or more of the molecules of the present invention, preferably one or more of the nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method using repeat elements to selectively isolate clones containing species specific DNA. In a preferred embodiment of the present invention, one or more of the *Glycine max* nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a GMS microarray based method to selectively isolate clones containing species specific DNA. A particular preferred microarray

embodiment of the present invention is a microarray comprising nucleic acid molecules encoding genes that are homologues of known genes or nucleic acid molecules that comprise genes or fragments thereof that elicit only limited or no matches to known genes. A further preferred microarray embodiment of the present invention is a microarray comprising nucleic acid molecules encoding genes or fragments thereof that are homologues of known genes and nucleic acid molecules that comprise genes or fragments thereof that elicit only limited or no matches to known genes. A further preferred microarray embodiment of the present invention is a microarray comprising nucleic acid molecules encoding genes or fragments thereof that elicit only limited or no matches to known genes.

It is understood that one or more of the molecules of the present invention, preferably one or more of the nucleic acid molecules or protein molecules or fragments thereof of the present invention may be utilized in a microarray based method. In a preferred embodiment of the present invention, one or more of the *Glycine max* nucleic acid molecules or protein molecules or fragments thereof of the present invention set forth in Table 1 may be utilized in a microarray based method.

Nucleic acid molecules of the present invention may be used in site directed mutagenesis. Site-directed mutagenesis may be utilized to modify nucleic acid sequences, particularly as it is a technique that allows one or more of the amino acids encoded by a nucleic acid molecule to be altered (e.g. a threonine to be replaced by a methionine). Three basic methods for site-directed mutagenesis are often employed. These are cassette mutagenesis (Wells *et al.*, *Gene 34*:315-23 (1985), the entirety of which is herein incorporated by reference), primer extension (Gilliam *et al.*, *Gene 12*:129-137 (1980), the entirety of which is herein incorporated by reference); Zoller and Smith, *Methods Enzymol. 100*:468-500 (1983), the entirety of which is herein incorporated

by reference; and Dalbadie-McFarland *et al., Proc. Natl. Acad. Sci.(U.S.A.) 79*:6409-6413 (1982), the entirety of which is herein incorporated by reference) and methods based upon PCR (Scharf *et al., Science 233*:1076-1078 (1986), the entirety of which is herein incorporated by reference; Higuchi *et al., Nucleic Acids Res. 16*:7351-7367 (1988), the entirety of which is herein incorporated by reference). Site-directed mutagenesis approaches are also described in European Patent 0 385 962, the entirety of which is herein incorporated by reference, European Patent 0 359 472, the entirety of which is herein incorporated by reference, and PCT Patent Application WO 93/07278, the entirety of which is herein incorporated by reference.

Site-directed mutagenesis strategies have been applied to plants for both *in vitro* as well as *in vivo* site-directed mutagenesis (Lanz *et al., J. Biol. Chem.* 266:9971-6 (1991), the entirety of which is herein incorporated by reference; Kovgan and Zhdanov, *Biotekhnologiya 5*:148-154, No. 207160n, Chemical Abstracts 110:225 (1989), the entirety of which is herein incorporated by reference; Ge *et al., Proc. Natl. Acad. Sci. (U.S.A.) 86*:4037-4041 (1989), the entirety of which is herein incorporated by reference, Zhu *et al., J. Biol. Chem. 271*:18494-18498 (1996), Chu *et al., Biochemistry 33*:6150-6157 (1994), the entirety of which is herein incorporated by reference, Small *et al., EMBO J. 11*:1291-1296 (1992), the entirety of which is herein incorporated by reference, Cho *et al., Mol. Biotechnol. 8*:13-16 (1997), Kita *et al., J. Biol. Chem. 271*:26529-26535 (1996), the entirety of which is herein incorporated by reference, Jin *et al., Mol. Microbiol. 7*:555-562 (1993), the entirety of which is herein incorporated by reference, Hatfield and Vierstra, *J. Biol. Chem. 267*:14799-14803 (1992), the entirety of which is herein incorporated by reference, Zhao *et al., Biochemistry 31*:5093-5099 (1992), the entirety of which is herein incorporated by reference).

Any of the nucleic acid molecules of the present invention may either be modified by site-directed mutagenesis or used as, for example, nucleic acid molecules that are used to target other nucleic acid molecules for modification. It is understood that mutants with more than one altered nucleotide can be constructed using techniques that practitioners skilled in the art are familiar with such as isolating restriction fragments and ligating such fragments into an expression vector (*see*, for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press (1989)). In a preferred embodiment of the present invention, one or more of the *Glycine max* nucleic acid molecules or fragments thereof of the present invention may be modified by site-directed mutagenesis.

Nucleic acid molecules of the present invention may be used in transformation. Exogenous genetic material may be transferred into a plant cell and the plant cell regenerated into a whole, fertile or sterile plant. Exogenous genetic material is any genetic material, whether naturally occurring or otherwise, from any source that is capable of being inserted into any organism. In a preferred embodiment of the present invention the exogenous genetic material can include *Glycine max* genetic material. In a preferred embodiment of the present invention, the exogenous genetic material comprises a nucleic acid molecule of the present invention. Such genetic material may be transferred into either monocotyledons and dicotyledons including but not limited to the plants, *Zea mays* and *Arabidopsis thaliana* and soybean (See specifically, Chistou, *Particle Bombardment for Genetic Engineering of Plants,* pp. 63-69 (*Zea mays*), pp50-60 (soybean), Biotechnology Intelligence Unit, Academic Press, San Diego, California (1996), the entirety of which is herein incorporated by reference and generally Chistou, *Particle Bombardment for Genetic Engineering of Plants,* Biotechnology Intelligence Unit, Academic Press, San Diego, California (1996), the entirety of which is herein incorporated by reference).

Transfer of a nucleic acid that encodes for a protein can result in overexpression of that protein in a transformed cell or transgenic plant. One or more of the proteins or fragments thereof encoded by nucleic acid molecules of the present invention may be overexpressed in a transformed cell or transformed plant. Such overexpression may be the result of transient or stable transfer of the exogenous material.

Exogenous genetic material may be transferred into a plant cell by the use of a DNA vector or construct designed for such a purpose. Vectors have been engineered for transformation of large DNA inserts into plant genomes. Vectors have been designed to replicate in both *E. coli* and *A. tumefaciens* and have all of the features required for transferring large inserts of DNA into plant chromosomes (Choi and Wing, http://genome.clemson.edu/protocols2-nj.html July, 1998). ApBACwich system has been developed to achieve site-directed integration of DNA into the genome. A 150 kb cotton BAC DNA is reported to have been transferred into a specific *lox* site in tobacco by biolistic bombardment and *Cre-lox* site specific recombination.

A construct or vector may include a plant promoter to express the protein or protein fragment of choice. A number of promoters which are active in plant cells have been described in the literature. These include the nopaline synthase (NOS) promoter (Ebert *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 84*:5745-5749 (1987), the entirety of which is herein incorporated by reference), the octopine synthase (OCS) promoter (which are carried on tumor-inducing plasmids of *Agrobacterium tumefaciens*), the caulimovirus promoters such as the cauliflower mosaic virus (CaMV) 19S promoter (Lawton *et al.*, *Plant Mol. Biol. 9*:315-324 (1987), the entirety of which is herein incorporated by reference) and the CAMV 35S promoter (Odell *et al.*, *Nature 313*:810-812 (1985), the entirety of which is herein incorporated by reference), the figwort mosaic virus 35S-promoter, the light-inducible promoter from the small subunit of ribulose-1,5-bis-phosphate

carboxylase (ssRUBISCO), the Adh promoter (Walker *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 84*:6624-6628 (1987), the entirety of which is herein incorporated by reference), the sucrose synthase promoter (Yang *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 87*:4144-4148 (1990), the entirety of which is herein incorporated by reference), the R gene complex promoter (Chandler *et al.*, *The Plant Cell 1*:1175-1183 (1989), the entirety of which is herein incorporated by reference), and the chlorophyll a/b binding protein gene promoter, etc. These promoters have been used to create DNA constructs which have been expressed in plants; *see*, *e.g.*, PCT publication WO 84/02913, herein incorporated by reference in its entirety.

Promoters which are known or are found to cause transcription of DNA in plant cells can be used in the present invention. Such promoters may be obtained from a variety of sources such as plants and plant viruses. It is preferred that the particular promoter selected should be capable of causing sufficient expression to result in the production of an effective amount of protein to cause the desired phenotype. In addition to promoters which are known to cause transcription of DNA in plant cells, other promoters may be identified for use in the current invention by screening a plant cDNA library for genes which are selectively or preferably expressed in the target tissues or cells.

For the purpose of expression in source tissues of the plant, such as the leaf, seed, root or stem, it is preferred that the promoters utilized in the present invention have relatively high expression in these specific tissues. For this purpose, one may choose from a number of promoters for genes with tissue- or cell-specific or -enhanced expression. Examples of such promoters reported in the literature include the chloroplast glutamine synthetase GS2 promoter from pea (Edwards *et al.*, *Proc. Natl. Acad. Sci. (U.S.A.) 87*:3459-3463 (1990), herein incorporated by reference in its entirety), the chloroplast fructose-1,6-biphosphatase (FBPase)

promoter from wheat (Lloyd *et al.*, *Mol. Gen. Genet. 225*:209-216 (1991), herein incorporated by reference in its entirety), the nuclear photosynthetic ST-LS1 promoter from potato (Stockhaus *et al.*, *EMBO J.. 8*:2445-2451 (1989), herein incorporated by reference in its entirety), the phenylalanine ammonia-lyase (PAL) promoter and the chalcone synthase (CHS) promoter from *Arabidopsis thaliana*. Also reported to be active in photosynthetically active tissues are the ribulose-1,5-bisphosphate carboxylase (RbcS) promoter from eastern larch (*Larix laricina*), the promoter for the *cab* gene, cab6, from pine (Yamamoto *et al.*, *Plant Cell Physiol. 35*:773-778 (1994), herein incorporated by reference in its entirety), the promoter for the Cab-1 gene from wheat (Fejes *et al.*, *Plant Mol. Biol. 15*:921-932 (1990), herein incorporated by reference in its entirety), the promoter for the CAB-1 gene from spinach (Lubberstedt *et al.*, *Plant Physiol. 104*:997-1006 (1994), herein incorporated by reference in its entirety), the promoter for the cab1R gene from rice (Luan *et al.*, *Plant Cell. 4*:971-981 (1992), the entirety of which is herein incorporated by reference), the pyruvate, orthophosphate dikinase (PPDK) promoter from *Zea mays* (Matsuoka *et al.*, *Proc. Natl. Acad. Sci.(U.S.A.) 90*:9586-9590 (1993), herein incorporated by reference in its entirety), the promoter for the tobacco Lhcb1*2 gene (Cerdan *et al.*, *Plant Mol. Biol. 33*:245-255. (1997), herein incorporated by reference in its entirety), the *Arabidopsis thaliana* SUC2 sucrose-H+ symporter promoter (Truernit *et al.*, *Planta. 196*:564-570 (1995), herein incorporated by reference in its entirety), and the promoter for the thylacoid membrane proteins from spinach (psaD, psaF, psaE, PC, FNR, atpC, atpD, cab, rbcS). Other promoters for the chlorophyll a/b-binding proteins may also be utilized in the present invention, such as the promoters for LhcB gene and PsbP gene from white mustard (*Sinapis alba*; Kretsch *et al.*, *Plant Mol. Biol. 28*:219-229 (1995), the entirety of which is herein incorporated by reference).

For the purpose of expression in sink tissues of the plant, such as the tuber of the potato plant, the fruit of tomato, or the seed of *Zea mays*, wheat, rice, and barley, it is preferred that the promoters utilized in the present invention have relatively high expression in these specific tissues. A number of promoters for genes with tuber-specific or -enhanced expression are known, including the class I patatin promoter (Bevan *et al.*, *EMBO J.. 8*:1899-1906 (1986); Jefferson *et al.*, *Plant Mol. Biol. 14*995-1006 (1990), both of which are herein incorporated by reference in its entirety), the promoter for the potato tuber ADPGPP genes, both the large and small subunits, the sucrose synthase promoter (Salanoubat and Belliard, *Gene. 60*:47-56 (1987), Salanoubat and Belliard, *Gene. 84*:181-185 (1989), both of which are incorporated by reference in their entirety), the promoter for the major tuber proteins including the 22 kd protein complexes and proteinase inhibitors (Hannapel, *Plant Physiol. 101*:703-704 (1993), herein incorporated by reference in its entirety), the promoter for the granule bound starch synthase gene (GBSS) (Visser *et al.*, *Plant Mol. Biol. 17*:691-699 (1991), herein incorporated by reference in its entirety), and other class I and II patatins promoters (Koster-Topfer *et al.*, *Mol. Gen. Genet. 219*:390-396 (1989); Mignery *et al.*, *Gene. 62*:27-44 (1988), both of which are herein incorporated by reference in their entirety).

Other promoters can also be used to express a fructose 1,6 bisphosphate aldolase gene in specific tissues, such as seeds or fruits. The promoter for β-conglycinin (Chen *et al.*, *Dev. Genet. 10*:112-122 (1989), herein incorporated by reference in its entirety) or other seed-specific promoters such as the napin and phaseolin promoters, can be used. The zeins are a group of storage proteins found in *Zea mays* endosperm. Genomic clones for zein genes have been isolated (Pedersen *et al.*, *Cell 29*:1015-1026 (1982), herein incorporated by reference in its entirety), and the promoters from these clones, including the 15 kD, 16 kD, 19 kD, 22 kD, 27 kD,

and gamma genes, could also be used. Other promoters known to function, for example, in *Zea mays*, include the promoters for the following genes: *waxy, Brittle, Shrunken 2*, Branching enzymes I and II, starch synthases, debranching enzymes, oleosins, glutelins, and sucrose synthases. A particularly preferred promoter for *Zea mays* endosperm expression is the promoter for the glutelin gene from rice, more particularly the Osgt-1 promoter (Zheng *et al.*, *Mol. Cell Biol. 13*:5829-5842 (1993), herein incorporated by reference in its entirety). Examples of promoters suitable for expression in wheat include those promoters for the ADPglucose pyrophosphorylase (ADPGPP) subunits, the granule bound and other starch synthases, the branching and debranching enzymes, the embryogenesis-abundant proteins, the gliadins, and the glutenins. Examples of such promoters in rice include those promoters for the ADPGPP subunits, the granule bound and other starch synthases, the branching enzymes, the debranching enzymes, sucrose synthases, and the glutelins. A particularly preferred promoter is the promoter for rice glutelin, Osgt-1. Examples of such promoters for barley include those for the ADPGPP subunits, the granule bound and other starch synthases, the branching enzymes, the debranching enzymes, sucrose synthases, the hordeins, the embryo globulins, and the aleurone specific proteins.

Root specific promoters may also be used. An example of such a promoter is the promoter for the acid chitinase gene (Samac *et al.*, *Plant Mol. Biol. 25*:587-596 (1994), the entirety of which is herein incorporated by reference). Expression in root tissue could also be accomplished by utilizing the root specific subdomains of the CaMV35S promoter that have been identified (Lam *et al.*, *Proc. Natl. Acad. Sci.(U.S.A.) 86*:7890-7894 (1989), herein incorporated by reference in its entirety). Other root cell specific promoters include those

reported by Conkling *et al.* (Conkling *et al.*, *Plant Physiol. 93*:1203-1211 (1990), the entirety of which is herein incorporated by reference).

Additional promoters that may be utilized are described, for example, in U.S. Patent Nos. 5,378,619, 5,391,725, 5,428,147, 5,447,858, 5,608,144, 5,608,144, 5,614,399, 5,633,441, 5,633,435, and 4,633,436, all of which are herein incorporated in their entirety. In addition, a tissue specific enhancer may be used (Fromm *et al.*, *The Plant Cell 1*:977-984 (1989), the entirety of which is herein incorporated by reference).

Constructs or vectors may also include, with the coding region of interest, a nucleic acid sequence that acts, in whole or in part, to terminate transcription of that region. For example, such sequences have been isolated including the Tr7 3' sequence and the nos 3' sequence (Ingelbrecht *et al.*, *The Plant Cell 1*:671-680 (1989), the entirety of which is herein incorporated by reference; Bevan *et al.*, *Nucleic Acids Res. 11*:369-385 (1983), the entirety of which is herein incorporated by reference), or the like.

A vector or construct may also include regulatory elements. Examples of such include the Adh intron 1 (Callis *et al.*, *Genes and Develop. 1*:1183-1200 (1987), the entirety of which is herein incorporated by reference), the sucrose synthase intron (Vasil et al., Plant Physiol. 91:1575-1579 (1989), the entirety of which is herein incorporated by reference) and the TMV omega element (Gallie *et al.*, *The Plant Cell 1*:301-311 (1989), the entirety of which is herein incorporated by reference). These and other regulatory elements may be included when appropriate.

A vector or construct may also include a selectable marker. Selectable markers may also be used to select for plants or plant cells that contain the exogenous genetic material. Examples of such include, but are not limited to, a neo gene (Potrykus *et al.*, *Mol. Gen. Genet. 199*:183-188

(1985), the entirety of which is herein incorporated by reference) which codes for kanamycin resistance and can be selected for using kanamycin, G418, etc.; a bar gene which codes for bialaphos resistance; a mutant EPSP synthase gene (Hinchee *et al.*, *Bio/Technology* 6:915-922 (1988), the entirety of which is herein incorporated by reference) which encodes glyphosate resistance; a nitrilase gene which confers resistance to bromoxynil (Stalker *et al.*, *J. Biol. Chem.* *263*:6310-6314 (1988), the entirety of which is herein incorporated by reference); a mutant acetolactate synthase gene (ALS) which confers imidazolinone or sulphonylurea resistance (European Patent Application 154,204 (Sept. 11, 1985), the entirety of which is herein incorporated by reference); and a methotrexate resistant DHFR gene (Thillet *et al.*, *J. Biol. Chem.* *263*:12500-12508 (1988), the entirety of which is herein incorporated by reference).

A vector or construct may also include a transit peptide. Incorporation of a suitable chloroplast transit peptide may also be employed (European Patent Application Publication Number 0218571, the entirety of which is herein incorporated by reference). Translational enhancers may also be incorporated as part of the vector DNA. DNA constructs could contain one or more 5' non-translated leader sequences which may serve to enhance expression of the gene products from the resulting mRNA transcripts. Such sequences may be derived from the promoter selected to express the gene or can be specifically modified to increase translation of the mRNA. Such regions may also be obtained from viral RNAs, from suitable eukaryotic genes, or from a synthetic gene sequence. For a review of optimizing expression of transgenes, see Koziel *et al.*, *Plant Mol. Biol.* *32*:393-405 (1996), the entirety of which is herein incorporated by reference.

A vector or construct may also include a screenable marker. Screenable markers may be used to monitor expression. Exemplary screenable markers include a β-glucuronidase or uidA

gene (GUS) which encodes an enzyme for which various chromogenic substrates are known (Jefferson, *Plant Mol. Biol, Rep. 5:*387-405 (1987), the entirety of which is herein incorporated by reference; Jefferson *et al., EMBO J.. 6:*3901-3907 (1987), the entirety of which is herein incorporated by reference); an R-locus gene, which encodes a product that regulates the production of anthocyanin pigments (red color) in plant tissues ((Dellaporta *et al.*, Stadler Symposium *11*:263-282 (1988), the entirety of which is herein incorporated by reference); a β-lactamase gene (Sutcliffe *et al.*, *Proc. Natl. Acad. Sci.(U.S.A.) 75*:3737-3741 (1978), the entirety of which is herein incorporated by reference), a gene which encodes an enzyme for which various chromogenic substrates are known (e.g., PADAC, a chromogenic cephalosporin); a luciferase gene (Ow *et al.*, *Science 234*:856-859 (1986), the entirety of which is herein incorporated by reference) a xylE gene (Zukowsky *et al.*, *Proc. Natl. Acad. Sci.(U.S.A.) 80*:1101-1105 (1983), the entirety of which is herein incorporated by reference) which encodes a catechol diozygenase that can convert chromogenic catechols; an α-amylase gene (Ikatu *et al.*, *Bio/Technol. 8*:241-242 (1990), the entirety of which is herein incorporated by reference); a tyrosinase gene (Katz *et al.*, *J. Gen. Microbiol. 129*:2703-2714 (1983), the entirety of which is herein incorporated by reference) which encodes an enzyme capable of oxidizing tyrosine to DOPA and dopaquinone which in turn condenses to melanin; an α-galactosidase, which will turn a chromogenic α-galactose substrate.

Included within the terms "selectable or screenable marker genes" are also genes which encode a secretable marker whose secretion can be detected as a means of identifying or selecting for transformed cells. Examples include markers which encode a secretable antigen that can be identified by antibody interaction, or even secretable enzymes which can be detected catalytically. Secretable proteins fall into a number of classes, including small, diffusible

proteins detectable, *e.g.,* by ELISA, small active enzymes detectable in extracellular solution (*e.g.,* α-amylase, β-lactamase, phosphinothricin transferase), or proteins which are inserted or trapped in the cell wall (such as proteins which include a leader sequence such as that found in the expression unit of extension or tobacco PR-S). Other possible selectable and/or screenable marker genes will be apparent to those of skill in the art.

Methods and compositions for transforming a bacteria and other microorganisms are known in the art (see for example Sambrook *et al., Molecular Cloning: A Laboratory Manual,* Second Edition, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., (1989), the entirety of which is herein incorporated by reference).

There are many methods for introducing transforming nucleic acid molecules into plant cells. Suitable methods are believed to include virtually any method by which nucleic acid molecules may be introduced into a cell, such as by *Agrobacterium* infection or direct delivery of nucleic acid molecules such as, for example, by PEG-mediated transformation, by electroporation or by acceleration of DNA coated particles, etc. (Pottykus, *Ann. Rev. Plant Physiol. Plant Mol. Biol. 42*:205-225 (1991), the entirety of which is herein incorporated by reference; Vasil, *Plant Mol. Biol. 25*:925-937 (1994), the entirety of which is herein incorporated by reference. For example, electroporation has been used to transform *Zea mays* protoplasts (Fromm *et al., Nature 312*:791-793 (1986), the entirety of which is herein incorporated by reference).

Technology for introduction of DNA into cells is well known to those of skill in the art. Four general methods for delivering a gene into cells have been described: (1) chemical methods (Graham and van der Eb, *Virology, 54*:536-539 (1973), the entirety of which is herein incorporated by reference); (2) physical methods such as microinjection (Capecchi, *Cell 22*:479-

488 (1980), electroporation (Wong and Neumann, *Biochem. Biophys. Res. Commun., 107*:584-587 (1982); Fromm *et al., Proc. Natl. Acad. Sci.(U.S.A.)*, 82:5824-5828 (1985); U.S. Patent No. 5,384,253; and the gene gun (Johnston and Tang, *Methods Cell Biol. 43*:353-365 (1994), all of which the entirety is herein incorporated by reference; (3) viral vectors (Clapp, *Clin. Perinatol., 20*:155-168 (1993); Lu *et al., J. Exp. Med., 178*:2089-2096 (1993); Eglitis and Anderson, *Biotechniques, 6*:608-614 (1988), all of which the entirety is herein incorporated by reference); and (4) receptor-mediated mechanisms (Curiel *et al., Hum. Gen. Ther., 3*:147-154 (1992); Wagner *et al., Proc. Natl. Acad. Sci. U.S.A., 89*:6099-6103 (1992), all of which the entirety is herein incorporated by reference).

Acceleration methods that may be used include, for example, microprojectile bombardment and the like. One example of a method for delivering transforming nucleic acid molecules to plant cells is microprojectile bombardment. This method has been reviewed by Yang and Christou, eds., *Particle Bombardment Technology for Gene Transfer*, Oxford Press, Oxford, England (1994), the entirety of which is herein incorporated by reference). Non-biological particles (microprojectiles) that may be coated with nucleic acids and delivered into cells by a propelling force. Exemplary particles include those comprised of tungsten, gold, platinum, and the like.

A particular advantage of microprojectile bombardment, in addition to it being an effective means of reproducibly, and stably transforming monocotyledons, is that neither the isolation of protoplasts (Cristou *et al., Plant Physiol. 87*:671-674 (1988), the entirety of which is herein incorporated by reference) nor the susceptibility of *Agrobacterium* infection is required. An illustrative embodiment of a method for delivering DNA into maize cells by acceleration is a biolistics-particle delivery system, which can be used to propel particles coated with DNA

through a screen, such as a stainless steel or Nytex screen, onto a filter surface covered with corn cells cultured in suspension. Gordon-Kamm *et al.,* describes the basic procedure for coating tungsten particles with DNA (Gordon-Kamm *et al.*, *Plant Cell 2*:603-618 (1990), the entirety of which is herein incorporated by reference). The screen disperses the tungsten nucleic acid particles so that they are not delivered to the recipient cells in large aggregates. A particle delivery system suitable for use with the present invention is the helium acceleration PDS-1000/He gun which is available from Bio-Rad Laboratories (Bio-Rad, Hercules, California)(Sanford *et al.*, *Technique 3*:3-16 (1991), the entirety of which is herein incorporated by reference).

For the bombardment, cells in suspension may be concentrated on filters. Filters containing the cells to be bombarded are positioned at an appropriate distance below the microprojectile stopping plate. If desired, one or more screens are also positioned between the gun and the cells to be bombarded.

Alternatively, immature embryos or other target cells may be arranged on solid culture medium. The cells to be bombarded are positioned at an appropriate distance below the macroprojectile stopping plate. If desired, one or more screens are also positioned between the acceleration device and the cells to be bombarded. Through the use of techniques set forth herein one may obtain up to 1000 or more foci of cells transiently expressing a marker gene. The number of cells in a focus which express the exogenous gene product 48 hours post-bombardment often range from one to ten and average one to three.

In bombardment transformation, one may optimize the prebombardment culturing conditions and the bombardment parameters to yield the maximum numbers of stable transformants. Both the physical and biological parameters for bombardment are important in

this technology. Physical factors are those that involve manipulating the DNA/microprojectile precipitate or those that affect the flight and velocity of either the macro- or microprojectiles. Biological factors include all steps involved in manipulation of cells before and immediately after bombardment, the osmotic adjustment of target cells to help alleviate the trauma associated with bombardment, and also the nature of the transforming DNA, such as linearized DNA or intact supercoiled plasmids. It is believed that pre-bombardment manipulations are especially important for successful transformation of immature embryos.

In another alternative embodiment, plastids can be stably transformed. Methods disclosed for plastid transformation in higher plants include particle gun delivery of DNA containing a selectable marker and targeting of the DNA to the plastid genome through homologous recombination (Svab *et al. Proc. Natl. Acad. Sci. (U.S.A.) 87*:8526-8530 (1990): Svab and Maliga *Proc. Natl. Acad. Sci. (U.S.A.) 90:*913-917 (1993)); (Staub, J.M. and Maliga, P. *EMBO J. 12:*601-606 (1993), U.S. Patents 5, 451,513 and 5,545,818 all of which are herein incorporated by reference in their entirety).

Accordingly, it is contemplated that one may wish to adjust various aspects of the bombardment parameters in small scale studies to fully optimize the conditions. One may particularly wish to adjust physical parameters such as gap distance, flight distance, tissue distance, and helium pressure. One may also minimize the trauma reduction factors by modifying conditions which influence the physiological state of the recipient cells and which may therefore influence transformation and integration efficiencies. For example, the osmotic state, tissue hydration and the subculture stage or cell cycle of the recipient cells may be adjusted for optimum transformation. The execution of other routine adjustments will be known to those of skill in the art in light of the present disclosure.

Agrobacterium-mediated transfer is a widely applicable system for introducing genes into plant cells because the DNA can be introduced into whole plant tissues, thereby bypassing the need for regeneration of an intact plant from a protoplast. The use of *Agrobacterium*-mediated plant integrating vectors to introduce DNA into plant cells is well known in the art. See, for example the methods described (Fraley *et al., Biotechnology 3*:629-635 (1985); Rogers *et al., Meth. In Enzymol, 153*:253-277 (1987), both of which are herein incorporated by reference in their entirety. Further, the integration of the Ti-DNA is a relatively precise process resulting in few rearrangements. The region of DNA to be transferred is defined by the border sequences, and intervening DNA is usually inserted into the plant genome as described (Spielmann *et al., Mol. Gen. Genet., 205*:34 (1986), the entirety of which is herein incorporated by reference).

Modern *Agrobacterium* transformation vectors are capable of replication in *E. coli* as well as *Agrobacterium*, allowing for convenient manipulations as described (Klee *et al., In: Plant DNA Infectious Agents*, T. Hohn and J. Schell, eds., Springer-Verlag, New York, pp. 179-203 (1985), the entirety of which is herein incorporated by reference. Moreover, recent technological advances in vectors for *Agrobacterium*-mediated gene transfer have improved the arrangement of genes and restriction sites in the vectors to facilitate construction of vectors capable of expressing various polypeptide coding genes. The vectors described have convenient multi-linker regions flanked by a promoter and a polyadenylation site for direct expression of inserted polypeptide coding genes and are suitable for present purposes (Rogers *et al., Meth. In Enzymol., 153*:253-277 (1987), the entirety of which is herein incorporated by reference). In addition, *Agrobacterium* containing both armed and disarmed Ti genes can be used for the transformations. In those plant strains where *Agrobacterium*-mediated transformation is efficient, it is the method of choice because of the facile and defined nature of the gene transfer.

A transgenic plant formed using *Agrobacterium* transformation methods typically contains a single gene on one chromosome. Such transgenic plants can be referred to as being heterozygous for the added gene. More preferred is a transgenic plant that is homozygous for the added structural gene; *i.e.*, a transgenic plant that contains two added genes, one gene at the same locus on each chromosome of a chromosome pair. A homozygous transgenic plant can be obtained by sexually mating (selfing) an independent segregant transgenic plant that contains a single added gene, germinating some of the seed produced and analyzing the resulting plants produced for the gene of interest.

It is also to be understood that two different transgenic plants can also be mated to produce offspring that contain two independently segregating added, exogenous genes. Selfing of appropriate progeny can produce plants that are homozygous for both added, exogenous genes that encode a polypeptide of interest. Back-crossing to a parental plant and out-crossing with a non-transgenic plant are also contemplated, as is vegetative propagation.

Transformation of plant protoplasts can be achieved using methods based on calcium phosphate precipitation, polyethylene glycol treatment, electroporation, and combinations of these treatments. See for example (Potrykus *et al., Mol. Gen. Genet., 205*:193-200 (1986); Lorz *et al., Mol. Gen. Genet., 199*:178, (1985); Fromm *et al., Nature, 319*:791,(1986); Uchimiya *et al., Mol. Gen. Genet.*:204:204, (1986); Callis *et al., Genes and Development, 1183*,(1987); Marcotte *et al., Nature, 335*:454, (1988), all of which the entirety is herein incorporated by reference).

Application of these systems to different plant strains depends upon the ability to regenerate that particular plant strain from protoplasts. Illustrative methods for the regeneration of cereals from protoplasts are described (Fujimura *et al., Plant Tissue Culture Letters, 2*:74,(1985); Toriyama *et al., Theor Appl. Genet. 205*:34. (1986); Yamada *et al., Plant Cell Rep.,*

4:85, (1986); Abdullah *et al., Biotechnology, 4*:1087, (1986), all of which the entirety is herein incorporated by reference).

To transform plant strains that cannot be successfully regenerated from protoplasts, other ways to introduce DNA into intact cells or tissues can be utilized. For example, regeneration of cereals from immature embryos or explants can be effected as described (Vasil, *Biotechnology, 6*:397,(1988), the entirety of which is herein incorporated by reference). In addition, "particle gun" or high-velocity microprojectile technology can be utilized (Vasil *et al., Bio/Technology 10*:667, (1992), the entirety of which is herein incorporated by reference).

Using the latter technology, DNA is carried through the cell wall and into the cytoplasm on the surface of small metal particles as described (Klein *et al., Nature, 328*:70, (1987); Klein *et al., Proc. Natl. Acad. Sci.(U.S.A.)*, 85:8502-8505, (1988); McCabe *et al., Biotechnology, 6*:923, (1988), all of which the entirety is herein incorporated by reference). The metal particles penetrate through several layers of cells and thus allow the transformation of cells within tissue explants.

Other methods of cell transformation can also be used and include but are not limited to introduction of DNA into plants by direct DNA transfer into pollen (Zhou *et al., Methods in Enzymology, 101*:433, (1983); Hess *et al., Intern Rev. Cytol., 107*:367, (1987); Luo *et al., Plant Mol. Biol. Reporter, 6*:165, (1988), all of which the entirety is herein incorporated by reference), by direct injection of DNA into reproductive organs of a plant (Pena et al., Nature, 325:274, (1987), the entirety of which is herein incorporated by reference), or by direct injection of DNA into the cells of immature embryos followed by the rehydration of dessicated embryos (Neuhaus *et al., Theor. Appl. Genet., 75*:30, (1987), the entirety of which is herein incorporated by reference).

The regeneration, development, and cultivation of plants from single plant protoplast transformants or from various transformed explants is well known in the art (Weissbach and Weissbach, *In: Methods for Plant Molecular Biology*, (Eds.), Academic Press, Inc., San Diego, CA, (1988), the entirety of which is herein incorporated by reference). This regeneration and growth process typically includes the steps of selection of transformed cells, culturing those individualized cells through the usual stages of embryonic development through the rooted plantlet stage. Transgenic embryos and seeds are similarly regenerated. The resulting transgenic rooted shoots are thereafter planted in an appropriate plant growth medium such as soil.

The development or regeneration of plants containing the foreign, exogenous gene that encodes a protein of interest is well known in the art. Preferably, the regenerated plants are self-pollinated to provide homozygous transgenic plants, as discussed before. Otherwise, pollen obtained from the regenerated plants is crossed to seed-grown plants of agronomically important lines. Conversely, pollen from plants of these important lines is used to pollinate regenerated plants. A transgenic plant of the present invention containing a desired polypeptide is cultivated using methods well known to one skilled in the art.

There are a variety of methods for the regeneration of plants from plant tissue. The particular method of regeneration will depend on the starting plant tissue and the particular plant species to be regenerated.

Methods for transforming dicots, primarily by use of *Agrobacterium tumefaciens*, and obtaining transgenic plants have been published for cotton (U.S. Patent No. 5,004,863, U.S. Patent No. 5,159,135, U.S. Patent No. 5,518,908, all of which the entirety is herein incorporated by reference); soybean (U.S. Patent No. 5,569,834, U.S. Patent No. 5,416,011, McCabe *et al.*, *Biotechnology 6*:923, (1988), Christou *et al.*, *Plant Physiol.*, *87*:671-674 (1988), all of which the

entirety is herein incorporated by reference); *Brassica* (U.S. Patent No. 5,463,174, the entirety of which is herein incorporated by reference); peanut (Cheng *et al., Plant Cell Rep. 15*:653-657 (1996), McKently *et al., Plant Cell Rep. 14*:699-703 (1995), all of which the entirety is herein incorporated by reference); papaya (Yang *et al.*, (1996), the entirety of which is herein incorporated by reference); pea (Grant *et al., Plant Cell Rep. 15*:254-258, (1995), the entirety of which is herein incorporated by reference).

Transformation of monocotyledons using electroporation, particle bombardment, and *Agrobacterium* have also been reported. Transformation and plant regeneration have been achieved in asparagus (Bytebier *et al., Proc. Natl. Acad. Sci.(U.S.A.) 84*:5345, (1987), the entirety of which is herein incorporated by reference); barley (Wan and Lemaux, *Plant Physiol 104*:37, (1994), the entirety of which is herein incorporated by reference); maize (Rhodes *et al., Science 240*:204, (1988), Gordon-Kamm *et al., Plant Cell, 2*:603, (1990), Fromm *et al., Bio/Technology 8*:833, (1990), Koziel *et al., Bio/Technology 11*:194, (1993), Armstrong *et al., Crop Science 35*:550-557, (1995), all of which the entirety is herein incorporated by reference); oat (Somers *et al., Bio/Technology, 10*:1589, (1992), the entirety of which is herein incorporated by reference); orchardgrass (Horn *et al., Plant Cell Rep. 7*:469, (1988), the entirety of which is herein incorporated by reference); rice (Toriyama *et al., Theor Appl. Genet. 205*:34, (1986); Park *et al., Plant Mol. Biol.,32*:1135-1148, (1996); Abedinia *et al., Aust. J. Plant Physiol.24*:133-141, (1997); Zhang and Wu, *Theor. Appl. Genet. 76*:835, (1988); Zhang *et al., Plant Cell Rep. 7*:379, (1988); Battraw and Hall, *Plant Sci. 86*:191-202, (1992); Christou *et al., Bio/Technology 9*:957, (1991), all of which the entirety is herein incorporated by reference); sugarcane (Bower and Birch, *Plant J.* 2:409, (1992), the entirety of which is herein incorporated by reference); tall fescue (Wang et al., Bio/Technology 10:691, (1992), the entirety of which is herein incorporated

by reference), and wheat (Vasil et al., Bio/Technology 10:667, (1992), the entirety of which is herein incorporated by reference; U.S. Patent No. 5,631,152, the entirety of which is herein incorporated by reference.

Assays for gene expression based on the transient expression of cloned nucleic acid constructs have been developed by introducing the nucleic acid molecules into plant cells by polyethylene glycol treatment, electroporation, or particle bombardment (Marcotte, *et al., Nature, 335*:454-457 (1988), the entirety of which is herein incorporated by reference; Marcotte, *et al., Plant Cell, 1*:523-532 (1989), the entirety of which is herein incorporated by reference; McCarty, *et al., Cell 66*:895-905 (1991), the entirety of which is herein incorporated by reference; Hattori, *et al., Genes Dev. 6*:609-618 (1992), the entirety of which is herein incorporated by reference; Goff, *et al., EMBO J.. 9*:2517-2522 (1990), the entirety of which is herein incorporated by reference). Transient expression systems may be used to functionally dissect gene constructs (*See generally*, Mailga *et al., Methods in Plant Molecular Biology,* Cold Spring Harbor Press (1995)).

Any of the nucleic acid molecules of the present invention may be introduced into a plant cell in a permanent or transient manner in combination with other genetic elements such as vectors, promoters enhancers etc. Further any of the nucleic acid molecules of the present invention may be introduced into a plant cell in a manner that allows for over expression of the protein or fragment thereof encoded by the nucleic acid molecule.

Nucleic acid molecules of the present invention may be used in cosuppression. Cosuppression is the reduction in expression levels, usually at the level of RNA, of a particular endogenous gene or gene family by the expression of a homologous sense construct that is capable of transcribing mRNA of the same strandedness as the transcript of the endogenous gene

(Napoli *et al., Plant Cell 2*:279-289 (1990), the entirety of which is herein incorporated by reference; van der Krol *et al., Plant Cell 2*:291-299 (1990), the entirety of which is herein incorporated by reference). Cosuppression may result from stable transformation with a single copy nucleic acid molecule that is homologous to a nucleic acid sequence found with the cell (Prolls and Meyer, *Plant J. 2*:465-475 (1992), the entirety of which is herein incorporated by reference) or with multiple copies of a nucleic acid molecule that is homologous to a nucleic acid sequence found with the cell (Mittlesten *et al., Mol. Gen. Genet. 244*: 325-330 (1994), the entirety of which is herein incorporated by reference). Genes, even though different, linked to homologous promoters may result in the cosuppression of the linked genes (Vaucheret, *C.R. Acad. Sci. III 316*: 1471-1483 (1993), the entirety of which is herein incorporated by reference).

This technique has, for example been applied to generate white flowers from red petunia and tomatoes that do not ripen on the vine. Up to 50% of petunia transformants that contained a sense copy of the chalcone synthase (CHS) gene produced white flowers or floral sectors; this was as a result of the post-transcriptional loss of mRNA encoding CHS (Flavell, *Proc. Natl. Acad. Sci. (U.S.A.) 91*:3490-3496 (1994)), the entirety of which is herein incorporated by reference). Cosuppression may require the coordinate transcription of the transgene and the endogenous gene, and can be reset by a developmental control mechanism (Jorgensen, *Trends Biotechnol, 8*:340344 (1990), the entirety of which is herein incorporated by reference; Meins and Kunz, In: *Gene Inactivation and Homologous Recombination in Plants* (Paszkowski, J., ed.), pp. 335-348. Kluwer Academic, Netherlands (1994), the entirety of which is herein incorporated by reference).

It is understood that one or more of the nucleic acids of the present invention, including nucleic acid molecules having a nucleic acid sequence selected from the group consisting of SEQ

ID NO:1 or complement thereof through SEQ ID NO:20082 or complement thereof or fragments thereof, may be introduced into a plant cell and transcribed using an appropriate promoter with such transcription resulting in the co-suppression of an endogenous protein.

Nucleic acid molecules of the present invention may be used to reduce gene function. Antisense approaches are a way of preventing or reducing gene function by targeting the genetic material (Mol *et al., FEBS Lett. 268*:427-430 (1990), the entirety of which is herein incorporated by reference). The objective of the antisense approach is to use a sequence complementary to the target gene to block its expression and create a mutant cell line or organism in which the level of a single chosen protein is selectively reduced or abolished. Antisense techniques have several advantages over other 'reverse genetic' approaches. The site of inactivation and its developmental effect can be manipulated by the choice of promoter for antisense genes or by the timing of external application or microinjection. Antisense can manipulate its specificity by selecting either unique regions of the target gene or regions where it shares homology to other related genes (Hiatt *et al., In Genetic Engineering,* Setlow (ed.), Vol. 11, New York: Plenum 49-63 (1989), the entirety of which is herein incorporated by reference).

The principle of regulation by antisense RNA is that RNA that is complementary to the target mRNA is introduced into cells, resulting in specific RNA:RNA duplexes being formed by base pairing between the antisense substrate and the target mRNA (Green *et al., Annu. Rev. Biochem. 55*:569-597 (1986), the entirety of which is herein incorporated by reference). Under one embodiment, the process involves the introduction and expression of an antisense gene sequence. Such a sequence is one in which part or all of the normal gene sequences are placed under a promoter in inverted orientation so that the 'wrong' or complementary strand is transcribed into a noncoding antisense RNA that hybridizes with the target mRNA and interferes

with its expression (Takayama and Inouye, *Crit. Rev. Biochem. Mol. Biol. 25*:155-184 (1990), the entirety of which is herein incorporated by reference). An antisense vector is constructed by standard procedures and introduced into cells by transformation, transfection, electroporation, microinjection, or by infection, etc. The type of transformation and choice of vector will determine whether expression is transient or stable. The promoter used for the antisense gene may influence the level, timing, tissue, specificity, or inducibility of the antisense inhibition.

It is understood that protein synthesis activity in a plant cell may be reduced or depressed by growing a transformed plant cell containing a nucleic acid molecule of the present invention.

Antibodies have been expressed in plants (Hiatt *et al., Nature 342:*76-78 (1989), the entirety of which is herein incorporated by reference; Conrad and Fielder, *Plant Mol. Biol. 26:*1023-1030 (1994), the entirety of which is herein incorporated by reference). Cytoplasmic expression of a scFv (single-chain Fv antibodies) has been reported to delay infection by artichoke mottled crinkle virus. Transgenic plants that express antibodies directed against endogenous proteins may exhibit a physiological effect (Philips *et al., EMBO J.. 16:*4489-4496 (1997), the entirety of which is herein incorporated by reference; Marion-Poll, *Trends in Plant Science 2:*447-448 (1997), the entirety of which is herein incorporated by reference). For example, expressed anti-abscisic antibodies reportedly result in a general perturbation of seed development (Philips *et al., EMBO J.. 16:*4489-4496 (1997)).

Nucleic acid molecules of the present invention may be used as antibodies. Antibodies that are catalytic may also be expressed in plants (abzymes). The principle behind abzymes is that since antibodies may be raised against many molecules, this recognition ability can be directed toward generating antibodies that bind transition states to force a chemical reaction forward (Persidas, *Nature Biotechnology 15*:1313-1315 (1997), the entirety of which is herein

incorporated by reference; Baca *et al., Ann. Rev. Biophys. Biomol. Struct. 26*:461-493 (1997), the entirety of which is herein incorporated by reference). The catalytic abilities of abzymes may be enhanced by site directed mutagenesis. Examples of abzymes are, for example, set forth in U.S. Patent No: 5,658,753; U.S. Patent No. 5,632,990; U.S. Patent No. 5,631,137; U.S. Patent 5,602,015; U.S. Patent No. 5,559,538; U.S. Patent No. 5,576,174; U.S. Patent No. 5,500,358; U.S. Patent 5,318,897; U.S. Patent No. 5,298,409; U.S. Patent No. 5,258,289 and U.S. Patent No. 5,194,585, all of which are herein incorporated in their entirety.

It is understood that any of the antibodies of the present invention may be expressed in plants and that such expression can result in a physiological effect. It is also understood that any of the expressed antibodies may be catalytic.

In addition to the above discussed procedures, practitioners are familiar with the standard resource materials which describe specific conditions and procedures for the construction, manipulation and isolation of macromolecules (e.g., DNA molecules, plasmids, etc.), generation of recombinant organisms and the screening and isolating of clones, (see for example, Sambrook *et al., Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Press (1989); Mailga *et al., Methods in Plant Molecular Biology,* Cold Spring Harbor Press (1995), the entirety of which is herein incorporated by reference; Birren *et al., Genome Analysis: Analyzing DNA,* 1, Cold Spring Harbor, New York, the entirety of which is herein incorporated by reference).

The nucleotide sequence provided in SEQ ID NO:1, through SEQ ID NO:20082 or fragment thereof, or complement thereof, or a nucleotide sequence at least 90% identical, preferably 95%, identical even more preferably 99% or 100% identical to the sequence provided in SEQ ID NO:1 through SEQ ID NO:20082 or fragment thereof, or complement thereof, can be

"provided" in a variety of mediums to facilitate use fragment thereof. Such a medium can also provide a subset thereof in a form that allows a skilled artisan to examine the sequences.

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc, storage medium, and magnetic tape: optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A skilled artisan can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising computer readable medium having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable medium. A skilled artisan can readily adopt any of the presently known methods for recording information on computer readable medium to generate media comprising the nucleotide sequence information of the present invention. A variety of data storage structures are available to a skilled artisan for creating a computer readable medium having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable medium. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database application, such as DB2, Sybase, Oracle, or the like. A skilled artisan can readily adapt

any number of data processor structuring formats (e.g., text file or database) in order to obtain computer readable medium having recorded thereon the nucleotide sequence information of the present invention.

By providing one or more of nucleotide sequences of the present invention, a skilled artisan can routinely access the sequence information for a variety of purposes. Computer software is publicly available which allows a skilled artisan to access sequence information provided in a computer readable medium. The examples which follow demonstrate how software which implements the BLAST (Altschul *et al., J. Mol. Biol. 215:*403-410 (1990)) and BLAZE (Brutlag *et al., Comp. Chem. 17:*203-207 (1993), the entirety of which is herein incorporated by reference) search algorithms on a Sybase system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs or proteins from other organisms. Such ORFs are protein-encoding fragments within the sequences of the present invention and are useful in producing commercially important proteins such as enzymes used in amino acid biosynthesis, metabolism, transcription, translation, RNA processing, nucleic acid and a protein degradation, protein modification, and DNA replication, restriction, modification, recombination, and repair.

The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the nucleic acid molecule of the present invention. As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled

artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention.

As indicated above, the computer-based systems of the present invention comprise a data storage means having stored therein a nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory that can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention. As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the sequence of the present invention that match a particular target sequence or target motif. A variety of known algorithms are disclosed publicly and a variety of commercially available software for conducting search means are available and can be used in the computer-based systems of the present invention. Examples of such software include, but are not limited to, MacPattern (EMBL), BLASTIN and BLASTIX (NCBIA). One of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is well recognized that during searches for commercially important fragments of the nucleic acid molecules of the present invention, such as sequence fragments involved in gene expression and protein processing, may be of shorter length.

As used herein, "a target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration which is formed upon the folding of the target motif. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymatic active sites and signal sequences. Nucleic acid target motifs include, but are not limited to, promoter sequences, *cis* elements, hairpin structures and inducible expression elements (protein binding sequences).

Thus, the present invention further provides an input means for receiving a target sequence, a data storage means for storing the target sequences of the present invention sequence identified using a search means as described above, and an output means for outputting the identified homologous sequences. A variety of structural formats for the input and output means can be used to input and output information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the sequence of the present invention by varying degrees of homology to the target sequence or target motif. Such presentation provides a skilled artisan with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments sequence of the present invention. For example, implementing software which implement the BLAST and BLAZE algorithms (Altschul *et al., J. Mol. Biol. 215:*403-410 (1990)) can be used to identify open frames within the nucleic acid molecules of the present invention. A skilled artisan can readily recognize that any

one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention.

Having now generally described the invention, the same will be more readily understood through reference to the following examples which are provided by way of illustration, and are not intended to be limiting of the present invention, unless specified.

Example 1

BACs are stable, non-chimeric cloning systems having genomic fragment inserts (100-300 kb) and their DNA can be prepared for most types of experiments including DNA sequencing. BAC vector, pBeloBAC11, is derived from the endogenous *E. coli* F-factor plasmid, which contains genes for strict copy number control and unidirectional origin of DNA replication. Additionally, pBeloBAC11 has three unique restriction enzyme sites (*Hind* III, *Bam* HI and *Sph* I) located within the *LacZ* gene which can be used as cloning sites for megabase-size plant DNA. Indigo, another BAC vector contains *Hind* III and *Eco* RI cloning sites. This vector also contains a random mutation in the *LacZ* gene that allows for darker blue colonies.

As an alternative, the P1-derived artificial chromosome (PAC) can be used as a large DNA fragment cloning vector (Ioannou, *et al.*, *Nature Genet. 6*:84-89 (1994), the entirety of which is herein incorporated by reference; Suzuki, *et al.*, *Gene 199*:133-137 (1997), the entirety of which is herein incorporated by reference). The PAC vector has most of the features of the BAC system, but also contains some of the elements of the bacteriophage P1 cloning system.

BAC libraries are generated by ligating size-selected restriction digested DNA with pBeloBAC11 followed by electroporation into *E. coli*. BAC library construction and characterization is extremely efficient when compared to YAC (yeast artificial chromosome)

library construction and analysis, particularly because of the chimerism associated with YACs and difficulties associated with extracting YAC DNA.

There are two general methods for preparing megabase-size DNA from plants. The protoplast method yields megabase-size DNA of high quality with minimal breakage. The process involves preparing young leaves which are manually feathered with a razor-blade before being incubated for four to five hours with cell-wall-degrading enzymes. The second method developed by Zhange *et al.*, *Plant J.* 7:175-184 (1995) the entirety of which is herein incorporated by reference is a universal nuclei method that works well for several divergent plant taxa. Fresh or frozen tissue is homogenized with a blender or mortar and pestle. Nuclei are then isolated and embedded. DNA is prepared by the nucleic method often more concentrated and is reported to contain lower amounts of chloroplast DNA than the protoplast method.

Once protoplasts or nuclei are produced, they are embedded in an agarose matrix as plugs or microbeads. The agarose provides a support matrix to prevent shearing of the DNA while allowing enzymes and buffers to diffuse into the DNA. The DNA is purified and manipulated in the agarose and is stable for more than one year at 4°C.

Once high molecular weight DNA has been prepared, it is fragmented to the desired size range. In general, DNA fragmentation utilizes two general approaches, 1) physical shearing and 2) partial digestion with a restriction enzyme that cuts relatively frequently within the genome. Since physical shearing is not dependent upon the frequency and distribution of particular restriction enzymes sites, this method should yield the most random distribution of DNA fragments. However, the ends of the sheared DNA fragments must be repaired and cloned directly or restriction enzyme sites added by the addition of synthetic linkers. Because of the subsequent steps required to clone DNA fragmented by shearing, most protocols fragment DNA

by partial restriction enzyme digestion. The advantage of partial restriction enzyme digestion is that no further enzymatic modification of the ends of the restriction fragments are necessary. Four common techniques that can be used to achieve reproducible partial digestion of megabase-size DNA are 1) varying the concentration of the restriction enzyme, 2) varying the time of incubation with the restriction enzyme 3) varying the concentration of an enzyme cofactor (e.g., Mg^{2+}) and 4) varying the ratio of endonuclease to methylase.

There are three cloning sites in pBeloBAC11, but only *Hind* III and *Bam* HI produce 5' overhangs for easy vector dephosphorylation. These two restriction enzymes are primarily used to construct BAC libraries. The optimal partial digestion conditions for megabase-size DNA are determined by wide and narrow window digestions. To optimize the optimum amount of *Hind* III, 1, 2, 3, 10, and 5- units of enzyme are each added to 50 ml aliquots of microbeads and incubated at 37 °C for 20 minutes

After partial digestion of megabase-size DNA, the DNA is run on a pulsed-field gel, and DNA in a size range of 100-500 kb is excised from the gel. This DNA is ligated to the BAC vector or subjected to a second size selection on a pulsed field gel under different running conditions. Studies have previously reported that two rounds of size selection can eliminate small DNA fragments co-migrating with the selected range in the first pulse-field fractionation. Such a strategy results in an increase in insert sizes and a more uniform insert size distribution. A practical approach to performing size selections is to first test for the number of clones/microliter of ligation and insert size from the first size selected material. If the numbers are good (500 to 2000 white colony/microliter of ligation) and the size range is also good (50 to 300 kb) then a second size selection is practical. When performing a second size selection one expects a 80 to 95% decrease in the number of recombinant clones per transformation.

Twenty to two hundred nanograms of the size-selected DNA is ligated to dephosphorylated BAC vector (molar ratio of 10 to 1 in BAC vector excess). Most BAC libraries use a molar ratio of 5 to 15 : 1 (size selected DNA:BAC vector).

Transformation is carried out by electroporation and the transformation efficiency for BACs is about 40 to 1,500 transformants from one microliter of ligation product or 20 to 1000 transformants/ng DNA.

Several tests can be carried out to determine the quality of a BAC library. Three basic tests to evaluate the quality include: the genome coverage of a BAC library-average insert size, average number of clones hybridizing with single copy probes and chloroplast DNA content.

The determination of the average insert size of the library is assessed in two ways. First, during library construction every ligation is tested to determine the average insert size by assaying 20-50 BAC clones per ligation. DNA is isolated from recombinant clones using a standard mini preparation protocol, digested with *Not* I to free the insert from the BAC vector and then sized using pulsed field gel electrophoresis (Maule, *Molecular Biotechnology* 9:107-126 (1998), the entirety of which is herein incorporated by reference).

To determine the genome coverage of the library, it is screened with single copy RFLP markers distributed randomly across the genome by hybridization. Microtiter plates containing BAC clones are spotted onto Hybond membranes. Bacteria from 48 or 72 plates are spotted twice onto one membrane resulting in 18,000 to 27,648 unique clones on each membrane in either a 4X4 or 5X5 orientation. Since each clone is present twice, false positives are easily eliminated and true positives are easily recognized and identified.

Finally, the chloroplast DNA content in the BAC library is estimated by hybridizing three chloroplast genes spaced evenly across the chloroplast genome to the library on high density hybridization filters.

There are strategies for isolating rare sequences within the genome. For example, higher plant genomes can range in size from 100 Mb/1C (*Arabidopsis*) to 15,966 Mb/C (*Triticum aestivum*), (Arumuganathan and Earle, *Plant Mol Bio Rep.*9:208-219 (1991), the entirety of which is herein incorporated by reference). The number of clones required to achieve a given probability that any DNA sequence will be represented in a genomic library is N = (ln(1-P))/(ln(1-L/G)) where N is the number of clones required, P is the probability desired to get the target sequence, L is the length of the average clone insert in base pairs and G is the haploid genome length in base pairs (Clarke *et al.*, *Cell* 9:91-100 (1976) the entirety of which is herein incorporated by reference).

The soybean BAC library of the present invention is constructed in the pBeloBAC11 or similar vector. Inserts are generated by partial *Eco* RI or other enzymatic digestion of DNA from the cultivar A3244. The library provides approximately twenty fold coverage of the soybean genome.

Example 2

Nucleic acid sequences are identified using a cascade of BLASTX, followed by BLASTN if no BLASTX hit is found.. Default BLAST parameters are used. BLASTX compares the six-frame conceptual translation products of a nucleotide query sequence (both strands) against a protein sequence database. BLASTN compares a nucleotide query sequence against a nucleotide

sequence database. Matches found with BLAST P-values equal or less than 1E-8 (probability) are classified as hits.

Example 3

Two basic methods can be used for DNA sequencing, the chain termination method of Sanger *et al., Proc. Natl. Acad. Sci.(U.S.A.) 74:*5463-5467 (1977), the entirety of which is herein incorporated by reference and the chemical degradation method of Maxam and Gilbert, *Proc. Natl. Acad. Sci.(U.S.A.) 74:*560-564 (1977), the entirety of which is herein incorporated by reference. Automation and advances in technology such as the replacement of radioisotopes with fluorescence-based sequencing have reduced the effort required to sequence DNA (Craxton, *Methods, 2:*20-26 (1991), the entirety of which is herein incorporated by reference; Ju *et al., Proc. Natl. Acad. Sci.(U.S.A.) 92:*4347-4351 (1995), the entirety of which is herein incorporated by reference; Tabor and Richardson, *Proc. Natl. Acad. Sci.(U.S.A.) 92:*6339-6343 (1995), the entirety of which is herein incorporated by reference). Automated sequencers are available from, for example, Pharmacia Biotech, Inc., Piscataway, New Jersey (Pharmacia ALF), LI-COR, Inc., Lincoln, Nebraska (LI-COR 4,000) and Millipore, Bedford, Massachusetts (Millipore BaseStation).

In addition, advances in capillary gel electrophoresis have also reduced the effort required to sequence DNA and such advances provide a rapid high resolution approach for sequencing DNA samples (Swerdlow and Gesteland, *Nucleic Acids Res. 18*:1415-1419 (1990); Smith, *Nature 349*:812-813 (1991); Luckey *et al., Methods Enzymol. 218*:154-172 (1993); Lu *et al., J. Chromatog. A. 680*:497-501 (1994); Carson *et al., Anal. Chem. 65*:3219-3226 (1993); Huang *et*

al., *Anal. Chem. 64*:2149-2154 (1992); Kheterpal *et al.*, *Electrophoresis 17*:1852-1859 (1996); Quesada and Zhang, *Electrophoresis 17*:1841-1851 (1996); Baba, *Yakugaku Zasshi 117*:265-281 (1997), all of which are herein incorporated by reference in their entirety).

A number of sequencing techniques are known in the art, including fluorescence-based sequencing methodologies. These methods have the detection, automation and instrumentation capability necessary for the analysis of large volumes of sequence data. Currently, the 377 DNA Sequencer (Perkin-Elmer Corp., Applied Biosystems Div., Foster City, CA) allows the most rapid electrophoresis and data collection. With these types of automated systems, fluorescent dye-labeled sequence reaction products are detected and data entered directly into the computer, producing a chromatogram that is subsequently viewed, stored, and analyzed using the corresponding software programs. These methods are known to those of skill in the art and have been described and reviewed (Birren *et al.*, *Genome Analysis: Analyzing DNA*,1, Cold Spring Harbor, New York, the entirety of which is herein incorporated by reference).

Example 4

To identify sequences containing microsatellites or simple sequence repeats (SSR), a SSR repeat pattern library is generated by using a Perl program, SSR_generator.pl, developed at Monsanto. The library contains repeat patterns of di-, tri-, tetra-, penta- and hexa- nucleotide repeats, a total of 5421 patterns. The length of di-, tri-, tetra-, penta- and hexa- nucleotide repeat units were 18, 12, 9, 5 and 4, respectively. These repeat patterns are used to search against the BAC-end sequence databases by the BLASTN program. If the search is performed on both strands, complementary and replicated patterns of an SSR library are removed from the library to avoid redundancy of SSRs. For di-nucleotide repeats, there are four unique patterns, i.e. (CA)n,

(CT)n, (CG)n and (AT)n. Product scores are used as a criteria to extract potential SSRs from BAC-ends. If a product score is equal or greater than 90, the sequences are further examined.

The SSR-containing sequences identified from BAC ends are searched against each other as well as the existing SSR collections by using BLASTN, and clustering of the sequences is performed by using CLUSTER2, a tool developed at Monsanto. The minimal match-length is set to 100 base pairs. Any redundant sequences are removed and the unique ones are then passed through a visible inspection to further remove those with not enough flanking sequences for primer design and those with substantial ambiguous nucleotides.

Primers are designed from good quality unique sequences. A public available primer design software program, PRIMER 3, (Cambridge, MA) is used. PRIMER 3 can be accessed though the internet at (http://www.genome.wi.mit.edu/cgi-bin/primer/primer3.cgi). Default parameters are used except those for product size and primer size are changed. Product Size is Min: 80, Opt: 100, Max: 120 , while Primer Size is Min: 18, Opt: 22 and Max: 27. Oligos are synthesized by Genosis Biotechnologies, Inc (Houston, Texas).

The above protocols are used to develop primers from Sequence id GM_M02_A2_B07_MR_MR containing the following nucleotide composition:

AGGCGTTTTNCCTTGATACCTTCGNAGGTCCANCCTTTTNCTTGCTGTATCGACTCAT

TAACACCAAGCTCGGTGAGCACTCTGAAGATTATGACAACTTTCGNTGATCTTTTTG

TCATCGATATTNTAGNAGAGACCAATCTTTCTTCTTCAAATGTCGCTCATGATATTTA

TTGTAATTATCTTCAATGTATGTCCAAAAAGTTAACCTTTTTTGGACCCCCACAATAG

AAATCTTTGAAATATTTAGCCATGTGTTGGCAAGCCATTCATATTTCTTTGCGGAGAA

ACATGATCTATTGTGTCTTTCGGATGCTTCTTCTATGTCTTCTTCTTCTTCTTCTTCTTC

TTCTTCTTCTTCATTGACCACAATATTATCCAACTCAACTTAGGTGCAAAATGGTGGA

ATTTGAGACTTTGACGCANAGTCAGATGGTGCGTCATGCTCTTTCATTACATTGGAC

ATCATNTACTACCCTTTGAAGACCCTCGATCCATGGAAGGGTTAATTGGTG

This sequence contains CTT dinucleotide repeats with a repeat unit of 11. Using the Primer 3 program, two primers are selected: SER157F GTGTCTTTCGGATGCTTCTTCT and SER157R CACCATTTTGCACCTAAGTTGA. When these two primers are used to amplify genomic DNAs from eight different varieties, Minsoy, Noir, PIC, HS-1, A3244, H6686, A0868 and H5088, three alleles are detected. Sizes of these alleles ranged from 80 to 110 bp The size variation in the PCR products result from repeat numbers in different varieties.

PCR reaction conditions

Genomic DNA is isolated from young leaves of *Glycine max* or *Glycine soja* plants. Two leaf discs are collected (approximately 40 mg) from a healthy leaf and stored on wet ice or at 4°C. Tissue samples are then freeze-dried and stored at -20°C or -80°C. The frozen samples are kept as dry as possible and sealed from contact with the atmosphere. The freeze-dried samples from -20°C or -80°C, are allowed to warm up to room temperature prior to unsealing or opening. One leaflet (or 2 leaf discs) is inserted into an 1.5ml Eppendorf tube, placed on dry ice, and crushed with a wooden dowel. Approximately 200 µl of microprep buffer (25 ml extraction buffer (350 mM sorbitol, 100 mM Tris-base, 5 mM EDTA-Na_2), 25 ml nuclei lysis buffer (1M Tris/HCl, 0.5 M EDTA, 5 M NaCl, 2% CTAB), 10ml 5% sarkosyl, 0.1g Na bisulfite) is added to each sample. The sample is then homogenized. An additional 550 µl of microprep buffer is added, vortexed for about 30-60 seconds, and incubated at 65°C for about 60 minutes. About 700 µl chloroform/isoamyl (24:1) is added, mixed well for about 10-30 seconds. Centrifugation of the tubes is performed at approximately 10,000 rpm for 5 minutes in a microcentrifuge. The aqueous phase is transferred into a new tube and RNA is removed from the extract by the

addition of 30 µl of RNase (10mg/ml) to the aqueous phase and incubated for 1 hour at room temperature. Approximately 500µl ice-cold isopropanol is added to the aqueous extract, and the tubes inverted until the DNA precipitated. The precipitated solution is kept at 4°C for about 1 hour or overnight. Centrifugation of the tubes is performed at approximately 10,000 rpm for 5 minutes in a microcentrifuge. The supernatant is discarded and the pellet washed 1-3 times with 200µl 70% ethanol. The ethanol is removed using a micropipette and pellet dried at 37°C for 10 minutes. The DNA is dissolved in 50 µl TE (10 mM Tris-HCl pH8.0, 0.1 mM EDTA), then kept overnight at 4°C. Centrifugation of the tubes is performed at approximately 10,000 rpm for 5 minutes and then the supernatant is transferred into new tubes. Using this method, approximately 2µg of DNA per mg of fresh leaf tissue is extracted.

DNA concentration is measured by a Spectrometry (Molecular Devices, Sunnyvale, California) and adjusted to proper concentration for use as template. The total volume for PCR reaction is 20 ul. The reaction mixture contains: Template DNA at a concentration of 15 ng, 0.15uM of primer, .03 unit of Taq DNA polymerase (Perkin Elmer) , 50uM of dNTP, the Reaction buffer contains, 10 mM Tris.HCl pH8.5, 1.5 mM MgCl2, 50 mM KCl and water is added to a total volume of 20 ul.

The PCR is performed on a Perkin Elmer DNA Thermal Cycler 9700 using the following cycle profile: hold at 94 °C for 3 min, 32 cycles of 94°C for 25 second, 47 °C for 25 second and 72 °C for 25 second, and 72 °C for 3min of final extension.

An acrylamide gel is prepared using 56.5 ml water, 3.5 ml 10x TAE buffer, 10.5 ml 40 acrylamide stock solution, 50 µl TEMED, 0.06 g ammonium persulfate. To each PCR, sample 20 µl of formamide loading dye is added to each sample and the samples are denatured at 90°C

for 3 minutes with a 4°C hold in a thermocycler. 1.5 μl of each sample is loaded onto the gel. Gels are run at constant wattage to give a constant heat development during electrophoresis at 40 to 50 Volt/cm of the gel length. Gels should be run at approximately 50°C during electrophoresis. Electrophoresis is stopped when the Bromophenol blue dye is at the bottom of the gel. After electrophoresis, the gel is stained in 1 x SYBR solution for 15 to 20 minutes with vigorous shaking. A Gel image is recorded using an Alpha-InnoTech imager.

Example 5

In order to create a file containing complex repeats, the GCG (Madison, WI) REPEAT program is used to determine initial internal repeats. Stringency is defined as 19 matched bases out of every contiguous 20 bases in the repeated diagonals part of the REPEAT program algorithm. After the REPEAT program is run on the STCs, a REPEAT output filed is processed with the UNIX utilities grep, sort, uniq and sed to produce a GCG pattern file. The GCG pattern file is broken into size groups: <20, 20-39, 40-59, 60-79, 80-89, 100-119, 120-139, 140-159, 160-179, 180-199, 200-219, and >220. Each pattern group is compared against the entire STC library using the GCG FINDPATTERNS program. Sequences of size 1-19 are allowed no mismatches. The 20-39 group are allowed one mismatch. A pattern of size n is allowed floor (n/20) mismatches. Patterns that occurred in at least 100 STCs are selected in this step. The results of the FINDPATTERNS program is post-processed with the UNIX utilities grep, sort and uniq and with the GCG REFORMAT program to produce GCG sequence files. Each sequence file is derived from a selected pattern and placed in a subdirectory that corresponds to its size group. GELSTART, GELENTER, GELMERGE and GELASSEMBLE are used to coalesce similar sequences of each size group. Patterns are 90% similar before they are aligned and the

patterns overlap by at least two thirds of the modal length in their length group. The GELSTART program creates a subdirectory which contains the individual and the coalesced consensus sequences. The consensus sequences are placed into a single directory and a FASTA style sequence library is constructed from it. The REPEAT-MASKER program is used to mask the original STCs. The unmasked sequences that remain afterward are concatenated into 100 KB pseudo-sequences. The pseudo-sequences are fed back into this algorithm and the new repeat patterns that result are added to the repeat library. The algorithm is iterated 3 times.

The repeat library is compared to the STCs using NCBI BLASTN version 2.0. HSPs are reported if they satisfied the criteria of:

"observed fractional match" >= "allowed fractional match"

where "observed fractional match" is defined as:

"fraction of HSP similarity" x "fraction of query sequence in HSP"

and "allowed fractional match" is defined as:

("repeat length" - "floor (repeat length/20)")/"repeat length"

Table 1

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1	GM_49_B2_A03_T7	g4063760	BLASTX	332	6e-28	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2	GM_49_B2_A04_MR	g3142328	BLASTN	1418	2e-57	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3	GM_49_B2_A06_T7	g2995405	BLASTX	167	2e-10	43	(Y12432) polyprotein [Ananas comosus]
4	GM_49_B2_B02_MR	g1769898	BLASTX	253	5e-20	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5	GM_49_B2_C01_MR	g2961390	BLASTX	199	3e-19	89	(AL022141) beta-galactosidase like protein [Arabidopsis thaliana]
6	GM_49_B2_C02_MR	g2995405	BLASTX	478	6e-44	55	(Y12432) polyprotein [Ananas comosus]
7	GM_49_B2_C03_MR	g587603	BLASTN	362	2e-09	64	P.falciparum gene for beta subunit RNA polymerase
8	GM_49_B2_C06_MR	g4063760	BLASTX	193	3e-14	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9	GM_49_B2_C07_MR	g2995405	BLASTX	356	8e-31	48	(Y12432) polyprotein [Ananas comosus]
10	GM_49_B2_C07_T7	g4063760	BLASTX	207	1e-14	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11	GM_49_B2_D02_T7	g2500724	BLASTX	277	3e-22	98	PREPROTEIN TRANSLOCASE SECA SUBUNIT PRECURSOR gi 2129894 pir S72453 secA protein precursor - garden pea gi 1122325 (X82404) chloroplast SecA protein [Pisum sativum]
12	GM_49_B2_D03_MR	g1769898	BLASTX	245	4e-19	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13	GM_49_B2_D08_MR	g18559	BLASTN	1100	7e-43	75	G.max gene for catalase
14	GM_49_B2_D11_T7	g4092470	BLASTN	412	1e-11	67	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
15	GM_49_B2_D12_MR	g18559	BLASTN	1055	8e-41	75	G.max gene for catalase
16	GM_49_B2_E02_MR	g2160694	BLASTX	162	3e-10	56	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
17	GM_49_B2_E02_T7	g2462058	BLASTX	302	4e-26	57	(Y13389) reverse transcriptase [Antirrhinum majus]
18	GM_49_B2_E03_MR	g2982431	BLASTX	224	2e-16	37	(AL022224) leucine rich repeat-like protein [Arabidopsis thaliana]
19	GM_49_B2_E03_T7	g3097320	BLASTN	830	1e-30	79	Glycine max gene for Bd 30K, complete cds
20	GM_49_B2_E04_MR	g1769898	BLASTX	245	4e-19	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
21	GM_49_B2_E09_MR	g477068	BLASTX	138	1e-08	39	reverse transcriptase (copia-like retrotransposon) - Pinus coulteri=pine (fragment) >gi 169382 (M94488) reverse transcriptase [Pinus coulteri]
22	GM_49_B2_E11_MR	g2346988	BLASTX	160	3e-10	70	(AB006606) ZPT4-4 [Petunia x hybrida]
23	GM_49_B2_F02_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
24	GM_49_B2_F02_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
25	GM_49_B2_F04_T7	g1666236	BLASTX	198	8e-15	30	(U76261) unknown [Hordeum vulgare]
26	GM_49_B2_F07_T7	g3075399	BLASTX	136	2e-10	50	(AC004484) SF16-like protein [Arabidopsis thaliana]
27	GM_49_B2_F09_T7	g1236920	BLASTN	375	5e-10	64	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
28	GM_49_B2_F10_T7	g3142303	BLASTX	257	7e-20	44	(AC002411) Strong similarity to MRP-like ABC transporter gb U92650 from A. thaliana and canalicular multi-drug resistance protein gb L49379 from Rattus norvegicus. [Arabidopsis thaliana]
29	GM_49_B2_F11_MR	g905361	BLASTX	624	3e-60	97	(U22103) gag-protease polyprotein [Glycine max]
30	GM_49_B2_G04_T7	g3650039	BLASTX	206	7e-15	43	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
31	GM_49_B2_G08_T7	g3402747	BLASTN	376	6e-10	64	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K22 (ESSAII project)
32	GM_49_B2_G09_MR	g3193221	BLASTN	373	7e-10	67	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
33	GM_49_B2_G12_MR	g1769897	BLASTX	198	3e-14	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
34	GM_49_B2_H06_MR	g4063760	BLASTX	281	2e-22	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
35	GM_49_B2_H06_T7	g507910	BLASTN	697	7e-25	86	Glycine max BSR-101 satellite SB92 genomic sequence.
36	GM_49_B2_H10_MR	g2129618	BLASTX	213	2e-15	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
37	GM_51_A1_A05_MR	g2463654	BLASTN	450	2e-13	62	Petunia vein clearing virus, complete genome
38	GM_51_A1_A12_MR	g100484	BLASTX	211	2e-15	47	hypothetical protein - garden snapdragon
39	GM_51_A1_B05_MR	g3319362	BLASTX	197	1e-13	41	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
40	GM_51_A1_B09_MR	g576762	BLASTN	364	8e-10	62	Myrmecia pilosula HI87-145 mitochondrion cytochrome b gene, partial cds.
41	GM_51_A1_C03_MR	g22490	BLASTX	186	7e-14	41	(X01380) ORF1 [Zea mays]
42	GM_51_A1_C04_MR	g2791289	BLASTX	129	5e-09	41	(AJ000387) protease [Drosophila melanogaster]
43	GM_51_A1_C05_T7	g2522228	BLASTX	187	3e-13	71	(AB007466) reverse transcriptase-like protein [Vicia faba]
44	GM_51_A1_D08_MR	g3319362	BLASTX	286	4e-26	46	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
45	GM_51_A1_D09_MR	g82231	BLASTX	157	8e-11	93	hypothetical protein 82 - common tobacco chloroplast gi 225200 prf 1211235AE ORF 82 [Nicotiana tabacum]
46	GM_51_A1_D09_T7	g11575	BLASTN	1003	5e-39	95	G.max chloroplast DNA for tRNA (Arg)
47	GM_51_A1_D11_MR	g3142328	BLASTN	471	3e-14	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
48	GM_51_A1_E02_T7	g4063760	BLASTX	164	4e-10	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
49	GM_51_A1_E07_T7	g507910	BLASTN	491	1e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
50	GM_51_A1_E12_MR	g4160362	BLASTN	439	9e-13	64	Saccharomyces cerevisiae complete mitochondrial genome
51	GM_51_A1_F07_T7	g3193284	BLASTX	264	5e-21	64	(AF069298) No definition line found [Arabidopsis thaliana]
52	GM_51_A1_F08_MR	g905361	BLASTX	252	7e-20	39	(U22103) gag-protease polyprotein [Glycine max]
53	GM_51_A1_F10_T7	g3142328	BLASTN	704	7e-25	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
54	GM_51_A1_G06_T7	g2995405	BLASTX	212	2e-15	50	(Y12432) polyprotein [Ananas comosus]
55	GM_51_A1_H04_T7	g100484	BLASTX	242	1e-18	52	hypothetical protein - garden snapdragon
56	GM_51_A1_H07_MR	g3142330	BLASTX	597	2e-57	84	(U96295) envelope-like [Glycine max]
57	GM_51_A1_H09_MR	g130582	BLASTX	213	3e-15	33	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
58	GM_51_A1_H10_MR	g3142379	BLASTX	204	1e-16	60	(AF053008) envelope-like [Glycine max]
59	GM_51_A2_A08_MR	g3097320	BLASTN	421	5e-12	66	Glycine max gene for Bd 30K, complete cds
60	GM_51_A2_A09_MR	g4063760	BLASTX	209	8e-15	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
61	GM_51_A2_A11_MR	g1785739	BLASTX	159	6e-11	39	(Y08502) orf240b [Arabidopsis thaliana]
62	GM_51_A2_A12_MR	g4063760	BLASTX	249	1e-20	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
63	GM_51_A2_C01_MR	g2995405	BLASTX	105	2e-10	54	(Y12432) polyprotein [Ananas comosus]
64	GM_51_A2_C05_MR	g3142328	BLASTN	587	1e-19	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
65	GM_51_A2_C12_MR	g2522227	BLASTX	205	7e-16	52	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
66	GM_51_A2_D02_MR	g2829133	BLASTX	170	7e-12	66	(AF043351) adenosine-5'-phosphosulfate-kinase [Arabidopsis thaliana]
67	GM_51_A2_E02_MR	g414831	BLASTN	354	1e-09	97	Glycine max (Rab1p) mRNA, complete cds.
68	GM_51_A2_E12_MR	g507910	BLASTN	686	2e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
69	GM_51_A2_F03_T7	g3097320	BLASTN	465	5e-14	83	Glycine max gene for Bd 30K, complete cds
70	GM_51_A2_F12_MR	g3645899	BLASTX	164	1e-18	42	(U68408) 5' end not determined experimentally [Zea mays]
71	GM_51_A2_G01_MR	g3406033	BLASTN	381	4e-10	64	Homo sapiens 12p13.3 RPCI4-773N5 (Roswell Park Cancer Institute Human PAC library) complete sequence [Homo sapiens]
72	GM_51_A2_G09_MR	g3142328	BLASTN	706	5e-25	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
73	GM_51_A2_G10_MR	g584862	BLASTX	301	5e-26	62	CYTOCHROME P450 LXXIA3 (P-450EG3) gi 480397 pir S36807 cytochrome P450 71A3 - eggplant (fragment) gi 408142 (X70982) P450 hydroxylase [Solanum melongena]
74	GM_51_A2_H01_MR	g3777527	BLASTX	159	2e-09	49	(AF053008) gag-pol polyprotein [Glycine max]
75	GM_51_A2_H07_MR	g3021696	BLASTN	374	7e-10	62	Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, cosmid clone: TY2F10, complete sequence [Homo sapiens]
76	GM_51_B2_A08_MR	g505129	BLASTN	402	3e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
77	GM_51_B2_A09_MR	g4063760	BLASTX	197	1e-13	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
78	GM_51_B2_A11_MR	g3845293	BLASTN	365	2e-09	61	Plasmodium falciparum chromosome 2, section 58 of 73 of the complete sequence
79	GM_51_B2_A12_MR	g2827717	BLASTX	148	1e-08	75	(AL021684) phosphoenolpyruvate carboxykinase (ATP) - like protein [Arabidopsis thaliana]
80	GM_51_B2_B03_MR	g3377848	BLASTX	166	7e-17	48	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
81	GM_51_B2_B04_MR	g2160155	BLASTN	364	1e-20	69	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
82	GM_51_B2_C03_MR	g905361	BLASTX	437	3e-40	97	(U22103) gag-protease polyprotein [Glycine max]
83	GM_51_B2_C05_MR	g2443320	BLASTX	343	5e-29	48	(D85597) polyprotein [Oryza australiensis]
84	GM_51_B2_C06_MR	g507910	BLASTN	393	4e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
85	GM_51_B2_C07_MR	g18695	BLASTN	464	4e-14	91	Soybean nodulin 22 gene
86	GM_51_B2_D04_MR	g4063760	BLASTX	237	2e-31	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
87	GM_51_B2_D07_MR	g18559	BLASTN	349	9e-09	69	G.max gene for catalase
88	GM_51_B2_D08_MR	g2244915	BLASTX	171	7e-11	34	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
89	GM_51_B2_D09_MR	g3695395	BLASTX	246	3e-19	35	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
90	GM_51_B2_D12_MR	g505267	BLASTX	151	2e-09	49	(X77111) chitinase, class V [Nicotiana tabacum]
91	GM_51_B2_F01_MR	g14222	BLASTN	458	1e-14	65	Saccharomyces cerevisiae mitochondrial gene aap1 for mitochondrial ATPase subunit 8
92	GM_51_B2_F06_MR	g130582	BLASTX	157	3e-09	34	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
93	GM_51_B2_F07_MR	g3269290	BLASTX	254	6e-20	38	(AL030978) putative receptor like kinase [Arabidopsis thaliana]
94	GM_51_B2_F08_MR	g2827635	BLASTX	184	6e-26	70	(AL021636) predicted protein [Arabidopsis thaliana]
95	GM_51_B2_F11_MR	g3319351	BLASTX	289	5e-26	56	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
96	GM_51_B2_G09_MR	g18559	BLASTN	938	2e-35	79	G.max gene for catalase
97	GM_51_B2_G12_MR	g3695412	BLASTX	368	4e-33	65	(AF096373) contains similarity to group 1 glycosyl transferases (Pfam: PF00534, E=2.1e-11) [Arabidopsis thaliana]
98	GM_51_B2_H02_MR	g1142702	BLASTN	404	9e-12	77	Glycine max satellite STR120-A.4.
99	GM_51_B2_H05_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
100	GM_51_B2_H07_MR	g4063756	BLASTN	492	3e-15	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
101	GM_51_B2_H09_MR	g507910	BLASTN	392	4e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
102	GM_51_B2_H10_MR	g3928086	BLASTX	305	2e-26	55	(AC005770) unknown protein [Arabidopsis thaliana]
103	GM_52_A1_A04_MR	g4063760	BLASTX	160	1e-09	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
104	GM_52_A1_A04_T7	g3645899	BLASTX	328	1e-27	53	(U68408) 5' end not determined experimentally [Zea mays]
105	GM_52_A1_A05_MR	g905361	BLASTX	409	5e-37	90	(U22103) gag-protease polyprotein [Glycine max]
106	GM_52_A1_A12_MR	g2384675	BLASTX	150	7e-17	71	(AF012659) putative potassium transporter AtKT4p [Arabidopsis thaliana]
107	GM_52_A1_B04_MR	g18559	BLASTN	596	5e-20	72	G.max gene for catalase
108	GM_52_A1_B06_MR	g2583130	BLASTX	234	2e-17	41	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
109	GM_52_A1_B07_MR	g3645899	BLASTX	199	8e-14	51	(U68408) 5' end not determined experimentally [Zea mays]
110	GM_52_A1_B08_MR	g100484	BLASTX	303	3e-25	55	hypothetical protein - garden snapdragon
111	GM_52_A1_B10_MR	g2995405	BLASTX	260	2e-20	52	(Y12432) polyprotein [Ananas comosus]
112	GM_52_A1_C07_MR	g18559	BLASTN	719	1e-25	73	G.max gene for catalase
113	GM_52_A1_D02_MR	g4063760	BLASTX	228	2e-21	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
114	GM_52_A1_D02_T7	g4063760	BLASTX	502	4e-46	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
115	GM_52_A1_D07_MR	g4063760	BLASTX	261	4e-22	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
116	GM_52_A1_D10_MR	g2085783	BLASTN	408	2e-11	68	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
117	GM_52_A1_D11_MR	g3645899	BLASTX	317	2e-26	52	(U68408) 5' end not determined experimentally [Zea mays]
118	GM_52_A1_E01_T7	g3639087	BLASTX	393	7e-35	71	(AF090444) phospholipase D2 [Brassica oleracea]
119	GM_52_A1_E02_T7	g3319351	BLASTX	338	2e-28	45	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
120	GM_52_A1_E04_MR	g2832304	BLASTX	130	5e-18	59	(AF044489) receptor-like protein kinase [Oryza sativa]
121	GM_52_A1_E08_MR	g3810596	BLASTX	134	1e-14	60	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
122	GM_52_A1_F02_T7	g2245107	BLASTX	108	6e-11	62	(Z97343) thioesterase homolog [Arabidopsis thaliana]
123	GM_52_A1_F03_T7	g100484	BLASTX	362	1e-31	56	hypothetical protein - garden snapdragon
124	GM_52_A1_F12_MR	g507910	BLASTN	339	1e-08	71	Glycine max BSR-101 satellite SB92 genomic sequence.
125	GM_52_A1_F12_T7	g3777526	BLASTN	1004	2e-38	87	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
126	GM_52_A1_G02_MR	g3097320	BLASTN	427	3e-12	71	Glycine max gene for Bd 30K, complete cds
127	GM_52_A1_G04_T7	g2764526	BLASTN	410	7e-19	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
128	GM_52_A1_G06_T7	g4038056	BLASTX	323	3e-27	48	(AC005897) putative transposon [Arabidopsis thaliana]
129	GM_52_A1_G08_T7	g4063760	BLASTX	347	2e-29	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
130	GM_52_A2_A04_MR	g2429543	BLASTX	164	4e-10	32	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]
131	GM_52_A2_A05_MR	g3033389	BLASTX	191	5e-13	39	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
132	GM_52_A2_A08_T7	g4063760	BLASTX	524	2e-48	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
133	GM_52_A2_A11_MR	g4038056	BLASTX	181	3e-20	46	(AC005897) putative transposon [Arabidopsis thaliana]
134	GM_52_A2_B08_MR	g3687234	BLASTX	113	5e-13	40	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
135	GM_52_A2_C01_MR	g3063460	BLASTX	154	6e-10	48	(AC003981) F22O13.22 [Arabidopsis thaliana]
136	GM_52_A2_C01_T7	g1480927	BLASTN	1266	1e-51	93	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
137	GM_52_A2_C08_MR	g3820757	BLASTN	345	9e-09	61	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
138	GM_52_A2_D05_T7	g507910	BLASTN	377	2e-10	81	Glycine max BSR-101 satellite SB92 genomic sequence.
139	GM_52_A2_D09_T7	g905361	BLASTX	436	4e-40	96	(U22103) gag-protease polyprotein [Glycine max]
140	GM_52_A2_E02_MR	g3097320	BLASTN	451	2e-13	68	Glycine max gene for Bd 30K, complete cds
141	GM_52_A2_E02_T7	g4063760	BLASTX	485	5e-50	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
142	GM_52_A2_E03_MR	g3777527	BLASTX	191	8e-13	77	(AF053008) gag-pol polyprotein [Glycine max]
143	GM_52_A2_E05_T7	g3510339	BLASTN	495	2e-15	71	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K3K7, complete sequence [Arabidopsis thaliana]
144	GM_52_A2_E10_MR	g3777526	BLASTN	389	1e-10	87	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
145	GM_52_A2_E12_T7	g3779026	BLASTX	341	9e-29	50	(AC005171) putative retrotransposon [Arabidopsis thaliana]
146	GM_52_A2_F07_MR	g4063760	BLASTX	270	2e-21	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
147	GM_52_A2_F07_T7	g507910	BLASTN	529	3e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
148	GM_52_A2_F11_T7	g3513747	BLASTX	173	7e-11	36	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
149	GM_52_A2_G03_T7	g3402704	BLASTX	142	6e-09	33	(AC004261) hypothetical protein [Arabidopsis thaliana]
150	GM_52_A2_G05_MR	g4038056	BLASTX	374	1e-32	52	(AC005897) putative transposon [Arabidopsis thaliana]
151	GM_52_A2_G05_T7	g1142701	BLASTN	1375	8e-56	86	Glycine max satellite STR120-A.3.
152	GM_52_A2_G07_T7	g3097836	BLASTN	389	2e-10	60	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
153	GM_52_A2_G11_T7	g3738339	BLASTX	227	3e-17	80	(AC005170) putative kinase [Arabidopsis thaliana]
154	GM_52_A2_H03_T7	g2558655	BLASTX	221	2e-16	61	(AC002354) No definition line found [Arabidopsis thaliana]
155	GM_52_A2_H05_MR	g2129618	BLASTX	167	2e-10	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
156	GM_52_A2_H07_MR	g3097320	BLASTN	450	2e-13	72	Glycine max gene for Bd 30K, complete cds
157	GM_52_B1_A07_MR	g3319362	BLASTX	308	2e-25	64	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
158	GM_52_B1_A08_MR	g3327392	BLASTX	171	6e-11	38	(AC004483) reverse-transcriptase-like protein [Arabidopsis thaliana]
159	GM_52_B1_A09_MR	g507910	BLASTN	382	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
160	GM_52_B1_B02_T7	g905361	BLASTX	170	5e-11	32	(U22103) gag-protease polyprotein [Glycine max]
161	GM_52_B1_B11_MR	g2760830	BLASTX	391	2e-35	70	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]
162	GM_52_B1_C01_MR	g3777527	BLASTX	448	4e-40	83	(AF053008) gag-pol polyprotein [Glycine max]
163	GM_52_B1_C02_T7	g1769898	BLASTX	173	3e-26	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
164	GM_52_B1_C08_MR	g18559	BLASTN	435	1e-12	67	G.max gene for catalase
165	GM_52_B1_C12_MR	g3319345	BLASTX	252	1e-19	38	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
166	GM_52_B1_C12_T7	g18559	BLASTN	947	6e-36	77	G.max gene for catalase
167	GM_52_B1_D04_MR	g2522230	BLASTX	305	2e-26	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
168	GM_52_B1_D08_MR	g99922	BLASTX	487	1e-45	63	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
169	GM_52_B1_D11_MR	g1142702	BLASTN	361	8e-10	75	Glycine max satellite STR120-A.4.
170	GM_52_B1_D12_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
171	GM_52_B1_D12_T7	g507910	BLASTN	388	6e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
172	GM_52_B1_E06_MR	g3688328	BLASTX	141	5e-09	54	(AJ228325) reverse transcriptase [Ginkgo biloba]
173	GM_52_B1_E06_T7	g1177046	BLASTX	153	3e-10	64	14 KD ZINC-BINDING PROTEIN (PROTEIN KINASE C INHIBITOR) (PKCI) gi 493053 (U09406) putative protein kinase C inhibitor [Brassica juncea]
174	GM_52_B1_E12_MR	g3142328	BLASTN	1676	4e-69	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
175	GM_52_B1_F03_T7	g99922	BLASTX	118	8e-10	67	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
176	GM_52_B1_F04_MR	g1061040	BLASTX	160	2e-10	53	(X89867) sterol-C-methyltransferase [Arabidopsis thaliana] gi 1587694 prf 2207220A sterol C-methyltransferase [Arabidopsis thaliana]
177	GM_52_B1_F04_T7	g4063760	BLASTX	175	3e-11	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
178	GM_52_B1_F05_MR	g2262155	BLASTN	332	2e-09	67	DNA sequence of Arabidopsis thaliana BAC F5J6 from chromosome IV, complete sequence [Arabidopsis thaliana]
179	GM_52_B1_F07_T7	g2462134	BLASTX	155	1e-09	29	(Y13368) reverse transcriptase [Beta vulgaris]
180	GM_52_B1_F09_T7	g130582	BLASTX	417	6e-37	57	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
181	GM_52_B1_G02_T7	g130582	BLASTX	246	3e-22	52	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
182	GM_52_B1_G07_T7	g2655227	BLASTN	345	9e-09	67	Zea mays Ty3/gypsy-type retrotransposon reverse transcriptase/integrase polyprotein pseudogene, partial sequence.
183	GM_52_B1_G09_MR	g1666236	BLASTX	158	1e-18	40	(U76261) unknown [Hordeum vulgare]
184	GM_52_B1_H02_MR	g4063760	BLASTX	380	5e-33	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
185	GM_52_B1_H05_T7	g2443320	BLASTX	246	9e-19	59	(D85597) polyprotein [Oryza australiensis]
186	GM_52_B1_H09_T7	g3810596	BLASTX	201	4e-14	53	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
187	GM_52_B2_A02_T7	g905361	BLASTX	215	7e-16	39	(U22103) gag-protease polyprotein [Glycine max]
188	GM_52_B2_A07_T7	g4151319	BLASTX	144	3e-16	83	(AF089084) putative auxin efflux carrier protein; AtPIN1 [Arabidopsis thaliana]
189	GM_52_B2_A09_MR	g4115365	BLASTX	231	4e-17	35	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
190	GM_52_B2_A10_T7	g1480927	BLASTN	1660	2e-69	90	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
191	GM_52_B2_A11_T7	g123601	BLASTX	250	4e-22	53	HEAT SHOCK 70 KD PROTEIN gi 99913 pir S14992 heat shock protein, 70K - soybean gi 18663 (X62799) Heat Shock 70kD protein [Glycine max]
192	GM_52_B2_A12_T7	g3097320	BLASTN	379	4e-10	70	Glycine max gene for Bd 30K, complete cds
193	GM_52_B2_B01_T7	g2351062	BLASTN	389	1e-10	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20
194	GM_52_B2_B02_T7	g2688839	BLASTX	134	2e-15	69	(AF003347) ATP phosphoribosyltransferase [Thlaspi goesingense]
195	GM_52_B2_B04_MR	g507910	BLASTN	577	2e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
196	GM_52_B2_B04_T7	g4063760	BLASTX	310	1e-25	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
197	GM_52_B2_B07_MR	g3777527	BLASTX	741	2e-71	93	(AF053008) gag-pol polyprotein [Glycine max]
198	GM_52_B2_B09_MR	g2522228	BLASTX	255	7e-32	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
199	GM_52_B2_B11_T7	g3142328	BLASTN	835	4e-59	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
200	GM_52_B2_C04_MR	g2129618	BLASTX	275	5e-22	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
201	GM_52_B2_C07_MR	g2586083	BLASTX	161	1e-12	42	(U72725) receptor kinase-like protein [Oryza longistaminata]
202	GM_52_B2_D01_MR	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
203	GM_52_B2_D01_T7	g507910	BLASTN	552	2e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
204	GM_52_B2_D06_MR	g3645899	BLASTX	141	9e-17	60	(U68408) 5' end not determined experimentally [Zea mays]
205	GM_52_B2_D06_T7	g3319363	BLASTX	154	6e-19	39	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 33.26) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
206	GM_52_B2_D08_MR	g1142701	BLASTN	1376	7e-56	86	Glycine max satellite STR120-A.3.
207	GM_52_B2_D09_MR	g100484	BLASTX	296	2e-24	53	hypothetical protein - garden snapdragon
208	GM_52_B2_D11_MR	g2829133	BLASTX	179	8e-20	73	(AF043351) adenosine-5'-phosphosulfate-kinase [Arabidopsis thaliana]
209	GM_52_B2_D11_T7	g3763998	BLASTN	325	2e-09	63	Plasmodium falciparum MAL3P4, complete sequence [Plasmodium falciparum]
210	GM_52_B2_E01_MR	g3142328	BLASTN	740	2e-26	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
211	GM_52_B2_E08_T7	g507910	BLASTN	370	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
212	GM_52_B2_E10_MR	g3777527	BLASTX	561	3e-52	92	(AF053008) gag-pol polyprotein [Glycine max]
213	GM_52_B2_F02_MR	g1518540	BLASTX	515	1e-48	88	(U53418) UDP-glucose dehydrogenase [Glycine max]
214	GM_52_B2_F12_MR	g507910	BLASTN	657	4e-23	84	Glycine max BSR-101 satellite SB92 genomic sequence.
215	GM_52_B2_G02_T7	g3645899	BLASTX	214	2e-18	51	(U68408) 5' end not determined experimentally [Zea mays]
216	GM_52_B2_G05_MR	g3097320	BLASTN	739	2e-26	77	Glycine max gene for Bd 30K, complete cds
217	GM_52_B2_H08_MR	g3645899	BLASTX	260	2e-32	58	(U68408) 5' end not determined experimentally [Zea mays]
218	GM_52_B2_H09_T7	g2443320	BLASTX	167	3e-10	33	(D85597) polyprotein [Oryza australiensis]
219	GM_52_B2_H10_T7	g3777527	BLASTX	137	2e-12	39	(AF053008) gag-pol polyprotein [Glycine max]
220	GM_53_A1_A01_T7	g3142328	BLASTN	1897	3e-79	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
221	GM_53_A1_A03_T7	g2969943	BLASTN	353	7e-09	60	Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS
222	GM_53_A1_B02_MR	g3097320	BLASTN	1331	3e-53	82	Glycine max gene for Bd 30K, complete cds
223	GM_53_A1_B04_MR	g130582	BLASTX	185	3e-12	33	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
224	GM_53_A1_B08_MR	g2655098	BLASTX	215	6e-16	37	(AF023472) peptide transporter [Hordeum vulgare]
225	GM_53_A1_B10_MR	g1666236	BLASTX	144	9e-09	27	(U76261) unknown [Hordeum vulgare]
226	GM_53_A1_C01_T7	g2245043	BLASTX	103	1e-11	55	(Z97342) resistance gene [Arabidopsis thaliana]
227	GM_53_A1_C04_T7	g170065	BLASTN	348	9e-09	70	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds.
228	GM_53_A1_C09_MR	g100484	BLASTX	300	6e-25	47	hypothetical protein - garden snapdragon
229	GM_53_A1_C11_T7	g3421384	BLASTX	201	1e-14	46	(AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]
230	GM_53_A1_C12_MR	g3645899	BLASTX	220	4e-16	46	(U68408) 5' end not determined experimentally [Zea mays]
231	GM_53_A1_D02_T7	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
232	GM_53_A1_D11_MR	g505129	BLASTN	374	6e-10	61	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
233	GM_53_A1_E01_MR	g3142328	BLASTN	2046	3e-86	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
234	GM_53_A1_F07_T7	g99729	BLASTX	195	8e-15	47	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
235	GM_53_A1_F12_MR	g857392	BLASTN	462	4e-14	68	Soybean mRNA for mitotic cyclin a1-type, complete cds
236	GM_53_A1_G05_MR	g507910	BLASTN	436	4e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
237	GM_53_A1_G08_T7	g2443320	BLASTX	223	3e-16	41	(D85597) polyprotein [Oryza australiensis]
238	GM_53_A1_G12_T7	g3810596	BLASTX	310	9e-26	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
239	GM_53_B1_A05_T7	g18559	BLASTN	767	9e-28	75	G.max gene for catalase
240	GM_53_B1_B04_T7	g2995405	BLASTX	408	2e-36	54	(Y12432) polyprotein [Ananas comosus]
241	GM_53_B1_B08_MR	g13767	BLASTN	249	2e-10	63	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
242	GM_53_B1_B10_T7	g3777527	BLASTX	172	9e-11	33	(AF053008) gag-pol polyprotein [Glycine max]
243	GM_53_B1_C02_T7	g507910	BLASTN	429	9e-13	73	Glycine max BSR-101 satellite SB92 genomic sequence.
244	GM_53_B1_C04_MR	g22447	BLASTN	360	3e-09	65	Zea mays ZMPMS2 gene for 19 kDa zein protein.
245	GM_53_B1_C08_MR	g507910	BLASTN	595	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
246	GM_53_B1_C09_T7	g130406	BLASTX	97	1e-10	42	RETROVIRUS-RELATED POL POLYPROTEIN (ENDONUCLEASE) gi 91265 pir A26621 retrovirus-related endonuclease (EC 3.1.-.-) - mouse (fragment) gi 61659 (X05165) endonuclease (391 AA) [Murine leukemia virus] gi 222106 gnl PID d1000518 (D00121) endonuclease [Murine leukemia virus]
247	GM_53_B1_C11_MR	g507910	BLASTN	562	9e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
248	GM_53_B1_C12_MR	g226407	BLASTX	162	9e-10	45	retrotransposon del1-46 [Lilium henryi]
249	GM_53_B1_D01_MR	g2443320	BLASTX	198	1e-13	41	(D85597) polyprotein [Oryza australiensis]
250	GM_53_B1_D05_MR	g2463568	BLASTN	363	1e-09	85	Glycine max mRNA for squalene synthase, complete cds
251	GM_53_B1_D09_MR	g245316	BLASTX	183	1e-13	81	reverse transcriptase [Petunia hybrida=petunias, cv. nana compacta, Peptide Transposon Partial, 76 aa]
252	GM_53_B1_E04_MR	g3777527	BLASTX	204	3e-14	39	(AF053008) gag-pol polyprotein [Glycine max]
253	GM_53_B1_E05_MR	g2129618	BLASTX	115	2e-12	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
254	GM_53_B1_E09_MR	g507910	BLASTN	492	1e-15	79	Glycine max BSR-101 satellite SB92 genomic sequence.
255	GM_53_B1_E11_T7	g3845268	BLASTN	386	2e-10	63	Plasmodium falciparum chromosome 2, section 53 of 73 of the complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
256	GM_53_B1_E12_MR	g507910	BLASTN	540	8e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
257	GM_53_B1_F10_MR	g1171591	BLASTN	361	3e-09	61	P.falciparum complete gene map of plastid-like DNA (IR-B)
258	GM_53_B1_G01_T7	g3493214	BLASTX	169	1e-10	33	(AF056940) pol polyprotein [Drosophila virilis]
259	GM_53_B1_G02_T7	g282881	BLASTX	207	7e-15	51	receptor-like protein kinase precursor - Arabidopsis thaliana gi 166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]
260	GM_53_B1_G07_MR	g18559	BLASTN	1348	4e-54	80	G.max gene for catalase
261	GM_53_B1_G10_MR	g3142328	BLASTN	1760	5e-73	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
262	GM_53_B1_G11_MR	g3283026	BLASTX	187	9e-13	33	putative transposase [Arabidopsis thaliana]
263	GM_53_B1_H10_T7	g2995405	BLASTX	208	6e-15	44	(Y12432) polyprotein [Ananas comosus]
264	GM_53_B2_A02_T7	g1142703	BLASTN	292	3e-16	78	Glycine max satellite STR120-B.1.
265	GM_53_B2_A12_MR	g3097836	BLASTN	396	7e-11	69	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
266	GM_53_B2_B10_MR	g4063760	BLASTX	392	2e-34	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
267	GM_53_B2_B11_MR	g2879886	BLASTN	384	2e-10	61	Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes
268	GM_53_B2_C03_MR	g2522228	BLASTX	462	5e-43	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
269	GM_53_B2_C05_MR	g3142328	BLASTN	1045	2e-40	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
270	GM_53_B2_D02_T7	g2264320	BLASTN	653	2e-22	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
271	GM_53_B2_E01_MR	g4115373	BLASTX	178	1e-11	35	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]
272	GM_53_B2_E02_MR	g3097320	BLASTN	384	2e-10	74	Glycine max gene for Bd 30K, complete cds
273	GM_53_B2_E02_T7	g4063756	BLASTN	416	9e-12	61	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
274	GM_53_B2_E04_MR	g3513747	BLASTX	247	5e-20	46	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
275	GM_53_B2_E06_T7	g3097320	BLASTN	394	8e-11	66	Glycine max gene for Bd 30K, complete cds
276	GM_53_B2_E07_T7	g3184508	BLASTN	393	1e-10	64	Homo sapiens chromosome 17, clone HRPC41C23, complete sequence [Homo sapiens]
277	GM_53_B2_E09_MR	g3142328	BLASTN	1844	7e-77	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
278	GM_53_B2_E10_T7	g3449327	BLASTN	468	4e-14	72	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]
279	GM_53_B2_F01_MR	g3377855	BLASTX	512	2e-48	68	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
280	GM_53_B2_F04_MR	g4151066	BLASTX	243	2e-27	90	(Y10861) ribonucleotide reductase [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
281	GM_53_B2_F05_T7	g18559	BLASTN	349	9e-09	77	G.max gene for catalase
282	GM_53_B2_F10_MR	g4063760	BLASTX	512	4e-47	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
283	GM_53_B2_F10_T7	g507910	BLASTN	542	7e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
284	GM_53_B2_G01_MR	g2522228	BLASTX	469	8e-44	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
285	GM_53_B2_G04_MR	g2895630	BLASTN	398	3e-11	61	Phoebis sennae large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
286	GM_53_B2_G09_MR	g3402703	BLASTX	145	9e-09	77	(AC004261) hypothetical protein [Arabidopsis thaliana]
287	GM_53_B2_G09_T7	g1769898	BLASTX	419	3e-38	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
288	GM_53_B2_G11_MR	g1167523	BLASTX	191	8e-13	39	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
289	GM_53_B2_H02_MR	g255572	BLASTN	1740	2e-72	96	small auxin up RNA gene cluster: orf 15A [Glycine max=soybeans, cv. Wayne, Genomic, 637 nt]
290	GM_54_A1_A02_MR	g1165321	BLASTN	378	4e-10	69	Glycine max extensin (SbHRGP3) gene, complete cds
291	GM_54_A1_A04_MR	g629693	BLASTX	136	1e-11	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
292	GM_54_A1_A05_MR	g507910	BLASTN	660	3e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
293	GM_54_A1_A07_T7	g507910	BLASTN	445	2e-13	78	Glycine max BSR-101 satellite SB92 genomic sequence.
294	GM_54_A1_A09_MR	g905361	BLASTX	195	1e-13	33	(U22103) gag-protease polyprotein [Glycine max]
295	GM_54_A1_B01_MR	g4063756	BLASTN	498	2e-15	72	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
296	GM_54_A1_B12_MR	g1785699	BLASTX	124	4e-12	44	(Y08501) orf145a [Arabidopsis thaliana]
297	GM_54_A1_C08_MR	g2760839	BLASTX	298	8e-25	48	(AC003105) putative receptor kinase [Arabidopsis thaliana]
298	GM_54_A1_D04_MR	g3142328	BLASTN	386	2e-10	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
299	GM_54_A1_D06_MR	g4063760	BLASTX	167	2e-10	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
300	GM_54_A1_D09_T7	g3097320	BLASTN	405	3e-11	74	Glycine max gene for Bd 30K, complete cds
301	GM_54_A1_D10_MR	g1666236	BLASTX	179	1e-12	31	(U76261) unknown [Hordeum vulgare]
302	GM_54_A1_D11_MR	g3687234	BLASTX	192	4e-13	54	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
303	GM_54_A1_D12_MR	g4063760	BLASTX	251	3e-19	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
304	GM_54_A1_E07_T7	g100484	BLASTX	248	2e-19	55	hypothetical protein - garden snapdragon
305	GM_54_A1_F07_MR	g507910	BLASTN	416	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
306	GM_54_A1_F08_MR	g4092471	BLASTN	441	7e-13	71	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
307	GM_54_A1_F09_MR	g1769897	BLASTX	217	3e-16	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
308	GM_54_A1_G03_MR	g4063760	BLASTX	184	4e-12	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
309	GM_54_A1_G04_MR	g18695	BLASTN	346	9e-09	67	Soybean nodulin 22 gene

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
310	GM_54_A1_G10_MR	g2388834	BLASTN	388	2e-10	65	Human DNA sequence from PAC 341I10 on chromosome 6q22.2-22.33. Contains 60S ribosomal protein L5 like (pseudo)gene, ESTs and STSs
311	GM_54_A1_G11_MR	g2995405	BLASTX	371	2e-32	51	(Y12432) polyprotein [Ananas comosus]
312	GM_54_A2_A12_T7	g4063760	BLASTX	245	1e-18	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
313	GM_54_A2_B05_MR	g3777527	BLASTX	216	2e-15	73	(AF053008) gag-pol polyprotein [Glycine max]
314	GM_54_A2_C03_T7	g4063760	BLASTX	160	1e-09	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
315	GM_54_A2_C04_T7	g3645899	BLASTX	128	1e-09	36	(U68408) 5' end not determined experimentally [Zea mays]
316	GM_54_A2_D12_T7	g4115365	BLASTX	156	4e-09	37	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
317	GM_54_A2_E01_T7	g18559	BLASTN	628	2e-21	76	G.max gene for catalase
318	GM_54_A2_E02_T7	g3645899	BLASTX	313	5e-26	50	(U68408) 5' end not determined experimentally [Zea mays]
319	GM_54_A2_E04_MR	g170606	BLASTN	700	4e-25	67	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
320	GM_54_A2_E06_T7	g1142700	BLASTN	698	5e-25	78	Glycine max satellite STR120-A.2.
321	GM_54_A2_E12_T7	g1658457	BLASTX	348	6e-31	75	(U75248) reverse transcriptase [Gossypium barbadense]
322	GM_54_A2_G11_T7	g3249073	BLASTX	123	4e-09	36	(AC004473) Contains similarity to reverse transcriptase-like protein gb 2244803 from A. thaliana chromosome 4 contig gb Z97336. [Arabidopsis thaliana]
323	GM_54_A2_H01_MR	g3142328	BLASTN	536	3e-17	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
324	GM_54_A2_H01_T7	g100484	BLASTX	386	3e-34	59	hypothetical protein - garden snapdragon
325	GM_54_A2_H02_T7	g99922	BLASTX	342	5e-32	74	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
326	GM_54_B1_A02_MR	g2342725	BLASTX	193	1e-14	67	(AC002341) hypothetical protein [Arabidopsis thaliana]
327	GM_54_B1_A03_MR	g507910	BLASTN	426	1e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
328	GM_54_B1_A06_MR	g507910	BLASTN	414	4e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
329	GM_54_B1_B03_T7	g3142328	BLASTN	624	3e-21	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
330	GM_54_B1_B09_T7	g4063760	BLASTX	285	5e-23	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
331	GM_54_B1_B10_T7	g18768	BLASTN	374	1e-10	69	Soybean Tgm6 transposable element 3' end
332	GM_54_B1_B11_MR	g1769897	BLASTX	178	5e-12	27	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
333	GM_54_B1_C01_MR	g19274	BLASTN	374	5e-10	66	L.esculentum mRNA for protein with leucine zipper.
334	GM_54_B1_C03_MR	g3319362	BLASTX	343	3e-29	48	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
335	GM_54_B1_C05_MR	g3746069	BLASTX	157	3e-09	35	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
336	GM_54_B1_C05_T7	g2443320	BLASTX	380	5e-33	53	(D85597) polyprotein [Oryza australiensis]
337	GM_54_B1_D01_T7	g905361	BLASTX	689	4e-67	95	(U22103) gag-protease polyprotein [Glycine max]
338	GM_54_B1_D03_T7	g3687234	BLASTX	214	2e-15	40	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
339	GM_54_B1_D08_T7	g18559	BLASTN	1789	3e-74	93	G.max gene for catalase
340	GM_54_B1_D10_MR	g1755186	BLASTX	405	5e-37	53	(U75204) germin-like protein [Arabidopsis thaliana]
341	GM_54_B1_D12_MR	g3777527	BLASTX	636	3e-60	91	(AF053008) gag-pol polyprotein [Glycine max]
342	GM_54_B1_E02_T7	g4038056	BLASTX	359	4e-31	54	(AC005897) putative transposon [Arabidopsis thaliana]
343	GM_54_B1_E05_T7	g2264312	BLASTN	503	1e-15	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]
344	GM_54_B1_F02_MR	g4063760	BLASTX	277	4e-22	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
345	GM_54_B1_F02_T7	g507910	BLASTN	747	4e-27	90	Glycine max BSR-101 satellite SB92 genomic sequence.
346	GM_54_B1_F04_MR	g1236949	BLASTX	273	7e-22	91	(U50075) lipoxygenase L-5 [Glycine max]
347	GM_54_B1_F11_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
348	GM_54_B1_F11_T7	g507910	BLASTN	379	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
349	GM_54_B1_G01_MR	g3068705	BLASTX	183	1e-13	62	(AF049236) unknown [Arabidopsis thaliana]
350	GM_54_B1_G02_MR	g4063760	BLASTX	303	7e-25	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
351	GM_54_B1_G02_T7	g507910	BLASTN	729	3e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
352	GM_54_B1_G08_MR	g421955	BLASTX	199	9e-33	56	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
353	GM_54_B1_G08_T7	g4115365	BLASTX	237	9e-18	39	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
354	GM_54_B1_G09_MR	g2443320	BLASTX	177	2e-11	35	(D85597) polyprotein [Oryza australiensis]
355	GM_54_B1_H01_MR	g507910	BLASTN	552	2e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
356	GM_54_B1_H01_T7	g507910	BLASTN	644	2e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
357	GM_54_B1_H02_MR	g905361	BLASTX	272	5e-22	39	(U22103) gag-protease polyprotein [Glycine max]
358	GM_54_B1_H03_T7	g18559	BLASTN	1712	1e-70	92	G.max gene for catalase
359	GM_54_B1_H05_MR	g3478665	BLASTN	350	9e-09	68	Homo sapiens PAC clone DJ0870F17 from 7q33-q36, complete sequence [Homo sapiens]
360	GM_54_B1_H11_MR	g507910	BLASTN	575	2e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
361	GM_54_B2_A01_T7	g3645899	BLASTX	339	9e-29	49	(U68408) 5' end not determined experimentally [Zea mays]
362	GM_54_B2_A03_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
363	GM_54_B2_A03_T7	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
364	GM_54_B2_A06_MR	g2315153	BLASTX	165	6e-11	70	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
365	GM_54_B2_A08_T7	g4038056	BLASTX	352	7e-33	41	(AC005897) putative transposon [Arabidopsis thaliana]
366	GM_54_B2_A10_MR	g2522228	BLASTX	475	2e-44	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
367	GM_54_B2_B05_MR	g1402881	BLASTX	199	6e-14	48	(X98130) non-ltr retrotransposon reverse transcriptase-like protein [Arabidopsis thaliana]
368	GM_54_B2_B06_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
369	GM_54_B2_B06_T7	g507910	BLASTN	397	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
370	GM_54_B2_B07_T7	g2879929	BLASTX	198	4e-15	31	(AB010897) secretory, endostyle (zone2) [Ciona intestinalis]
371	GM_54_B2_B08_MR	g3894391	BLASTX	237	4e-18	42	(AF053997) Hcr2-5B [Lycopersicon esculentum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
372	GM_54_B2_C02_T7	g2895866	BLASTX	175	3e-15	68	(AF045770) methylmalonate semi-aldehyde dehydrogenase [Oryza sativa]
373	GM_54_B2_C06_T7	g132770	BLASTX	183	1e-13	88	CHLOROPLAST 50S RIBOSOMAL PROTEIN L20 gi 71275 pir R5NT20 ribosomal protein L20 - common tobacco chloroplast gi 11852 (Z00044) ribosomal protein L20 [Nicotiana tabacum] gi 225221 prf 1211235BC ribosomal protein L20 [Nicotiana tabacum]
374	GM_54_B2_C08_MR	g505129	BLASTN	352	6e-09	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
375	GM_54_B2_C09_MR	g3097320	BLASTN	1734	2e-71	83	Glycine max gene for Bd 30K, complete cds
376	GM_54_B2_C12_T7	g2598579	BLASTX	240	1e-18	68	(Y15295) L-ascorbate oxidase [Medicago truncatula]
377	GM_54_B2_D01_MR	g3142379	BLASTX	174	2e-13	54	(AF053008) envelope-like [Glycine max]
378	GM_54_B2_D01_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
379	GM_54_B2_D09_MR	g18559	BLASTN	390	1e-10	68	G.max gene for catalase
380	GM_54_B2_D12_MR	g3549664	BLASTX	212	9e-17	51	(AL031394) putative protein [Arabidopsis thaliana]
381	GM_54_B2_E02_T7	g2583106	BLASTN	433	2e-12	72	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]
382	GM_54_B2_E03_MR	g131289	BLASTX	509	5e-48	85	PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN) (CP43) gi 72709 pir F2NT44 photosystem II chlorophyll a-binding protein psbC - common tobacco chloroplast gi 225285 prf 1211235W photosystem II 44kD protein [Nicotiana tabacum]
383	GM_54_B2_E03_T7	g131269	BLASTX	277	7e-23	79	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) gi 72708 pir QJLV6A photosystem II chlorophyll a-binding protein psbB - liverwort (Marchantia polymorpha) chloroplast gi 11700 (X04465) psbB gene product [Marchantia polymorpha]
384	GM_54_B2_E05_MR	g2129618	BLASTX	204	2e-14	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
385	GM_54_B2_E09_MR	g4063760	BLASTX	540	3e-50	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
386	GM_54_B2_E09_T7	g3319362	BLASTX	212	3e-15	53	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
387	GM_54_B2_E11_MR	g4126312	BLASTN	444	5e-13	61	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
388	GM_54_B2_E11_T7	g2695704	BLASTN	456	1e-13	66	A.thaliana constans gene.
389	GM_54_B2_F05_MR	g1431738	BLASTN	410	1e-11	67	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
390	GM_54_B2_F09_MR	g3810596	BLASTX	165	2e-17	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
391	GM_54_B2_F09_T7	g2414348	BLASTN	377	5e-10	65	Caenorhabditis elegans cosmid Y37A1A, complete sequence [Caenorhabditis elegans]
392	GM_54_B2_F12_MR	g3176673	BLASTX	222	1e-17	44	(AC003671) Similar to serine/threonine kinase gb Y12531 from Brassica oleracea. [Arabidopsis thaliana]
393	GM_54_B2_G02_T7	g1666236	BLASTX	154	3e-23	33	(U76261) unknown [Hordeum vulgare]
394	GM_54_B2_G03_MR	g3873174	BLASTN	452	2e-13	67	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]
395	GM_54_B2_G05_MR	g2656030	BLASTN	827	3e-30	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL8
396	GM_54_B2_G09_MR	g507910	BLASTN	405	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
397	GM_54_B2_G09_T7	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
398	GM_54_B2_G10_MR	g2129626	BLASTX	173	9e-21	47	J-domain protein - Arabidopsis thaliana gi 928936 (Z49238) J-domain protein [Arabidopsis thaliana] gi 1585434 prf 2124427A diamide resistance gene [Arabidopsis thaliana]
399	GM_54_B2_G12_T7	g4063760	BLASTX	311	1e-25	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
400	GM_54_B2_H01_MR	g18559	BLASTN	989	8e-38	77	G.max gene for catalase
401	GM_54_B2_H02_T7	g1421750	BLASTN	383	2e-10	83	Pisum sativum S-adenosylmethionine decarboxylase mRNA, complete cds.
402	GM_54_B2_H04_MR	g3319362	BLASTX	262	1e-20	47	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
403	GM_54_B2_H07_MR	g2522228	BLASTX	304	2e-43	59	(AB007466) reverse transcriptase-like protein [Vicia faba]
404	GM_54_B2_H09_MR	g1769897	BLASTX	348	2e-34	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
405	GM_54_B2_H09_T7	g2462936	BLASTX	235	7e-32	60	(Y12321) open reading frame 2 [Brassica oleracea]
406	GM_54_B2_H12_MR	g3319362	BLASTX	187	9e-27	55	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
407	GM_55_A1_A02_T7	g3377848	BLASTX	195	4e-14	37	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
408	GM_55_A1_A03_T7	g507910	BLASTN	387	7e-11	78	Glycine max BSR-101 satellite SB92 genomic sequence.
409	GM_55_A1_A05_T7	g3513747	BLASTX	404	2e-35	53	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
410	GM_55_A1_A08_MR	g4092471	BLASTN	443	6e-13	66	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
411	GM_55_A1_A11_T7	g3805845	BLASTX	226	9e-17	63	(AL031986) putative protein [Arabidopsis thaliana]
412	GM_55_A1_B03_MR	g3859610	BLASTN	862	6e-32	67	Arabidopsis thaliana BAC T9E19
413	GM_55_A1_B04_MR	g3402755	BLASTX	230	6e-28	47	(AL031187) putative transposable element [Arabidopsis thaliana]
414	GM_55_A1_B06_MR	g3142328	BLASTN	2136	2e-90	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
415	GM_55_A1_B10_T7	g3645899	BLASTX	157	2e-09	41	(U68408) 5' end not determined experimentally [Zea mays]
416	GM_55_A1_C03_MR	g2791937	BLASTX	315	2e-27	64	(AJ001200) reverse transcriptase [Alstroemeria aurea]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
417	GM_55_A1_C05_MR	g3777527	BLASTX	770	2e-74	97	(AF053008) gag-pol polyprotein [Glycine max]
418	GM_55_A1_C07_MR	g18559	BLASTN	1346	5e-54	87	G.max gene for catalase
419	GM_55_A1_C08_MR	g3142328	BLASTN	651	2e-22	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
420	GM_55_A1_C11_MR	g2522230	BLASTX	288	1e-24	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
421	GM_55_A1_D03_T7	g99726	BLASTX	169	5e-12	47	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976) orf 3 [Arabidopsis thaliana]
422	GM_55_A1_D05_MR	g2522228	BLASTX	416	3e-38	71	(AB007466) reverse transcriptase-like protein [Vicia faba]
423	GM_55_A1_D12_T7	g1707642	BLASTX	205	1e-14	33	(Y07748) TMK [Oryza sativa]
424	GM_55_A1_E02_T7	g3097320	BLASTN	928	5e-35	81	Glycine max gene for Bd 30K, complete cds
425	GM_55_A1_E06_T7	g3142328	BLASTN	951	4e-36	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
426	GM_55_A1_E09_MR	g130582	BLASTX	422	2e-37	55	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
427	GM_55_A1_E11_T7	g3650039	BLASTX	258	2e-20	42	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
428	GM_55_A1_F01_MR	g3142328	BLASTN	1169	5e-46	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
429	GM_55_A1_F02_T7	g99730	BLASTX	256	1e-20	56	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
430	GM_55_A1_F04_T7	g3859610	BLASTN	586	2e-19	66	Arabidopsis thaliana BAC T9E19
431	GM_55_A1_F10_MR	g99922	BLASTX	460	8e-43	65	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
432	GM_55_A1_G03_MR	g2656031	BLASTN	496	2e-15	72	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20
433	GM_55_A1_G08_T7	g3287695	BLASTX	153	5e-09	60	(AC003979) Similar to hypothetical protein C34B7.2 gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis thaliana]
434	GM_55_A1_G10_T7	g130582	BLASTX	154	7e-09	38	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
435	GM_55_A1_H01_T7	g4063760	BLASTX	464	4e-42	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
436	GM_55_A1_H02_T7	g1769898	BLASTX	295	1e-24	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
437	GM_55_A1_H05_MR	g3142328	BLASTN	1163	9e-46	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
438	GM_55_A1_H10_MR	g3097320	BLASTN	430	2e-12	72	Glycine max gene for Bd 30K, complete cds
439	GM_55_A1_H11_MR	g3334667	BLASTX	212	8e-16	77	(Y10493) putative cytochrome P450 [Glycine max]
440	GM_55_A1_H12_MR	g3777527	BLASTX	699	6e-67	94	(AF053008) gag-pol polyprotein [Glycine max]
441	GM_55_A2_A02_MR	g2522228	BLASTX	264	6e-22	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
442	GM_55_A2_A03_T7	g507910	BLASTN	386	8e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
443	GM_55_A2_A05_MR	g507910	BLASTN	630	7e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
444	GM_55_A2_A05_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
445	GM_55_A2_A10_MR	g665934	BLASTX	130	8e-13	39	(U20341) ORF III [Cassava vein mosaic virus] gi 1399884 (U59751) ORF 3 [Cassava vein mosaic virus]
446	GM_55_A2_B01_T7	g4038056	BLASTX	295	3e-24	43	(AC005897) putative transposon [Arabidopsis thaliana]
447	GM_55_A2_B03_MR	g505129	BLASTN	378	4e-10	61	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
448	GM_55_A2_B10_T7	g2865437	BLASTX	219	8e-16	53	(AF039376) polyprotein [Arabidopsis arenosa]
449	GM_55_A2_B12_MR	g507910	BLASTN	351	3e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
450	GM_55_A2_B12_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
451	GM_55_A2_C01_MR	g905361	BLASTX	690	3e-67	92	(U22103) gag-protease polyprotein [Glycine max]
452	GM_55_A2_C02_MR	g905361	BLASTX	303	2e-44	85	(U22103) gag-protease polyprotein [Glycine max]
453	GM_55_A2_C05_MR	g1568664	BLASTX	216	1e-16	38	(U70873) O-methyltransferase [Pinus radiata]
454	GM_55_A2_C08_T7	g3930515	BLASTX	121	4e-12	47	(AF059674) putative gag protein [Nicotiana tabacum]
455	GM_55_A2_C09_T7	g1666236	BLASTX	160	1e-10	30	(U76261) unknown [Hordeum vulgare]
456	GM_55_A2_C12_T7	g522302	BLASTX	171	3e-14	48	(L35053) endonuclease [Magnaporthe grisea]
457	GM_55_A2_D05_MR	g100484	BLASTX	115	4e-09	63	hypothetical protein - garden snapdragon
458	GM_55_A2_D09_T7	g1708314	BLASTX	532	2e-50	76	HEAT SHOCK PROTEIN 83 gi 169296 (M99431) heat shock protein 83 [Pharbitis nil] gi 445625 prf 1909372A heat shock protein 83 [Ipomoea nil]
459	GM_55_A2_E02_MR	g507910	BLASTN	393	4e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
460	GM_55_A2_E09_MR	g3687234	BLASTX	170	1e-10	34	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
461	GM_55_A2_E10_MR	g507910	BLASTN	348	4e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
462	GM_55_A2_E10_T7	g507910	BLASTN	467	2e-14	77	Glycine max BSR-101 satellite SB92 genomic sequence.
463	GM_55_A2_F02_MR	g507910	BLASTN	436	4e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
464	GM_55_A2_F03_MR	g3831457	BLASTX	349	4e-31	64	(AC005700) putative ion channel protein [Arabidopsis thaliana]
465	GM_55_A2_F04_MR	g2522228	BLASTX	417	3e-38	73	(AB007466) reverse transcriptase-like protein [Vicia faba]
466	GM_55_A2_F06_MR	g3645899	BLASTX	144	7e-20	50	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
467	GM_55_A2_F08_T7	g2073447	BLASTN	416	9e-12	67	L.japonicus gln1, pge1 & krm genes
468	GM_55_A2_F12_MR	g2244996	BLASTX	385	5e-34	59	(Z97341) similarity to a membrane-associated salt-inducible protein [Arabidopsis thaliana]
469	GM_55_A2_G02_MR	g3142328	BLASTN	797	4e-29	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
470	GM_55_A2_G04_T7	g2462134	BLASTX	328	1e-28	47	(Y13368) reverse transcriptase [Beta vulgaris]
471	GM_55_A2_G09_MR	g905361	BLASTX	171	4e-11	29	(U22103) gag-protease polyprotein [Glycine max]
472	GM_55_A2_H03_T7	g2583130	BLASTX	156	7e-13	32	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
473	GM_55_A2_H05_MR	g2995405	BLASTX	450	6e-41	64	(Y12432) polyprotein [Ananas comosus]
474	GM_55_A2_H06_T7	g1666236	BLASTX	180	9e-13	28	(U76261) unknown [Hordeum vulgare]
475	GM_55_A2_H08_T7	g130582	BLASTX	358	1e-30	61	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
476	GM_55_A2_H11_T7	g13767	BLASTN	441	9e-14	63	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
477	GM_55_B1_A03_T7	g1706522	BLASTX	206	2e-31	87	DIHYDROFOLATE REDUCTASE / THYMIDYLATE SYNTHASE (DHFR-TS) gi 1362048 pir S55683 dihydrofolate reductase-thymidylate synthase - soybean gi 999190 bbs 166832 (S78087) dihydrofolate reductase-thymidylate synthase, DHFR-TS=bifunctional enzyme {EC 1.5.1.3} [Glycine max, seedling, Peptide, 530 aa] [Glycine max] gi 1096144 prf 2111237A dihydrofolate reductase-thymidylate synthase [Glycine max]
478	GM_55_B1_A04_MR	g3687234	BLASTX	172	5e-19	55	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
479	GM_55_B1_A04_T7	g1666236	BLASTX	170	1e-11	27	(U76261) unknown [Hordeum vulgare]
480	GM_55_B1_A05_MR	g13619	BLASTN	503	1e-16	65	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
481	GM_55_B1_A12_MR	g2982576	BLASTN	353	5e-14	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-105, complete sequence [Plasmodium falciparum]
482	GM_55_B1_B05_MR	g2194136	BLASTX	344	4e-29	51	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
483	GM_55_B1_B05_T7	g2815075	BLASTN	470	3e-14	62	Caenorhabditis elegans cosmid Y38H8A, complete sequence [Caenorhabditis elegans]
484	GM_55_B1_B06_MR	g3097320	BLASTN	545	1e-17	81	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
485	GM_55_B1_B11_MR	g4140712	BLASTX	197	2e-20	48	(AF110183) putative integrase [Oryza sativa]
486	GM_55_B1_B12_MR	g4063760	BLASTX	492	5e-45	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
487	GM_55_B1_B12_T7	g4063760	BLASTX	458	2e-41	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
488	GM_55_B1_C02_T7	g507910	BLASTN	424	2e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
489	GM_55_B1_C03_MR	g2760832	BLASTX	170	6e-12	43	(AC003105) similar to barley ids-4 gene product [Arabidopsis thaliana]
490	GM_55_B1_C05_T7	g18767	BLASTN	424	7e-23	83	Soybean Tgm6 transposable element 5' end
491	GM_55_B1_C06_MR	g18559	BLASTN	452	2e-13	75	G.max gene for catalase
492	GM_55_B1_C09_MR	g170029	BLASTN	389	1e-10	80	Glycine max cv. Dare nodulin 26 gene fragment.
493	GM_55_B1_C10_MR	g3097320	BLASTN	776	4e-28	80	Glycine max gene for Bd 30K, complete cds
494	GM_55_B1_C11_T7	g3176768	BLASTN	372	9e-11	62	Homo sapiens allele 1 fragile site locus (FRA10B) minisatellite, 3' sequence
495	GM_55_B1_D05_T7	g2708743	BLASTX	191	8e-13	39	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
496	GM_55_B1_D09_T7	g342952	BLASTN	348	1e-09	60	paramecium species 1,168 mt dna dimer: replication init. region.
497	GM_55_B1_D11_MR	g4063760	BLASTX	390	4e-34	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
498	GM_55_B1_D11_T7	g507910	BLASTN	565	6e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
499	GM_55_B1_D12_MR	g2121303	BLASTN	471	3e-14	60	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
500	GM_55_B1_E05_T7	g1167523	BLASTX	417	6e-37	52	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
501	GM_55_B1_E07_MR	g4063760	BLASTX	411	2e-36	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
502	GM_55_B1_F05_T7	g4115942	BLASTX	152	3e-09	84	(AF118223) contains similarity to eukaryotic protein kinase domains (Pfam: PF00069, score=238.4, E= 1e-67, N=1) and EF hand domains (Pfam: PF00036, score=109.0, E=8.9e-29, N=5) [Arabidopsis thaliana]
503	GM_55_B1_F09_MR	g1076286	BLASTX	534	7e-51	82	amidophosphoribosyltransferase - Arabidopsis thaliana gi 469193 gnl PID d1006574 (D28868) amidophosphoribosyltransferase [Arabidopsis thaliana]
504	GM_55_B1_F12_T7	g3645899	BLASTX	146	2e-09	63	(U68408) 5' end not determined experimentally [Zea mays]
505	GM_55_B1_G02_T7	g3097320	BLASTN	1585	9e-65	83	Glycine max gene for Bd 30K, complete cds
506	GM_55_B1_G03_MR	g2522230	BLASTX	151	4e-10	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
507	GM_55_B1_G04_MR	g3831457	BLASTX	340	3e-30	63	(AC005700) putative ion channel protein [Arabidopsis thaliana]
508	GM_55_B1_G08_MR	g2982291	BLASTX	195	7e-22	82	(AF051230) heat shock protein [Picea mariana]
509	GM_55_B1_H06_MR	g2244915	BLASTX	293	6e-24	42	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
510	GM_55_B1_H09_MR	g1666236	BLASTX	219	3e-17	32	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
511	GM_55_B1_H10_MR	g2522230	BLASTX	270	1e-22	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
512	GM_55_B2_A02_MR	g2780996	BLASTX	160	5e-10	54	Chain A, Crystal Structure Of A Eukaryotic (Pea Seedling) Copper-Containing Amine Oxidase At 2.2a Resolution Oxidase, Copper, Pea Seedling, Oxidoreductase Mol_id: 1; Molecule: Copper Amine Oxidase; Chain: A, B; Ec: 1.4.3.6; Biolog... gi 2780997 pdb 1KSI B Chain B, Crystal Structure Of A Eukaryotic (Pea Seedling) Copper-Containing Amine Oxidase At 2.2a Resolution Oxidase, Copper, Pea Seedling, Oxidoreductase Mol_id: 1; Molecule: Copper Amine Oxidase; Chain: A, B; Ec: 1.4.3.6; Biolog...
513	GM_55_B2_A07_T7	g507910	BLASTN	351	3e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
514	GM_55_B2_B05_MR	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
515	GM_55_B2_B06_T7	g18767	BLASTN	340	5e-09	65	Soybean Tgm6 transposable element 5' end
516	GM_55_B2_B09_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
517	GM_55_B2_C04_MR	g4063760	BLASTX	226	1e-16	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
518	GM_55_B2_C09_T7	g3426334	BLASTN	439	7e-13	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
519	GM_55_B2_C12_T7	g1142701	BLASTN	734	7e-27	85	Glycine max satellite STR120-A.3.
520	GM_55_B2_D06_T7	g4063760	BLASTX	490	8e-45	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
521	GM_55_B2_D07_T7	g507910	BLASTN	456	5e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.
522	GM_55_B2_D08_MR	g402616	BLASTN	401	3e-11	93	G.max satellite DNA
523	GM_55_B2_E06_T7	g4050011	BLASTN	471	3e-14	62	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
524	GM_55_B2_F03_T7	g2997694	BLASTX	158	3e-20	36	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
525	GM_55_B2_F10_T7	g3845197	BLASTN	395	8e-11	65	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
526	GM_55_B2_G04_MR	g2462058	BLASTX	148	9e-10	46	(Y13389) reverse transcriptase [Antirrhinum majus]
527	GM_55_B2_G05_MR	g2462056	BLASTX	178	6e-13	48	(Y13388) reverse transcriptase [Antirrhinum majus]
528	GM_55_B2_H12_MR	g507910	BLASTN	501	5e-16	84	Glycine max BSR-101 satellite SB92 genomic sequence.
529	GM_56_A1_A02_MR	g1769898	BLASTX	520	3e-49	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
530	GM_56_A1_A03_MR	g507910	BLASTN	340	9e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
531	GM_56_A1_A03_T7	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
532	GM_56_A1_A05_T7	g81869	BLASTX	313	2e-27	62	hydroxyproline-rich glycoprotein (clone Hyp2.13) - kidney bean (fragment) gi 169349 (M18095) hydroxyproline-rich glycoprotein [Phaseolus vulgaris]
533	GM_56_A1_A06_MR	g2656031	BLASTN	354	6e-09	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20
534	GM_56_A1_B02_MR	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
535	GM_56_A1_B03_MR	g3059060	BLASTN	386	2e-10	58	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
536	GM_56_A1_B04_MR	g3142328	BLASTN	968	7e-37	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
537	GM_56_A1_B06_MR	g4038056	BLASTX	241	2e-18	51	(AC005897) putative transposon [Arabidopsis thaliana]
538	GM_56_A1_C01_MR	g507910	BLASTN	564	7e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
539	GM_56_A1_C01_T7	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
540	GM_56_A1_C04_T7	g99729	BLASTX	238	3e-19	42	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
541	GM_56_A1_D05_MR	g2191182	BLASTX	353	6e-31	44	(AF007271) similar to N. tabacum membrane-associated salt-inducible protein (PID:g473874) [Arabidopsis thaliana]
542	GM_56_A1_D06_T7	g2982243	BLASTX	163	2e-11	47	(AF051204) hypothetical protein [Picea mariana]
543	GM_56_A1_D07_MR	g475599	BLASTN	320	3e-11	71	Glycine max Century 84 BiP isoform B mRNA, complete cds.
544	GM_56_A1_D08_MR	g1167523	BLASTX	665	2e-63	64	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
545	GM_56_A1_D12_MR	g4063760	BLASTX	111	8e-11	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
546	GM_56_A1_E02_MR	g3687828	BLASTN	376	6e-10	63	Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence [Homo sapiens]
547	GM_56_A1_E02_T7	g1619602	BLASTX	134	3e-10	53	(Y08726) MtN3 [Medicago truncatula]
548	GM_56_A1_E03_MR	g3834324	BLASTX	145	4e-09	83	(AC005679) Similar to gb X92762 tafazzins protein from Homo sapiens. [Arabidopsis thaliana]
549	GM_56_A1_E03_T7	g1171583	BLASTN	321	9e-12	67	P.falciparum complete gene map of plastid-like DNA (IR-A)
550	GM_56_A1_E07_MR	g4063760	BLASTX	646	1e-61	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
551	GM_56_A1_E09_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
552	GM_56_A1_E10_T7	g4063760	BLASTX	687	6e-66	77	(AC005561) putative POL3 protein [Arabidopsis thaliana]
553	GM_56_A1_F11_MR	g1666236	BLASTX	259	2e-24	38	(U76261) unknown [Hordeum vulgare]
554	GM_56_A1_F12_T7	g2335061	BLASTN	397	7e-11	63	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence [Homo sapiens]
555	GM_56_A1_G02_MR	g1931642	BLASTX	162	1e-14	47	(U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]
556	GM_56_A1_G07_MR	g507910	BLASTN	600	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
557	GM_56_A1_G07_T7	g507910	BLASTN	570	4e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
558	GM_56_A1_G08_MR	g995751	BLASTN	519	1e-16	66	Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence
559	GM_56_A1_G08_T7	g2661071	BLASTX	218	2e-35	74	(AF035309) similar to 26S proteasome subunit p45 [Homo sapiens]
560	GM_56_A1_G10_MR	g3319351	BLASTX	310	2e-25	34	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
561	GM_56_A1_G12_T7	g13581	BLASTN	472	4e-15	63	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTCG10 Saccharomyces cerevisiae mitochondrion DNA segment.
562	GM_56_A1_H01_MR	g2979597	BLASTN	520	2e-16	64	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
563	GM_56_A1_H05_MR	g2688839	BLASTX	128	2e-14	78	(AF003347) ATP phosphoribosyltransferase [Thlaspi goesingense]
564	GM_56_A1_H06_T7	g2995405	BLASTX	321	5e-27	56	(Y12432) polyprotein [Ananas comosus]
565	GM_56_A1_H08_MR	g3097320	BLASTN	1007	1e-38	76	Glycine max gene for Bd 30K, complete cds
566	GM_56_A1_H09_MR	g3695395	BLASTX	224	7e-17	38	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
567	GM_56_A1_H10_T7	g18559	BLASTN	542	2e-17	71	G.max gene for catalase
568	GM_56_A2_A04_T7	g507910	BLASTN	352	3e-09	75	Glycine max BSR-101 satellite SB92 genomic sequence.
569	GM_56_A2_A08_T7	g3845197	BLASTN	475	2e-14	63	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
570	GM_56_A2_B01_MR	g4063760	BLASTX	251	3e-19	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
571	GM_56_A2_B02_T7	g3193221	BLASTN	407	2e-11	73	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
572	GM_56_A2_B06_MR	g1666236	BLASTX	205	3e-18	37	(U76261) unknown [Hordeum vulgare]
573	GM_56_A2_B07_MR	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
574	GM_56_A2_B09_T7	g4038056	BLASTX	313	4e-26	45	(AC005897) putative transposon [Arabidopsis thaliana]
575	GM_56_A2_B10_T7	g21376	BLASTN	352	5e-09	70	Sesbania rostrata Srglb3 gene for leghemoglobin
576	GM_56_A2_B11_MR	g905361	BLASTX	408	6e-37	91	(U22103) gag-protease polyprotein [Glycine max]
577	GM_56_A2_B12_T7	g99727	BLASTX	173	2e-11	31	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345510 gnl PID e73213 (X53975) orf 1 [Arabidopsis thaliana]
578	GM_56_A2_C07_MR	g3097320	BLASTN	437	9e-13	69	Glycine max gene for Bd 30K, complete cds
579	GM_56_A2_C11_MR	g1769897	BLASTX	304	9e-26	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
580	GM_56_A2_D01_MR	g4063760	BLASTX	256	9e-21	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
581	GM_56_A2_D01_T7	g4063760	BLASTX	343	4e-29	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
582	GM_56_A2_D07_MR	g3142328	BLASTN	621	4e-21	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
583	GM_56_A2_E05_T7	g507910	BLASTN	593	3e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
584	GM_56_A2_E07_MR	g2522227	BLASTX	152	8e-10	46	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
585	GM_56_A2_E09_T7	g2995405	BLASTX	364	9e-44	63	(Y12432) polyprotein [Ananas comosus]
586	GM_56_A2_E11_MR	g505129	BLASTN	348	9e-09	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
587	GM_56_A2_E12_MR	g3914449	BLASTX	204	5e-15	75	26S PROTEASE REGULATORY SUBUNIT 7 (26S PROTEASOME SUBUNIT 7) >gi 3172331 (AF041258) 26S proteasome subunit 7 [Prunus persica]
588	GM_56_A2_F02_T7	g3097320	BLASTN	1265	3e-50	80	Glycine max gene for Bd 30K, complete cds
589	GM_56_A2_F06_T7	g507910	BLASTN	483	3e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
590	GM_56_A2_G02_T7	g1669680	BLASTN	507	7e-16	63	Human DNA sequence from PAC 293E14 contains ESTs, STS
591	GM_56_A2_G07_T7	g2522228	BLASTX	398	2e-36	56	(AB007466) reverse transcriptase-like protein [Vicia faba]
592	GM_56_A2_G08_MR	g4063760	BLASTX	372	3e-32	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
593	GM_56_A2_G09_T7	g2443320	BLASTX	292	1e-23	43	(D85597) polyprotein [Oryza australiensis]
594	GM_56_A2_G12_MR	g507910	BLASTN	453	7e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
595	GM_56_A2_G12_T7	g507910	BLASTN	509	2e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
596	GM_56_A2_H01_T7	g3777527	BLASTX	144	3e-25	42	(AF053008) gag-pol polyprotein [Glycine max]
597	GM_56_A2_H02_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
598	GM_56_A2_H04_MR	g3142328	BLASTN	2184	1e-92	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
599	GM_56_A2_H05_T7	g2443887	BLASTX	187	2e-12	59	(AC002294) Similar to transcription factor gb Z46606 1658307 and others [Arabidopsis thaliana]
600	GM_56_A2_H06_MR	g2564051	BLASTN	515	3e-16	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]
601	GM_56_A2_H07_T7	g3033399	BLASTX	246	3e-19	43	(AC004238) hypothetical protein [Arabidopsis thaliana]
602	GM_56_A2_H08_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
603	GM_56_A2_H08_T7	g4063760	BLASTX	371	4e-32	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
604	GM_56_B1_A04_MR	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
605	GM_56_B1_A04_T7	g507910	BLASTN	374	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
606	GM_56_B1_A05_MR	g968986	BLASTN	365	1e-09	73	Glycine max ferritin gene, nuclear gene encoding chloroplast protein, complete cds
607	GM_56_B1_A05_T7	g3068704	BLASTX	411	1e-43	87	(AF049236) unknown [Arabidopsis thaliana]
608	GM_56_B1_A06_T7	g3820976	BLASTN	427	3e-12	65	Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complet...
609	GM_56_B1_A07_MR	g1171583	BLASTN	376	6e-10	63	P.falciparum complete gene map of plastid-like DNA (IR-A)
610	GM_56_B1_A10_MR	g2801676	BLASTN	755	6e-28	72	Glycine max telomere-associated sequence STAS5
611	GM_56_B1_B02_T7	g280411	BLASTX	178	7e-16	54	hypothetical protein - rice transposon Tos1 (fragment) gi 218244 gnl PID d1002752 (D12825) reverse transcriptase [Oryza sativa]
612	GM_56_B1_B03_T7	g4092471	BLASTN	471	3e-14	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
613	GM_56_B1_B05_MR	g1666236	BLASTX	154	7e-13	30	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
614	GM_56_B1_B07_T7	g1769896	BLASTN	563	2e-18	75	A.thaliana lectin receptor kinase gene
615	GM_56_B1_C01_MR	g100484	BLASTX	166	4e-17	54	hypothetical protein - garden snapdragon
616	GM_56_B1_C08_MR	g2337888	BLASTN	406	3e-11	75	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]
617	GM_56_B1_C09_MR	g507910	BLASTN	633	5e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
618	GM_56_B1_C12_MR	g18559	BLASTN	647	3e-22	71	G.max gene for catalase
619	GM_56_B1_D02_MR	g2129618	BLASTX	225	1e-16	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
620	GM_56_B1_E01_T7	g3319345	BLASTX	209	5e-15	36	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
621	GM_56_B1_E02_T7	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
622	GM_56_B1_E03_MR	g3645899	BLASTX	322	6e-27	56	(U68408) 5' end not determined experimentally [Zea mays]
623	GM_56_B1_E03_T7	g4063760	BLASTX	559	3e-52	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
624	GM_56_B1_E04_T7	g3142328	BLASTN	1287	2e-51	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
625	GM_56_B1_E05_MR	g507910	BLASTN	389	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
626	GM_56_B1_E05_T7	g507910	BLASTN	402	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
627	GM_56_B1_E06_MR	g2443320	BLASTX	117	7e-13	48	(D85597) polyprotein [Oryza australiensis]
628	GM_56_B1_E07_T7	g3426334	BLASTN	554	4e-18	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
629	GM_56_B1_E08_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
630	GM_56_B1_E08_T7	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
631	GM_56_B1_E12_T7	g2245104	BLASTX	174	5e-11	44	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
632	GM_56_B1_F02_T7	g3142328	BLASTN	1088	2e-42	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
633	GM_56_B1_F04_T7	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
634	GM_56_B1_F05_MR	g3930515	BLASTX	113	1e-11	42	(AF059674) putative gag protein [Nicotiana tabacum]
635	GM_56_B1_F08_T7	g507910	BLASTN	454	7e-14	81	Glycine max BSR-101 satellite SB92 genomic sequence.
636	GM_56_B1_F10_MR	g99922	BLASTX	612	5e-59	86	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
637	GM_56_B1_G01_T7	g3142328	BLASTN	1303	4e-52	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
638	GM_56_B1_G08_MR	g3777527	BLASTX	149	2e-09	30	(AF053008) gag-pol polyprotein [Glycine max]
639	GM_56_B1_G09_MR	g3777527	BLASTX	243	3e-18	44	(AF053008) gag-pol polyprotein [Glycine max]
640	GM_56_B1_G12_MR	g507910	BLASTN	591	4e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
641	GM_56_B1_H04_T7	g226407	BLASTX	298	3e-24	52	retrotransposon del1-46 [Lilium henryi]
642	GM_56_B1_H06_MR	g507910	BLASTN	394	3e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
643	GM_56_B1_H06_T7	g3142328	BLASTN	2037	9e-86	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
644	GM_56_B1_H08_T7	g3142328	BLASTN	1999	5e-84	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
645	GM_56_B2_A05_MR	g3869068	BLASTN	359	3e-09	59	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]
646	GM_56_B2_A06_MR	g2924729	BLASTN	697	2e-24	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]
647	GM_56_B2_A08_MR	g3873182	BLASTN	600	5e-20	70	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
648	GM_56_B2_B01_MR	g507910	BLASTN	401	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
649	GM_56_B2_B01_T7	g4063760	BLASTX	105	1e-11	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
650	GM_56_B2_B04_MR	g18559	BLASTN	1035	6e-40	75	G.max gene for catalase
651	GM_56_B2_B04_T7	g3142328	BLASTN	1755	9e-73	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
652	GM_56_B2_B11_T7	g4063760	BLASTX	210	1e-35	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
653	GM_56_B2_B12_T7	g1769899	BLASTX	190	3e-14	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
654	GM_56_B2_C06_T7	g4063760	BLASTX	290	4e-26	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
655	GM_56_B2_C10_T7	g3377855	BLASTX	473	3e-44	72	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
656	GM_56_B2_D04_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
657	GM_56_B2_D04_T7	g507910	BLASTN	555	2e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
658	GM_56_B2_D06_T7	g2522228	BLASTX	336	1e-29	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
659	GM_56_B2_D10_MR	g2129618	BLASTX	276	4e-22	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
660	GM_56_B2_D12_T7	g3777527	BLASTX	201	7e-14	38	(AF053008) gag-pol polyprotein [Glycine max]
661	GM_56_B2_E02_MR	g3142328	BLASTN	538	2e-17	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
662	GM_56_B2_E03_T7	g3777527	BLASTX	413	2e-36	58	(AF053008) gag-pol polyprotein [Glycine max]
663	GM_56_B2_E08_T7	g505129	BLASTN	398	5e-11	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
664	GM_56_B2_E09_MR	g2894612	BLASTX	153	3e-15	56	(AL021889) putative protein [Arabidopsis thaliana]
665	GM_56_B2_E10_MR	g3377816	BLASTX	114	4e-09	35	(AF076275) contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]
666	GM_56_B2_E11_T7	g507910	BLASTN	436	4e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
667	GM_56_B2_E12_T7	g130582	BLASTX	299	2e-24	42	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
668	GM_56_B2_F04_T7	g3241935	BLASTN	517	3e-16	64	Arabidopsis thaliana chromosome IV from 19 cM, complete sequence [Arabidopsis thaliana]
669	GM_56_B2_F06_MR	g2961349	BLASTX	279	2e-22	44	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
670	GM_56_B2_G01_MR	g2924341	BLASTN	478	8e-15	63	Saccharomyces cerevisiae mitochondrial Tyr-tRNA, Asn-tRNA and Met-tRNA genes
671	GM_56_B2_G03_T7	g629693	BLASTX	305	2e-26	48	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
672	GM_56_B2_G10_MR	g3097320	BLASTN	632	1e-21	86	Glycine max gene for Bd 30K, complete cds
673	GM_56_B2_G12_T7	g100484	BLASTX	248	2e-19	57	hypothetical protein - garden snapdragon
674	GM_56_B2_H02_T7	g2245004	BLASTX	283	2e-23	53	(Z97341) similarity to membrane transport protein [Arabidopsis thaliana]
675	GM_56_B2_H04_T7	g18768	BLASTN	408	4e-12	68	Soybean Tgm6 transposable element 3' end
676	GM_56_B2_H05_MR	g3319351	BLASTX	271	2e-21	43	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
677	GM_56_B2_H08_T7	g342963	BLASTN	479	3e-15	67	paramecium species 5,87 mt dna dimer: replication init. region.
678	GM_56_B2_H12_MR	g1840106	BLASTN	396	1e-11	62	Human fragile site locus (FRA16B) minisatellite repeat
679	GM_57_A1_A02_T7	g99726	BLASTX	138	1e-08	52	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976) orf 3 [Arabidopsis thaliana]
680	GM_57_A1_A05_MR	g3746069	BLASTX	237	9e-18	33	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
681	GM_57_A1_B03_T7	g3777527	BLASTX	237	1e-17	93	(AF053008) gag-pol polyprotein [Glycine max]
682	GM_57_A1_B05_MR	g1769897	BLASTX	257	1e-20	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
683	GM_57_A1_C04_MR	g507910	BLASTN	555	2e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
684	GM_57_A1_C05_T7	g2982452	BLASTX	211	4e-15	68	(AL022223) receptor protein kinase - like protein [Arabidopsis thaliana]
685	GM_57_A1_D02_MR	g2335100	BLASTX	465	9e-43	59	(AC002339) unknown protein [Arabidopsis thaliana]
686	GM_57_A1_D05_MR	g3097320	BLASTN	1148	6e-45	81	Glycine max gene for Bd 30K, complete cds
687	GM_57_A1_D05_T7	g2995405	BLASTX	230	3e-17	67	(Y12432) polyprotein [Ananas comosus]
688	GM_57_A1_D11_MR	g507910	BLASTN	438	4e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
689	GM_57_A1_E06_MR	g3426334	BLASTN	367	1e-09	69	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
690	GM_57_A1_E07_MR	g2642445	BLASTX	87	5e-10	55	(AC002391) putative serine/threonine protein kinase [Arabidopsis thaliana]
691	GM_57_A1_E08_MR	g2462134	BLASTX	190	2e-13	28	(Y13368) reverse transcriptase [Beta vulgaris]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
692	GM_57_A1_E08_T7	g1167523	BLASTX	211	6e-15	64	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
693	GM_57_A1_F10_MR	g2129618	BLASTX	257	2e-21	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
694	GM_57_A1_G09_MR	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
695	GM_57_A1_G11_MR	g1707007	BLASTX	256	3e-20	32	(U78721) hypothetical protein [Arabidopsis thaliana]
696	GM_57_A1_H01_MR	g3097320	BLASTN	707	6e-25	73	Glycine max gene for Bd 30K, complete cds
697	GM_57_A1_H10_MR	g2853072	BLASTX	453	4e-42	61	(AL021768) putative protein [Arabidopsis thaliana]
698	GM_57_A2_A01_MR	g130582	BLASTX	315	3e-28	57	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
699	GM_57_A2_A02_T7	g2996647	BLASTN	509	6e-16	66	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
700	GM_57_A2_A03_MR	g4063760	BLASTX	460	1e-41	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
701	GM_57_A2_A03_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
702	GM_57_A2_A05_MR	g507910	BLASTN	615	4e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
703	GM_57_A2_A05_T7	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
704	GM_57_A2_B01_T7	g3319362	BLASTX	101	6e-09	30	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
705	GM_57_A2_B03_MR	g507910	BLASTN	407	9e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
706	GM_57_A2_B03_T7	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
707	GM_57_A2_B04_MR	g18559	BLASTN	1043	3e-40	75	G.max gene for catalase
708	GM_57_A2_B05_MR	g18559	BLASTN	865	3e-32	75	G.max gene for catalase
709	GM_57_A2_B08_MR	g421955	BLASTX	325	1e-28	48	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
710	GM_57_A2_B08_T7	g3063465	BLASTX	224	9e-17	51	(AC003981) F22O13.27 [Arabidopsis thaliana]
711	GM_57_A2_B10_MR	g3241854	BLASTX	542	2e-51	62	(AB006009) thaumatin-like protein precursor [Pyrus pyrifolia]
712	GM_57_A2_B10_T7	g1769897	BLASTX	142	1e-10	33	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
713	GM_57_A2_B11_MR	g99922	BLASTX	270	1e-22	53	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
714	GM_57_A2_B12_MR	g2462058	BLASTX	290	7e-25	50	(Y13389) reverse transcriptase [Antirrhinum majus]
715	GM_57_A2_C01_MR	g99922	BLASTX	442	6e-41	64	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
716	GM_57_A2_C05_MR	g1663549	BLASTX	300	8e-30	52	(U55809) disease resistance protein homolog [Glycine max]
717	GM_57_A2_C05_T7	g3935164	BLASTX	101	1e-11	57	(AC004557) F17L21.7 [Arabidopsis thaliana]
718	GM_57_A2_C07_MR	g387902	BLASTX	244	4e-26	53	(L23524) ORF [Hordeum vulgare]
719	GM_57_A2_C08_MR	g3426334	BLASTN	374	7e-10	65	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
720	GM_57_A2_C08_T7	g170606	BLASTN	879	2e-33	68	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
721	GM_57_A2_C09_MR	g170080	BLASTN	358	3e-09	67	Soybean seed lectin gene transposable element tgm1.
722	GM_57_A2_C09_T7	g13767	BLASTN	344	2e-09	64	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
723	GM_57_A2_C12_T7	g1619956	BLASTX	120	5e-13	71	(U72151) voltage-gated chloride channel [Arabidopsis thaliana]
724	GM_57_A2_D01_MR	g2465923	BLASTX	194	2e-15	55	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]
725	GM_57_A2_D06_T7	g507910	BLASTN	498	7e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
726	GM_57_A2_D07_MR	g3142328	BLASTN	1916	3e-80	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
727	GM_57_A2_D07_T7	g4063770	BLASTX	130	5e-14	43	(AB004906) transposase [Ipomoea purpurea]
728	GM_57_A2_E03_MR	g3319362	BLASTX	345	2e-29	49	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
729	GM_57_A2_E04_T7	g2462936	BLASTX	236	4e-24	56	(Y12321) open reading frame 2 [Brassica oleracea]
730	GM_57_A2_E07_T7	g3250673	BLASTN	381	4e-10	68	Arabidopsis thaliana DNA chromosome 4, BAC clone T16H5 (ESSAII project)
731	GM_57_A2_E09_T7	g3451066	BLASTX	333	2e-29	60	(AL031326) hypothetical protein [Arabidopsis thaliana]
732	GM_57_A2_E10_T7	g3097320	BLASTN	458	1e-13	69	Glycine max gene for Bd 30K, complete cds
733	GM_57_A2_E11_T7	g3097320	BLASTN	506	7e-16	70	Glycine max gene for Bd 30K, complete cds
734	GM_57_A2_F04_MR	g507910	BLASTN	500	6e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
735	GM_57_A2_F08_T7	g2895628	BLASTN	343	9e-09	67	Pieris rapae large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
736	GM_57_A2_F11_MR	g3777527	BLASTX	199	2e-18	92	(AF053008) gag-pol polyprotein [Glycine max]
737	GM_57_A2_F11_T7	g507910	BLASTN	623	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
738	GM_57_A2_G02_MR	g3335341	BLASTX	254	2e-20	43	(AC004512) T8F5.10 [Arabidopsis thaliana]
739	GM_57_A2_G04_MR	g507910	BLASTN	565	6e-19	79	Glycine max BSR-101 satellite SB92 genomic sequence.
740	GM_57_A2_G04_T7	g507910	BLASTN	601	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
741	GM_57_A2_G06_MR	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
742	GM_57_A2_G06_T7	g4063760	BLASTX	298	6e-48	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
743	GM_57_A2_H01_MR	g3599418	BLASTN	353	6e-09	83	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
744	GM_57_A2_H03_MR	g3135962	BLASTN	457	1e-13	64	Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
745	GM_57_A2_H04_MR	g1171591	BLASTN	269	8e-09	63	P.falciparum complete gene map of plastid-like DNA (IR-B)
746	GM_57_A2_H08_MR	g1785744	BLASTX	359	4e-32	57	(Y08502) orf158 [Arabidopsis thaliana]
747	GM_57_A2_H08_T7	g3097320	BLASTN	402	4e-11	71	Glycine max gene for Bd 30K, complete cds
748	GM_57_A2_H10_MR	g349378	BLASTN	237	3e-09	72	Helianthus annuus homeodomain containing protein (HAHB-1) mRNA, partial cds.
749	GM_57_A2_H12_MR	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
750	GM_57_A2_H12_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
751	GM_57_B1_A04_T7	g2660670	BLASTX	100	2e-14	64	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]
752	GM_57_B1_A08_T7	g2764525	BLASTN	483	6e-15	65	Pisum sativum genomic DNA encoding truncated Ty3/Gypsy-like retroelement Cyclops-1
753	GM_57_B1_A10_T7	g507910	BLASTN	368	5e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
754	GM_57_B1_B02_MR	g3021268	BLASTX	234	6e-25	63	(AL022347) putative protein [Arabidopsis thaliana]
755	GM_57_B1_B03_T7	g3695387	BLASTX	225	1e-16	64	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
756	GM_57_B1_B08_MR	g2583128	BLASTX	152	2e-09	66	(AC002387) hypothetical protein [Arabidopsis thaliana]
757	GM_57_B1_C03_MR	g3097320	BLASTN	419	6e-12	78	Glycine max gene for Bd 30K, complete cds
758	GM_57_B1_C03_T7	g2522230	BLASTX	162	3e-11	32	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
759	GM_57_B1_C06_T7	g2252634	BLASTX	172	3e-11	41	(U95973) hypothetical protein [Arabidopsis thaliana]
760	GM_57_B1_D02_MR	g3845314	BLASTN	430	2e-12	61	Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence
761	GM_57_B1_D06_MR	g3777527	BLASTX	612	1e-57	85	(AF053008) gag-pol polyprotein [Glycine max]
762	GM_57_B1_E01_MR	g4038056	BLASTX	163	3e-20	55	(AC005897) putative transposon [Arabidopsis thaliana]
763	GM_57_B1_E03_MR	g4063760	BLASTX	196	2e-13	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
764	GM_57_B1_E09_T7	g3695387	BLASTX	222	3e-16	64	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
765	GM_57_B1_E10_MR	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
766	GM_57_B1_F05_T7	g3059060	BLASTN	385	2e-10	63	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
767	GM_57_B1_F06_T7	g18559	BLASTN	710	4e-25	72	G.max gene for catalase
768	GM_57_B1_F10_MR	g18559	BLASTN	464	5e-14	70	G.max gene for catalase
769	GM_57_B1_F10_T7	g2522228	BLASTX	398	3e-36	76	(AB007466) reverse transcriptase-like protein [Vicia faba]
770	GM_57_B1_G06_MR	g4063760	BLASTX	227	9e-17	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
771	GM_57_B1_G06_T7	g507910	BLASTN	583	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
772	GM_57_B1_G07_MR	g18700	BLASTN	683	4e-24	77	Soybean nodulin-23 gene

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
773	GM_57_B1_G09_MR	g2462936	BLASTX	166	1e-11	40	(Y12321) open reading frame 2 [Brassica oleracea]
774	GM_57_B1_G09_T7	g3319362	BLASTX	185	4e-28	50	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
775	GM_57_B1_G10_T7	g1167523	BLASTX	193	5e-23	54	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
776	GM_57_B1_H01_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
777	GM_57_B1_H01_T7	g507910	BLASTN	354	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
778	GM_57_B2_A01_MR	g2633727	BLASTX	200	1e-14	58	(Z99111) ykrT [Bacillus subtilis]
779	GM_57_B2_A04_T7	g226407	BLASTX	203	4e-14	39	retrotransposon del1-46 [Lilium henryi]
780	GM_57_B2_A05_T7	g3947437	BLASTN	366	2e-09	64	Homo sapiens BAC clone NH0342K06 from 2, complete sequence [Homo sapiens]
781	GM_57_B2_A10_T7	g507910	BLASTN	495	9e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
782	GM_57_B2_A12_MR	g3097320	BLASTN	942	1e-35	78	Glycine max gene for Bd 30K, complete cds
783	GM_57_B2_B07_MR	g3367534	BLASTX	533	2e-49	83	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis thaliana]
784	GM_57_B2_B08_MR	g3930515	BLASTX	121	4e-13	47	(AF059674) putative gag protein [Nicotiana tabacum]
785	GM_57_B2_B09_MR	g18559	BLASTN	947	6e-36	74	G.max gene for catalase
786	GM_57_B2_B12_T7	g3319362	BLASTX	103	4e-09	32	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
787	GM_57_B2_C03_T7	g4063756	BLASTN	377	5e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
788	GM_57_B2_C05_MR	g2160155	BLASTN	374	7e-10	64	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
789	GM_57_B2_C10_MR	g18559	BLASTN	744	1e-26	73	G.max gene for catalase
790	GM_57_B2_C10_T7	g3777527	BLASTX	334	5e-28	49	(AF053008) gag-pol polyprotein [Glycine max]
791	GM_57_B2_D02_MR	g2367675	BLASTX	169	1e-10	31	(AF017040) Pol [Dictyostelium discoideum]
792	GM_57_B2_D02_T7	g100484	BLASTX	252	1e-21	50	hypothetical protein - garden snapdragon
793	GM_57_B2_D04_MR	g173088	BLASTX	180	1e-11	35	has homology to retroviral pol genes; ORF2 TYB3-2 (5' end of coding region not precisely determined)
794	GM_57_B2_D05_MR	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
795	GM_57_B2_D06_MR	g3510505	BLASTX	234	2e-17	36	(AF030881) pol polyprotein [Fugu rubripes]
796	GM_57_B2_D06_T7	g2129618	BLASTX	159	1e-09	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
797	GM_57_B2_D07_T7	g3930515	BLASTX	120	2e-12	47	(AF059674) putative gag protein [Nicotiana tabacum]
798	GM_57_B2_D08_MR	g2494115	BLASTX	98	2e-13	100	(AC002376) Strong similarity to Arabidopsis ATHSAR1 (gb M90418). ESTs gb T44122,gb N65276,gb AA041135 come from this gene. [Arabidopsis thaliana]
799	GM_57_B2_D09_MR	g3785992	BLASTN	411	2e-11	64	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
800	GM_57_B2_E03_MR	g1871190	BLASTX	307	1e-26	52	(U90439) Ser/Thr kinase isolog [Arabidopsis thaliana]
801	GM_57_B2_E05_T7	g3935164	BLASTX	157	9e-11	43	(AC004557) F17L21.7 [Arabidopsis thaliana]
802	GM_57_B2_E06_T7	g2522230	BLASTX	246	4e-20	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
803	GM_57_B2_E09_T7	g18559	BLASTN	936	2e-35	76	G.max gene for catalase
804	GM_57_B2_F02_MR	g2642661	BLASTX	204	1e-14	63	(AF034545) copalyl pyrophosphate synthase [Stevia rebaudiana]
805	GM_57_B2_F05_T7	g3645899	BLASTX	209	7e-15	52	(U68408) 5' end not determined experimentally [Zea mays]
806	GM_57_B2_F08_MR	g2462134	BLASTX	115	5e-15	36	(Y13368) reverse transcriptase [Beta vulgaris]
807	GM_57_B2_F12_T7	g3599418	BLASTN	723	9e-26	83	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
808	GM_57_B2_G01_T7	g4063760	BLASTX	323	3e-30	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
809	GM_57_B2_G06_T7	g3142328	BLASTN	1038	4e-40	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
810	GM_57_B2_G08_MR	g3702324	BLASTX	209	1e-15	39	(AC005397) hypothetical protein [Arabidopsis thaliana]
811	GM_57_B2_G09_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
812	GM_57_B2_G09_T7	g507910	BLASTN	398	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
813	GM_57_B2_H01_T7	g1277164	BLASTX	287	1e-24	98	(U51853) cysteine proteinase inhibitor [Glycine max]
814	GM_57_B2_H02_MR	g2367675	BLASTX	169	1e-10	31	(AF017040) Pol [Dictyostelium discoideum]
815	GM_57_B2_H02_T7	g100484	BLASTX	260	1e-23	51	hypothetical protein - garden snapdragon
816	GM_57_B2_H05_T7	g1769897	BLASTX	315	2e-34	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
817	GM_57_B2_H06_MR	g421954	BLASTX	160	6e-10	50	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
818	GM_57_B2_H08_T7	g4038056	BLASTX	350	4e-30	51	(AC005897) putative transposon [Arabidopsis thaliana]
819	GM_57_B2_H09_MR	g2246449	BLASTN	352	7e-09	64	Lycopersicon esculentum copia-like retrotransposon ToRTL1, 3-hydroxy-3-methylglutaryl CoA reductase 2 (HMG2) gene, complete cds.
820	GM_57_B2_H11_T7	g3645899	BLASTX	233	2e-26	53	(U68408) 5' end not determined experimentally [Zea mays]
821	GM_58_A1_A03_T7	g3142328	BLASTN	1374	2e-55	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
822	GM_58_A1_A04_MR	g505129	BLASTN	413	1e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
823	GM_58_A1_A04_T7	g3142328	BLASTN	1681	2e-69	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
824	GM_58_A1_A05_MR	g3758836	BLASTN	372	9e-10	60	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
825	GM_58_A1_A08_T7	g2982529	BLASTN	374	7e-10	60	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-09, complete sequence [Plasmodium falciparum]
826	GM_58_A1_A09_MR	g18559	BLASTN	1299	6e-52	74	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
827	GM_58_A1_A10_T7	g2618684	BLASTX	184	6e-13	85	(AC002510) putative UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase [Arabidopsis thaliana] gi 3241947 (AC004625) putative UDP-N-acetylglucosamine--dolichyl-phosphate N-acetylglucosaminephosphotransferase [Arabidopsis thaliana]
828	GM_58_A1_A12_MR	g4160362	BLASTN	269	6e-09	63	Saccharomyces cerevisiae complete mitochondrial genome
829	GM_58_A1_A12_T7	g3810596	BLASTX	124	7e-12	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
830	GM_58_A1_B01_MR	g507910	BLASTN	553	2e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
831	GM_58_A1_B04_MR	g3142328	BLASTN	1112	2e-43	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
832	GM_58_A1_B08_MR	g3142379	BLASTX	308	1e-26	65	(AF053008) envelope-like [Glycine max]
833	GM_58_A1_B08_T7	g507910	BLASTN	348	4e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
834	GM_58_A1_B09_MR	g18695	BLASTN	392	1e-13	72	Soybean nodulin 22 gene
835	GM_58_A1_B11_MR	g2708743	BLASTX	183	2e-13	36	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
836	GM_58_A1_B11_T7	g4063760	BLASTX	164	5e-10	25	(AC005561) putative POL3 protein [Arabidopsis thaliana]
837	GM_58_A1_C01_T7	g3097320	BLASTN	758	3e-27	71	Glycine max gene for Bd 30K, complete cds
838	GM_58_A1_C04_MR	g3478637	BLASTX	154	3e-09	57	(AC005546) R29425_1 [Homo sapiens]
839	GM_58_A1_C05_MR	g2961349	BLASTX	321	8e-27	44	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
840	GM_58_A1_C05_T7	g18559	BLASTN	1427	1e-57	76	G.max gene for catalase
841	GM_58_A1_C08_T7	g3080353	BLASTX	165	4e-11	66	(AL022580) cytochrome P450 [Arabidopsis thaliana]
842	GM_58_A1_C09_MR	g3777527	BLASTX	821	5e-80	81	(AF053008) gag-pol polyprotein [Glycine max]
843	GM_58_A1_C10_MR	g3645899	BLASTX	395	9e-35	44	(U68408) 5' end not determined experimentally [Zea mays]
844	GM_58_A1_C11_T7	g3033389	BLASTX	233	2e-17	40	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
845	GM_58_A1_D01_T7	g3645899	BLASTX	479	9e-44	56	(U68408) 5' end not determined experimentally [Zea mays]
846	GM_58_A1_D06_T7	g1769898	BLASTX	302	2e-33	39	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
847	GM_58_A1_D07_MR	g3758836	BLASTN	362	3e-09	61	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
848	GM_58_A1_D07_T7	g13096	BLASTN	442	5e-13	65	Leishmania tarentolae maxicircle DNA fragment
849	GM_58_A1_D09_T7	g130582	BLASTX	141	2e-13	42	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
850	GM_58_A1_E02_T7	g3142328	BLASTN	1673	5e-69	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
851	GM_58_A1_E04_T7	g1666236	BLASTX	183	3e-25	31	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
852	GM_58_A1_E05_MR	g3176803	BLASTN	506	9e-17	62	Homo sapiens allele 15 fragile site locus (FRA10B) minisatellite sequence
853	GM_58_A1_E06_MR	g3831469	BLASTX	154	3e-09	26	(AC005700) hypothetical protein [Arabidopsis thaliana]
854	GM_58_A1_E09_MR	g1076414	BLASTX	401	7e-36	47	subtilisin-like proteinase (EC 3.4.21.-) - Arabidopsis thaliana (fragment) gi 757534 (X85974) subtilisin-like protease [Arabidopsis thaliana]
855	GM_58_A1_E10_MR	g1840106	BLASTN	473	2e-15	61	Human fragile site locus (FRA16B) minisatellite repeat
856	GM_58_A1_E12_T7	g3645899	BLASTX	522	2e-48	60	(U68408) 5' end not determined experimentally [Zea mays]
857	GM_58_A1_F03_T7	g507910	BLASTN	435	5e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
858	GM_58_A1_F06_T7	g18559	BLASTN	1075	1e-41	75	G.max gene for catalase
859	GM_58_A1_F08_T7	g3142328	BLASTN	775	5e-57	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
860	GM_58_A1_F09_T7	g3777527	BLASTX	896	5e-88	95	(AF053008) gag-pol polyprotein [Glycine max]
861	GM_58_A1_F12_MR	g1171583	BLASTN	602	4e-20	63	P.falciparum complete gene map of plastid-like DNA (IR-A)
862	GM_58_A1_G01_T7	g3492889	BLASTN	396	7e-11	61	Homo sapiens chromosome 17, clone hRPK.746_E_8, complete sequence [Homo sapiens]
863	GM_58_A1_G04_MR	g4150930	BLASTN	496	2e-15	61	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
864	GM_58_A1_G07_MR	g2827715	BLASTX	263	1e-20	47	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
865	GM_58_A1_G10_MR	g4063760	BLASTX	254	1e-19	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
866	GM_58_A1_G10_T7	g507910	BLASTN	738	1e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
867	GM_58_A1_G12_MR	g4063770	BLASTX	231	2e-17	39	(AB004906) transposase [Ipomoea purpurea]
868	GM_58_A1_H01_MR	g2462134	BLASTX	272	2e-28	43	(Y13368) reverse transcriptase [Beta vulgaris]
869	GM_58_A1_H05_MR	g2104683	BLASTX	201	3e-14	56	(X97908) transcription factor [Vicia faba]
870	GM_58_A1_H06_MR	g576756	BLASTN	488	1e-15	63	Myrmecia pilosula HI87-133 mitochondrion cytochrome b gene, partial cds.
871	GM_58_A1_H07_T7	g3281868	BLASTX	484	2e-45	63	(AL031004) putative protein [Arabidopsis thaliana]
872	GM_58_A1_H08_MR	g2129618	BLASTX	215	1e-15	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
873	GM_58_A1_H08_T7	g2129618	BLASTX	187	1e-12	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
874	GM_58_A1_H10_MR	g3142328	BLASTN	1181	1e-46	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
875	GM_58_A2_A01_MR	g4063760	BLASTX	516	1e-47	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
876	GM_58_A2_A04_T7	g3097320	BLASTN	707	6e-25	77	Glycine max gene for Bd 30K, complete cds
877	GM_58_A2_A07_T7	g4063760	BLASTX	310	1e-25	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
878	GM_58_A2_A10_MR	g507910	BLASTN	629	8e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
879	GM_58_A2_A10_T7	g507910	BLASTN	405	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
880	GM_58_A2_B03_T7	g2342686	BLASTX	179	2e-19	46	(AC000106) Similar to Saccharomyces hypothetical protein YDR051c (gb Z49209). ESTs gb T44436,gb 42252 come from this gene. [Arabidopsis thaliana]
881	GM_58_A2_B04_MR	g3461840	BLASTX	299	3e-24	38	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
882	GM_58_A2_B04_T7	g3599418	BLASTN	360	3e-09	81	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
883	GM_58_A2_B11_T7	g531389	BLASTX	224	3e-16	46	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
884	GM_58_A2_B12_MR	g130582	BLASTX	207	1e-14	40	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
885	GM_58_A2_C02_T7	g4063760	BLASTX	613	5e-58	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
886	GM_58_A2_C06_MR	g3097320	BLASTN	636	9e-22	77	Glycine max gene for Bd 30K, complete cds
887	GM_58_A2_D01_MR	g3097320	BLASTN	914	2e-34	79	Glycine max gene for Bd 30K, complete cds
888	GM_58_A2_D03_T7	g3777527	BLASTX	786	3e-76	96	(AF053008) gag-pol polyprotein [Glycine max]
889	GM_58_A2_D08_MR	g2829923	BLASTX	153	2e-09	67	(AC002291) Similar to uridylyl transferases [Arabidopsis thaliana]
890	GM_58_A2_E03_T7	g2522228	BLASTX	197	2e-14	51	(AB007466) reverse transcriptase-like protein [Vicia faba]
891	GM_58_A2_E04_MR	g18559	BLASTN	679	2e-38	79	G.max gene for catalase
892	GM_58_A2_E04_T7	g905361	BLASTX	411	3e-37	91	(U22103) gag-protease polyprotein [Glycine max]
893	GM_58_A2_E11_T7	g2564750	BLASTN	359	3e-09	69	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
894	GM_58_A2_F02_T7	g3337395	BLASTN	351	8e-09	61	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
895	GM_58_A2_F03_MR	g2995405	BLASTX	145	3e-24	63	(Y12432) polyprotein [Ananas comosus]
896	GM_58_A2_F04_T7	g2522228	BLASTX	217	1e-16	63	(AB007466) reverse transcriptase-like protein [Vicia faba]
897	GM_58_A2_F06_MR	g632992	BLASTN	421	5e-12	64	Homo sapiens interleukin 9 receptor precursor (IL9R) gene, complete cds
898	GM_58_A2_F07_MR	g4063760	BLASTX	493	3e-45	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
899	GM_58_A2_F07_T7	g507910	BLASTN	367	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
900	GM_58_A2_F08_MR	g3452140	BLASTX	416	3e-38	78	(AJ004901) resistance protein [Glycine max]
901	GM_58_A2_F09_MR	g665934	BLASTX	204	1e-14	35	(U20341) ORF III [Cassava vein mosaic virus] gi 1399884 (U59751) ORF 3 [Cassava vein mosaic virus]
902	GM_58_A2_F09_T7	g3097320	BLASTN	404	3e-11	68	Glycine max gene for Bd 30K, complete cds
903	GM_58_A2_G01_MR	g1899158	BLASTN	560	1e-18	65	Saccharomyces cerevisiae synthetic green fluorescent protein (cox3::GFPm) gene, mitochondrial gene construct, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
904	GM_58_A2_G02_MR	g529353	BLASTX	224	6e-17	47	(U12757) diphenol oxidase [Acer pseudoplatanus]
905	GM_58_A2_G03_MR	g3334663	BLASTX	244	3e-19	95	(Y10491) putative cytochrome P450 [Glycine max]
906	GM_58_A2_G04_MR	g2995405	BLASTX	325	2e-27	53	(Y12432) polyprotein [Ananas comosus]
907	GM_58_A2_G05_MR	g4063756	BLASTN	455	2e-13	71	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
908	GM_58_A2_G07_MR	g3097320	BLASTN	1445	2e-58	82	Glycine max gene for Bd 30K, complete cds
909	GM_58_A2_G09_MR	g4160362	BLASTN	313	7e-10	60	Saccharomyces cerevisiae complete mitochondrial genome
910	GM_58_A2_G12_T7	g629693	BLASTX	146	7e-09	41	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
911	GM_58_A2_H02_MR	g529353	BLASTX	289	5e-24	48	(U12757) diphenol oxidase [Acer pseudoplatanus]
912	GM_58_A2_H08_MR	g2281092	BLASTX	236	4e-19	72	(AC002333) hypothetical protein [Arabidopsis thaliana]
913	GM_58_A2_H09_T7	g18559	BLASTN	354	5e-09	75	G.max gene for catalase
914	GM_58_B1_A04_T7	g2522230	BLASTX	255	4e-21	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
915	GM_58_B1_A05_MR	g100484	BLASTX	349	3e-30	55	hypothetical protein - garden snapdragon
916	GM_58_B1_A10_MR	g507910	BLASTN	540	8e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
917	GM_58_B1_A10_T7	g4063760	BLASTX	412	2e-36	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
918	GM_58_B1_B01_MR	g3319362	BLASTX	154	4e-09	42	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
919	GM_58_B1_B03_MR	g3810596	BLASTX	274	6e-22	43	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
920	GM_58_B1_B05_MR	g3033389	BLASTX	185	2e-12	32	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
921	GM_58_B1_B08_MR	g3979928	BLASTN	413	1e-11	67	Caenorhabditis elegans cosmid Y18D10A, complete sequence [Caenorhabditis elegans]
922	GM_58_B1_B09_MR	g3097320	BLASTN	765	1e-27	72	Glycine max gene for Bd 30K, complete cds
923	GM_58_B1_B11_MR	g4140712	BLASTX	138	2e-21	59	(AF110183) putative integrase [Oryza sativa]
924	GM_58_B1_C02_MR	g3097320	BLASTN	903	7e-34	78	Glycine max gene for Bd 30K, complete cds
925	GM_58_B1_C06_MR	g3097320	BLASTN	1222	3e-48	81	Glycine max gene for Bd 30K, complete cds
926	GM_58_B1_C08_T7	g4140712	BLASTX	303	3e-26	59	(AF110183) putative integrase [Oryza sativa]
927	GM_58_B1_D10_MR	g507910	BLASTN	342	7e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
928	GM_58_B1_D10_T7	g507910	BLASTN	346	5e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
929	GM_58_B1_E01_T7	g3097320	BLASTN	1191	6e-47	77	Glycine max gene for Bd 30K, complete cds
930	GM_58_B1_E02_T7	g18559	BLASTN	1085	3e-42	78	G.max gene for catalase
931	GM_58_B1_E04_MR	g507910	BLASTN	433	6e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
932	GM_58_B1_E04_T7	g3142379	BLASTX	422	7e-41	64	(AF053008) envelope-like [Glycine max]
933	GM_58_B1_E06_T7	g18559	BLASTN	726	7e-26	73	G.max gene for catalase
934	GM_58_B1_E07_MR	g905361	BLASTX	421	2e-38	95	(U22103) gag-protease polyprotein [Glycine max]
935	GM_58_B1_F01_MR	g507910	BLASTN	444	2e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
936	GM_58_B1_F01_T7	g3142330	BLASTX	467	1e-43	67	(U96295) envelope-like [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
937	GM_58_B1_F07_MR	g18559	BLASTN	950	5e-36	76	G.max gene for catalase
938	GM_58_B1_F08_T7	g3097320	BLASTN	589	1e-19	73	Glycine max gene for Bd 30K, complete cds
939	GM_58_B1_G04_MR	g399940	BLASTX	328	4e-46	100	MITOCHONDRIAL HEAT SHOCK 70 KD PROTEIN PRECURSOR gi 100004 pir S25005 heat shock protein, 70K - kidney bean gi 22636 (X66874) 70 kDa heat shock protein [Phaseolus vulgaris]
940	GM_58_B1_G05_T7	g3645899	BLASTX	172	5e-11	50	(U68408) 5' end not determined experimentally [Zea mays]
941	GM_58_B1_G09_MR	g3426334	BLASTN	404	3e-11	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
942	GM_58_B1_G09_T7	g18559	BLASTN	866	3e-32	85	G.max gene for catalase
943	GM_58_B1_H01_T7	g2129618	BLASTX	204	2e-14	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
944	GM_58_B1_H02_T7	g2443320	BLASTX	292	1e-23	50	(D85597) polyprotein [Oryza australiensis]
945	GM_58_B1_H04_MR	g2924257	BLASTN	478	1e-14	82	Tobacco chloroplast genome DNA
946	GM_58_B1_H07_T7	g3426334	BLASTN	432	2e-12	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
947	GM_58_B2_A01_T7	g4063760	BLASTX	181	8e-12	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
948	GM_58_B2_A06_MR	g3097320	BLASTN	1197	3e-47	81	Glycine max gene for Bd 30K, complete cds
949	GM_58_B2_A07_MR	g905361	BLASTX	172	3e-11	37	(U22103) gag-protease polyprotein [Glycine max]
950	GM_58_B2_A10_MR	g3097320	BLASTN	857	9e-32	73	Glycine max gene for Bd 30K, complete cds
951	GM_58_B2_A10_T7	g84801	BLASTX	252	2e-19	36	hypothetical protein 2 - silkworm transposon mag
952	GM_58_B2_B02_T7	g2764526	BLASTN	531	6e-17	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
953	GM_58_B2_B03_T7	g2764526	BLASTN	528	8e-17	65	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
954	GM_58_B2_B04_T7	g629693	BLASTX	370	2e-33	58	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
955	GM_58_B2_B12_T7	g2522228	BLASTX	262	1e-21	50	(AB007466) reverse transcriptase-like protein [Vicia faba]
956	GM_58_B2_C01_T7	g1144551	BLASTN	337	6e-09	60	Anopheles melas 12S ribosomal RNA, D-loop, and tRNA-Ile mitochondrial genes, partial sequence.
957	GM_58_B2_C02_T7	g1666236	BLASTX	163	7e-11	27	(U76261) unknown [Hordeum vulgare]
958	GM_58_B2_C04_MR	g2656026	BLASTN	371	1e-09	77	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20
959	GM_58_B2_C05_MR	g3283026	BLASTX	223	5e-19	40	putative transposase [Arabidopsis thaliana]
960	GM_58_B2_C05_T7	g3820757	BLASTN	452	1e-13	66	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
961	GM_58_B2_C07_MR	g507910	BLASTN	499	6e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
962	GM_58_B2_C07_T7	g3097320	BLASTN	348	1e-08	72	Glycine max gene for Bd 30K, complete cds
963	GM_58_B2_C11_T7	g507910	BLASTN	355	2e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
964	GM_58_B2_E01_T7	g3777527	BLASTX	150	9e-21	45	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
965	GM_58_B2_E03_MR	g4063760	BLASTX	249	9e-33	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
966	GM_58_B2_E03_T7	g4063760	BLASTX	115	2e-12	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
967	GM_58_B2_E04_MR	g170605	BLASTN	542	7e-18	65	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
968	GM_58_B2_E05_T7	g3645899	BLASTX	211	4e-15	33	(U68408) 5' end not determined experimentally [Zea mays]
969	GM_58_B2_E06_MR	g1666236	BLASTX	177	2e-12	35	(U76261) unknown [Hordeum vulgare]
970	GM_58_B2_E08_MR	g3142328	BLASTN	1115	1e-43	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
971	GM_58_B2_E08_T7	g2655309	BLASTN	344	8e-09	66	Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence
972	GM_58_B2_E11_MR	g507910	BLASTN	635	4e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
973	GM_58_B2_E12_MR	g2522227	BLASTX	150	1e-09	38	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
974	GM_58_B2_F01_MR	g2264320	BLASTN	543	2e-17	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
975	GM_58_B2_F04_MR	g3033389	BLASTX	172	5e-11	32	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
976	GM_58_B2_F05_T7	g2809247	BLASTX	122	1e-10	36	(AC002560) F21B7.16 [Arabidopsis thaliana]
977	GM_58_B2_F07_T7	g3176804	BLASTN	378	6e-11	62	Homo sapiens allele 15 fragile site locus (FRA10B) minisatellite, 3' sequence
978	GM_58_B2_F08_MR	g507910	BLASTN	380	1e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
979	GM_58_B2_F08_T7	g507910	BLASTN	349	4e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
980	GM_58_B2_F09_T7	g2129618	BLASTX	233	2e-17	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
981	GM_58_B2_F11_T7	g507910	BLASTN	588	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
982	GM_58_B2_G04_MR	g507910	BLASTN	491	1e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
983	GM_58_B2_G04_T7	g507910	BLASTN	481	4e-15	79	Glycine max BSR-101 satellite SB92 genomic sequence.
984	GM_58_B2_G09_MR	g905361	BLASTX	223	9e-17	37	(U22103) gag-protease polyprotein [Glycine max]
985	GM_58_B2_G09_T7	g3650039	BLASTX	250	6e-25	56	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
986	GM_58_B2_G12_MR	g1666236	BLASTX	147	4e-09	30	(U76261) unknown [Hordeum vulgare]
987	GM_59_A1_A03_T7	g3834313	BLASTX	220	2e-17	76	(AC005679) Strong similarity to T16B12.3 gi 3746060 unknown protein from Arabidopsis thaliana BAC gb AC005311. [Arabidopsis thaliana]
988	GM_59_A1_A06_MR	g18559	BLASTN	655	1e-22	72	G.max gene for catalase
989	GM_59_A1_A11_MR	g4115365	BLASTX	157	3e-09	30	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
990	GM_59_A1_A11_T7	g861155	BLASTX	169	5e-11	40	(Z35162) beta-fructofuranosidase; cell wall invertase I; fructosidase [Vicia faba]
991	GM_59_A1_B04_T7	g2462134	BLASTX	192	1e-13	41	(Y13368) reverse transcriptase [Beta vulgaris]
992	GM_59_A1_B10_MR	g4063760	BLASTX	263	2e-22	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
993	GM_59_A1_C02_MR	g1785699	BLASTX	162	3e-11	34	(Y08501) orf145a [Arabidopsis thaliana]
994	GM_59_A1_C07_MR	g507910	BLASTN	480	4e-15	79	Glycine max BSR-101 satellite SB92 genomic sequence.
995	GM_59_A1_C07_T7	g507910	BLASTN	352	3e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
996	GM_59_A1_C09_T7	g3142328	BLASTN	920	1e-34	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
997	GM_59_A1_D05_T7	g507910	BLASTN	352	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
998	GM_59_A1_D07_MR	g2522228	BLASTX	154	1e-09	56	(AB007466) reverse transcriptase-like protein [Vicia faba]
999	GM_59_A1_D08_MR	g629693	BLASTX	258	2e-21	45	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
1000	GM_59_A1_D09_T7	g3024450	BLASTX	102	2e-11	57	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi 2143323 gnl PID e319087 (Y13328) 51kDa chlorophyll a protein [Populus deltoides]
1001	GM_59_A1_D11_MR	g3128166	BLASTN	364	2e-09	70	Arabidopsis thaliana chromosome II BAC F4I1 genomic sequence, complete sequence [Arabidopsis thaliana]
1002	GM_59_A1_F01_T7	g2465923	BLASTX	235	6e-22	72	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]
1003	GM_59_A1_F05_T7	g3142379	BLASTX	242	3e-19	66	(AF053008) envelope-like [Glycine max]
1004	GM_59_A1_F10_T7	g422418	BLASTX	112	5e-12	42	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
1005	GM_59_A1_G01_T7	g1709970	BLASTX	308	1e-26	81	60S RIBOSOMAL PROTEIN L10A
1006	GM_59_A1_G07_MR	g1769897	BLASTX	202	7e-25	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1007	GM_59_A1_H03_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
1008	GM_59_A1_H05_T7	g3650039	BLASTX	179	5e-12	39	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
1009	GM_59_A1_H11_T7	g3834313	BLASTX	191	2e-14	63	(AC005679) Strong similarity to T16B12.3 gi 3746060 unknown protein from Arabidopsis thaliana BAC gb AC005311. [Arabidopsis thaliana]
1010	GM_59_A2_B01_T7	g1431738	BLASTN	564	1e-18	91	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
1011	GM_59_A2_B02_MR	g1142701	BLASTN	228	5e-11	67	Glycine max satellite STR120-A.3.
1012	GM_59_A2_B03_T7	g130582	BLASTX	188	5e-17	44	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
1013	GM_59_A2_B08_T7	g507910	BLASTN	500	6e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
1014	GM_59_A2_C01_T7	g1769898	BLASTX	160	2e-13	39	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1015	GM_59_A2_C05_T7	g1346388	BLASTX	183	6e-13	86	KNOTTED-LIKE HOMEOBOX PROTEIN 4 gi 1045044 (X92393) KNAT4 homeobox protein [Arabidopsis thaliana]
1016	GM_59_A2_D02_MR	g100484	BLASTX	196	7e-16	46	hypothetical protein - garden snapdragon
1017	GM_59_A2_D03_T7	g1167523	BLASTX	111	5e-10	71	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
1018	GM_59_A2_D06_MR	g507910	BLASTN	574	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
1019	GM_59_A2_D06_T7	g507910	BLASTN	536	1e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
1020	GM_59_A2_D09_T7	g18695	BLASTN	505	5e-16	75	Soybean nodulin 22 gene
1021	GM_59_A2_D10_MR	g1840106	BLASTN	216	4e-10	72	Human fragile site locus (FRA16B) minisatellite repeat
1022	GM_59_A2_D10_T7	g18559	BLASTN	1004	2e-38	77	G.max gene for catalase
1023	GM_59_A2_D12_T7	g507910	BLASTN	523	5e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
1024	GM_59_A2_F02_T7	g1142699	BLASTN	1100	2e-43	80	Glycine max satellite STR120-A.1.
1025	GM_59_A2_F05_MR	g3142328	BLASTN	503	9e-16	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1026	GM_59_A2_F09_MR	g2879886	BLASTN	426	2e-12	68	Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes
1027	GM_59_A2_F09_T7	g3169170	BLASTX	207	5e-16	67	(AC004401) putative chloroplast envelope Ca2+-ATPase, 5' partial [Arabidopsis thaliana]
1028	GM_59_A2_G03_T7	g3377848	BLASTX	257	4e-21	56	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
1029	GM_59_A2_G07_MR	g3097320	BLASTN	350	8e-09	67	Glycine max gene for Bd 30K, complete cds
1030	GM_59_A2_H04_MR	g507910	BLASTN	402	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1031	GM_59_A2_H06_T7	g2145356	BLASTX	116	1e-09	80	(Y11122) HD-Zip protein [Arabidopsis thaliana] gi 3132474 (AC003096) homeobox protein, ATHB-14 [Arabidopsis thaliana]
1032	GM_59_A2_H09_MR	g2129618	BLASTX	183	3e-12	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
1033	GM_59_B1_A05_MR	g1769897	BLASTX	159	6e-15	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1034	GM_59_B1_A05_T7	g3142328	BLASTN	1097	9e-43	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1035	GM_59_B1_A10_T7	g4063760	BLASTX	192	5e-13	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1036	GM_59_B1_B01_T7	g4038056	BLASTX	211	3e-15	47	(AC005897) putative transposon [Arabidopsis thaliana]
1037	GM_59_B1_B02_T7	g99922	BLASTX	535	9e-51	69	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
1038	GM_59_B1_B10_T7	g2462134	BLASTX	137	1e-12	42	(Y13368) reverse transcriptase [Beta vulgaris]
1039	GM_59_B1_C03_T7	g2121303	BLASTN	351	8e-09	63	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
1040	GM_59_B1_C07_T7	g2764526	BLASTN	424	4e-12	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1041	GM_59_B1_C10_MR	g99922	BLASTX	352	2e-31	66	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
1042	GM_59_B1_C10_T7	g99721	BLASTX	362	4e-31	50	retrovirus-related polyprotein - Arabidopsis thaliana retrotransposon Ta1-3 gi 16534 (X13291) polyprotein [Arabidopsis thaliana]
1043	GM_59_B1_D05_MR	g99922	BLASTX	560	2e-53	87	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
1044	GM_59_B1_D12_MR	g4063760	BLASTX	389	5e-34	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1045	GM_59_B1_D12_T7	g507910	BLASTN	528	3e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
1046	GM_59_B1_E09_MR	g2506276	BLASTX	250	9e-20	64	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) gi 2129561 pir S71235 chaperonin-60 alpha chain - Arabidopsis thaliana gi 1223910 (U49357) chaperonin-60 alpha subunit [Arabidopsis thaliana]
1047	GM_59_B1_E12_T7	g3142328	BLASTN	1922	2e-80	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1048	GM_59_B1_F10_T7	g2739003	BLASTN	684	3e-24	85	Glycine max cytochrome P450 monooxygenase CYP82C1p (CYP82C1) mRNA, complete cds
1049	GM_59_B1_G03_MR	g507910	BLASTN	383	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1050	GM_59_B1_G04_T7	g1666236	BLASTX	184	3e-13	28	(U76261) unknown [Hordeum vulgare]
1051	GM_59_B1_G10_MR	g840618	BLASTN	346	8e-09	58	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
1052	GM_59_B1_G12_T7	g905361	BLASTX	155	7e-22	51	(U22103) gag-protease polyprotein [Glycine max]
1053	GM_59_B1_H06_T7	g3021266	BLASTX	136	7e-09	69	(AL022347) serine/threonine kinase - like protein [Arabidopsis thaliana] gi 3292840 gnl PID e1310083 (AL031018) serine/threonine kinase - like protein [Arabidopsis thaliana]
1054	GM_59_B1_H07_T7	g20834	BLASTN	347	9e-09	72	P.sativum PHSP1 mRNA for HSP70
1055	GM_59_B1_H08_MR	g2995405	BLASTX	121	2e-13	51	(Y12432) polyprotein [Ananas comosus]
1056	GM_59_B1_H09_MR	g507910	BLASTN	389	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1057	GM_59_B1_H09_T7	g905361	BLASTX	432	1e-39	95	(U22103) gag-protease polyprotein [Glycine max]
1058	GM_59_B1_H12_T7	g507910	BLASTN	403	1e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
1059	GM_59_B2_A05_MR	g1666236	BLASTX	168	2e-11	35	(U76261) unknown [Hordeum vulgare]
1060	GM_59_B2_A11_MR	g1666236	BLASTX	103	1e-09	33	(U76261) unknown [Hordeum vulgare]
1061	GM_59_B2_A12_MR	g2522230	BLASTX	151	2e-14	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
1062	GM_59_B2_B01_T7	g4063760	BLASTX	254	1e-19	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1063	GM_59_B2_B04_T7	g18559	BLASTN	1106	4e-43	76	G.max gene for catalase
1064	GM_59_B2_B07_T7	g3738114	BLASTN	396	7e-11	62	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1065	GM_59_B2_B08_MR	g3142328	BLASTN	462	6e-14	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1066	GM_59_B2_B09_T7	g507910	BLASTN	584	9e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
1067	GM_59_B2_B10_T7	g322663	BLASTX	157	2e-25	53	S-receptor kinase-related protein - Chinese kale gi 17917 (Z18884) S-receptor kinase related protein [Brassica oleracea]
1068	GM_59_B2_C01_MR	g1769898	BLASTX	316	8e-27	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1069	GM_59_B2_C01_T7	g4063756	BLASTN	434	1e-12	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
1070	GM_59_B2_C08_T7	g2462828	BLASTX	165	2e-21	45	(AF000657) hypothetical protein [Arabidopsis thaliana]
1071	GM_59_B2_C10_T7	g3599418	BLASTN	647	1e-25	71	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
1072	GM_59_B2_C11_MR	g18559	BLASTN	595	6e-20	75	G.max gene for catalase
1073	GM_59_B2_D01_MR	g3142328	BLASTN	1199	2e-47	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1074	GM_59_B2_D06_T7	g2522230	BLASTX	245	5e-20	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
1075	GM_59_B2_D07_MR	g507910	BLASTN	470	1e-14	77	Glycine max BSR-101 satellite SB92 genomic sequence.
1076	GM_59_B2_D07_T7	g3777527	BLASTX	338	2e-28	49	(AF053008) gag-pol polyprotein [Glycine max]
1077	GM_59_B2_D10_MR	g3877502	BLASTX	159	4e-10	34	(Z49967) ATP-binding protein (CDC48/PAS1/SEC18 family) with strong similarity to the yeast BCS1 protein (Swiss Prot accession number P32839); cDNA EST EMBL:C07371 comes from this gene; cDNA EST EMBL:C08716 comes from this ge...
1078	GM_59_B2_D11_MR	g2245136	BLASTX	381	2e-33	79	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]
1079	GM_59_B2_D11_T7	g4092471	BLASTN	473	3e-14	70	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
1080	GM_59_B2_E01_MR	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1081	GM_59_B2_E01_T7	g576752	BLASTN	345	6e-09	61	Myrmecia pilosula HI91-035 mitochondrion cytochrome b gene, partial cds.
1082	GM_59_B2_E02_MR	g507910	BLASTN	398	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1083	GM_59_B2_E04_T7	g4063743	BLASTX	239	3e-24	63	(AC005851) hypothetical protein [Arabidopsis thaliana]
1084	GM_59_B2_E07_T7	g507910	BLASTN	412	5e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1085	GM_59_B2_E10_MR	g13767	BLASTN	384	3e-11	63	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1086	GM_59_B2_E11_T7	g2501460	BLASTX	172	1e-19	71	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) gi 1545952 gnl PID e244584 (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]
1087	GM_59_B2_F05_T7	g3777527	BLASTX	734	1e-70	97	(AF053008) gag-pol polyprotein [Glycine max]
1088	GM_59_B2_F06_T7	g1666236	BLASTX	188	1e-13	28	(U76261) unknown [Hordeum vulgare]
1089	GM_59_B2_F07_T7	g629693	BLASTX	227	8e-18	44	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
1090	GM_59_B2_F10_T7	g2864621	BLASTX	146	6e-16	48	hypothetical protein [Arabidopsis thaliana]
1091	GM_59_B2_G02_MR	g1480927	BLASTN	373	6e-10	68	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
1092	GM_59_B2_H02_T7	g479124	BLASTN	471	2e-14	64	C.parapsilosos mitochondrial DNA for right telomeric region and ATP6 gene
1093	GM_59_B2_H03_T7	g4063760	BLASTX	355	2e-30	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1094	GM_59_B2_H12_T7	g2462058	BLASTX	222	1e-17	37	(Y13389) reverse transcriptase [Antirrhinum majus]
1095	GM_60_A1_A02_T7	g2459445	BLASTX	245	8e-20	64	(AC002332) putative ribonucleoprotein [Arabidopsis thaliana]
1096	GM_60_A1_A04_MR	g3777527	BLASTX	244	4e-24	48	(AF053008) gag-pol polyprotein [Glycine max]
1097	GM_60_A1_A10_T7	g2462058	BLASTX	287	2e-24	64	(Y13389) reverse transcriptase [Antirrhinum majus]
1098	GM_60_A1_A11_T7	g100484	BLASTX	203	2e-14	47	hypothetical protein - garden snapdragon
1099	GM_60_A1_B04_MR	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1100	GM_60_A1_B04_T7	g507910	BLASTN	611	5e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
1101	GM_60_A1_B09_MR	g4038056	BLASTX	261	2e-23	42	(AC005897) putative transposon [Arabidopsis thaliana]
1102	GM_60_A1_B10_MR	g2213632	BLASTX	148	4e-11	41	(AC000103) F21J9.24 [Arabidopsis thaliana]
1103	GM_60_A1_C04_MR	g507910	BLASTN	575	2e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
1104	GM_60_A1_C04_T7	g4063756	BLASTN	363	2e-09	66	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
1105	GM_60_A1_C12_MR	g4150930	BLASTN	371	1e-09	64	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
1106	GM_60_A1_D09_T7	g3777527	BLASTX	178	2e-11	35	(AF053008) gag-pol polyprotein [Glycine max]
1107	GM_60_A1_E04_MR	g507910	BLASTN	581	1e-19	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1108	GM_60_A1_E04_T7	g4063756	BLASTN	422	5e-12	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
1109	GM_60_A1_F01_T7	g3142328	BLASTN	571	7e-19	68	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1110	GM_60_A1_F04_MR	g2244915	BLASTX	192	4e-13	36	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
1111	GM_60_A1_F05_MR	g4038056	BLASTX	330	6e-28	48	(AC005897) putative transposon [Arabidopsis thaliana]
1112	GM_60_A1_F07_MR	g3097320	BLASTN	898	1e-33	79	Glycine max gene for Bd 30K, complete cds
1113	GM_60_A1_F08_MR	g2465527	BLASTX	342	5e-30	63	(AF000354) phosphate transporter [Medicago truncatula]
1114	GM_60_A1_G05_MR	g2522230	BLASTX	241	1e-19	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
1115	GM_60_A1_G09_MR	g4063760	BLASTX	437	4e-39	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1116	GM_60_A1_G10_T7	g18559	BLASTN	667	3e-23	74	G.max gene for catalase
1117	GM_60_A1_H05_T7	g3142328	BLASTN	1245	2e-49	83	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1118	GM_60_A1_H08_T7	g3688328	BLASTX	293	4e-25	61	(AJ228325) reverse transcriptase [Ginkgo biloba]
1119	GM_60_A1_H10_MR	g507910	BLASTN	517	9e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1120	GM_60_A1_H10_T7	g507910	BLASTN	446	1e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1121	GM_60_A2_A03_T7	g2522227	BLASTX	143	9e-09	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
1122	GM_60_A2_A08_T7	g3059060	BLASTN	365	2e-09	66	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
1123	GM_60_A2_B02_MR	g20749	BLASTN	374	9e-11	66	Pea PSU2 gene for U2 snRNA
1124	GM_60_A2_B03_MR	g507910	BLASTN	394	3e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
1125	GM_60_A2_C04_MR	g3097320	BLASTN	424	4e-12	68	Glycine max gene for Bd 30K, complete cds
1126	GM_60_A2_C07_MR	g905361	BLASTX	211	2e-15	65	(U22103) gag-protease polyprotein [Glycine max]
1127	GM_60_A2_C08_MR	g3269288	BLASTX	182	2e-13	70	(AL030978) putative protein [Arabidopsis thaliana]
1128	GM_60_A2_C10_MR	g3859610	BLASTN	484	8e-15	64	Arabidopsis thaliana BAC T9E19
1129	GM_60_A2_D01_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1130	GM_60_A2_D04_MR	g3142328	BLASTN	1090	2e-42	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1131	GM_60_A2_D04_T7	g4038056	BLASTX	275	4e-22	46	(AC005897) putative transposon [Arabidopsis thaliana]
1132	GM_60_A2_D08_MR	g3777527	BLASTX	158	1e-15	36	(AF053008) gag-pol polyprotein [Glycine max]
1133	GM_60_A2_D09_T7	g3097320	BLASTN	879	9e-33	78	Glycine max gene for Bd 30K, complete cds
1134	GM_60_A2_D11_MR	g3097320	BLASTN	466	5e-14	66	Glycine max gene for Bd 30K, complete cds
1135	GM_60_A2_E03_T7	g3777527	BLASTX	424	1e-37	85	(AF053008) gag-pol polyprotein [Glycine max]
1136	GM_60_A2_E12_MR	g3738089	BLASTX	154	4e-10	40	(AC005617) similar to symbiotic ammonium transporter, SAT1 [Arabidopsis thaliana]
1137	GM_60_A2_F02_MR	g1769898	BLASTX	413	1e-37	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1138	GM_60_A2_F03_MR	g22490	BLASTX	176	3e-15	48	(X01380) ORF1 [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1139	GM_60_A2_F04_MR	g507910	BLASTN	403	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1140	GM_60_A2_G02_MR	g3142328	BLASTN	845	3e-31	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1141	GM_60_A2_G06_MR	g4063760	BLASTX	252	1e-20	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1142	GM_60_A2_G07_MR	g4063760	BLASTX	260	3e-20	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1143	GM_60_B1_A08_T7	g507910	BLASTN	520	7e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
1144	GM_60_B1_A11_T7	g3777527	BLASTX	454	9e-41	85	(AF053008) gag-pol polyprotein [Glycine max]
1145	GM_60_B1_C01_T7	g507910	BLASTN	407	9e-12	79	Glycine max BSR-101 satellite SB92 genomic sequence.
1146	GM_60_B1_C05_MR	g4038056	BLASTX	201	3e-21	55	(AC005897) putative transposon [Arabidopsis thaliana]
1147	GM_60_B1_C07_T7	g1143318	BLASTN	809	9e-31	92	Glycine max biotin carboxyl carrier protein precursor (accB-1) mRNA, complete cds
1148	GM_60_B1_C09_T7	g2864624	BLASTX	167	1e-10	50	(AL021811) putative protein [Arabidopsis thaliana]
1149	GM_60_B1_C12_T7	g2583119	BLASTX	175	6e-14	42	(AC002387) hypothetical protein [Arabidopsis thaliana]
1150	GM_60_B1_D01_MR	g507910	BLASTN	409	7e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1151	GM_60_B1_D03_T7	g1769898	BLASTX	158	9e-10	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1152	GM_60_B1_D04_MR	g3930515	BLASTX	107	3e-11	40	(AF059674) putative gag protein [Nicotiana tabacum]
1153	GM_60_B1_D04_T7	g3645899	BLASTX	173	5e-11	57	(U68408) 5' end not determined experimentally [Zea mays]
1154	GM_60_B1_D05_MR	g22490	BLASTX	145	7e-12	60	(X01380) ORF1 [Zea mays]
1155	GM_60_B1_D10_MR	g3695387	BLASTX	269	9e-23	58	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
1156	GM_60_B1_D12_T7	g4063760	BLASTX	156	4e-09	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1157	GM_60_B1_E01_T7	g1431738	BLASTN	355	9e-16	92	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
1158	GM_60_B1_E06_MR	g2275207	BLASTX	93	2e-09	46	(AC002337) hypothetical protein [Arabidopsis thaliana]
1159	GM_60_B1_F01_MR	g3600044	BLASTX	98	3e-09	44	(AF080119) contains similarity to proteases [Arabidopsis thaliana]
1160	GM_60_B1_F03_T7	g4063760	BLASTX	331	7e-28	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1161	GM_60_B1_F04_T7	g3319362	BLASTX	234	5e-19	53	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
1162	GM_60_B1_F06_T7	g2501448	BLASTX	89	2e-12	76	UBIQUITIN-LIKE PROTEIN SMT3 gi 1707372 gnl PID e259962 (X99609) ubiquitin-like protein [Arabidopsis thaliana]
1163	GM_60_B1_F09_MR	g507910	BLASTN	628	9e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
1164	GM_60_B1_F12_MR	g3426334	BLASTN	532	5e-17	60	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
1165	GM_60_B1_H02_MR	g3377834	BLASTX	210	3e-15	34	(AF075598) No definition line found [Arabidopsis thaliana]
1166	GM_60_B1_H06_MR	g3097320	BLASTN	483	8e-15	75	Glycine max gene for Bd 30K, complete cds
1167	GM_60_B2_A03_T7	g3810596	BLASTX	192	1e-20	40	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
1168	GM_60_B2_A04_MR	g4063760	BLASTX	384	2e-33	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1169	GM_60_B2_A04_T7	g4063760	BLASTX	664	2e-63	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1170	GM_60_B2_A05_MR	g13597	BLASTN	308	9e-14	63	Yeast mitochondrial tRNA genes for tRNA-Ala, tRNA-Tyr and tRNA-Ile
1171	GM_60_B2_A10_MR	g3142328	BLASTN	1136	2e-44	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1172	GM_60_B2_B09_MR	g1468969	BLASTX	138	1e-13	51	(D30666) brain acyl-CoA synthtase II [Rattus norvegicus]
1173	GM_60_B2_B11_MR	g3097320	BLASTN	390	1e-10	76	Glycine max gene for Bd 30K, complete cds
1174	GM_60_B2_C03_MR	g2130016	BLASTX	209	2e-32	50	homeotic protein 1 - common sunflower gi 1208940 (L76588) homeodomain protein 1 [Helianthus annuus]
1175	GM_60_B2_C04_MR	g2443320	BLASTX	407	9e-50	54	(D85597) polyprotein [Oryza australiensis]
1176	GM_60_B2_C05_T7	g1431738	BLASTN	355	9e-16	92	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
1177	GM_60_B2_C10_T7	g18559	BLASTN	1109	3e-43	73	G.max gene for catalase
1178	GM_60_B2_C11_MR	g507910	BLASTN	387	7e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1179	GM_60_B2_D03_MR	g3599418	BLASTN	617	6e-21	73	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
1180	GM_60_B2_D05_MR	g2443320	BLASTX	233	2e-17	35	(D85597) polyprotein [Oryza australiensis]
1181	GM_60_B2_D06_MR	g3242700	BLASTN	364	2e-09	65	Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence, complete sequence [Arabidopsis thaliana]
1182	GM_60_B2_D07_MR	g505129	BLASTN	398	5e-11	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
1183	GM_60_B2_E03_T7	g4063760	BLASTX	655	2e-62	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1184	GM_60_B2_E04_MR	g505129	BLASTN	417	2e-15	68	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
1185	GM_60_B2_E05_MR	g2245044	BLASTX	204	1e-21	38	(Z97342) similarity to reverse transcriptase - Arabidopsis thaliana retrotransposon 2 (fragment) [Arabidopsis thaliana]
1186	GM_60_B2_E06_T7	g2764525	BLASTN	746	6e-27	68	Pisum sativum genomic DNA encoding truncated Ty3/Gypsy-like retroelement Cyclops-1
1187	GM_60_B2_E07_MR	g3777527	BLASTX	621	1e-58	83	(AF053008) gag-pol polyprotein [Glycine max]
1188	GM_60_B2_E09_MR	g2522230	BLASTX	182	2e-13	35	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1189	GM_60_B2_E10_T7	g136636	BLASTX	222	1e-17	100	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana gi 442594 pdb 1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) gi 2981894 pdb 2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana Ubiquitin Conjugation, Ligase Mol_id: 1; Molecule: Ubiquitin Conjugating Enzyme; Chain: Null; Synonym: Ubc1; Ec: 6.3.2.19; Engineered: Yes gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] gi 431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]
1190	GM_60_B2_E11_T7	g2522230	BLASTX	255	4e-21	44	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
1191	GM_60_B2_E12_T7	g2443320	BLASTX	324	5e-27	44	(D85597) polyprotein [Oryza australiensis]
1192	GM_60_B2_F02_T7	g99922	BLASTX	348	2e-51	85	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
1193	GM_60_B2_F03_MR	g995751	BLASTN	533	2e-17	59	Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence
1194	GM_60_B2_F05_T7	g3142328	BLASTN	894	2e-33	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1195	GM_60_B2_F06_MR	g507910	BLASTN	597	2e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
1196	GM_60_B2_F06_T7	g507910	BLASTN	642	2e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
1197	GM_60_B2_F07_T7	g507910	BLASTN	557	1e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
1198	GM_60_B2_F08_T7	g905361	BLASTX	439	2e-40	97	(U22103) gag-protease polyprotein [Glycine max]
1199	GM_60_B2_G01_MR	g3319362	BLASTX	457	2e-41	51	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
1200	GM_60_B2_G02_MR	g2558654	BLASTX	411	3e-36	55	(AC002354) No definition line found [Arabidopsis thaliana]
1201	GM_60_B2_G06_MR	g3319345	BLASTX	225	1e-16	35	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
1202	GM_60_B2_G07_T7	g4063760	BLASTX	212	4e-15	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1203	GM_60_B2_G08_MR	g507910	BLASTN	430	8e-13	78	Glycine max BSR-101 satellite SB92 genomic sequence.
1204	GM_60_B2_G08_T7	g4063760	BLASTX	463	6e-42	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1205	GM_60_B2_G10_T7	g125568	BLASTX	780	9e-77	95	PROTEIN KINASE PVPK-1 gi 100013 pir A30311 protein kinase C (EC 2.7.1.-) homolog - kidney bean gi 169361 (J04555) PVPK-1 protein [Phaseolus vulgaris]
1206	GM_60_B2_H02_T7	g1171583	BLASTN	317	8e-12	64	P.falciparum complete gene map of plastid-like DNA (IR-A)
1207	GM_60_B2_H03_MR	g3777527	BLASTX	326	3e-34	50	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1208	GM_60_B2_H05_MR	g3142328	BLASTN	822	3e-30	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1209	GM_60_B2_H07_MR	g2098816	BLASTN	362	3e-09	59	Arabidopsis thaliana BAC F19G10, complete sequence
1210	GM_60_B2_H07_T7	g1769897	BLASTX	490	5e-46	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1211	GM_60_B2_H09_T7	g3063461	BLASTX	156	3e-09	32	(AC003981) F22O13.23 [Arabidopsis thaliana]
1212	GM_61_A1_A04_T7	g18559	BLASTN	413	1e-11	70	G.max gene for catalase
1213	GM_61_A1_A05_T7	g2522228	BLASTX	263	8e-22	74	(AB007466) reverse transcriptase-like protein [Vicia faba]
1214	GM_61_A1_A06_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1215	GM_61_A1_A06_T7	g507910	BLASTN	389	6e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
1216	GM_61_A1_A08_T7	g2462058	BLASTX	196	1e-18	53	(Y13389) reverse transcriptase [Antirrhinum majus]
1217	GM_61_A1_A09_MR	g4038037	BLASTX	183	4e-12	55	(AC005936) hypothetical protein [Arabidopsis thaliana]
1218	GM_61_A1_B02_MR	g4092471	BLASTN	431	2e-12	70	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
1219	GM_61_A1_B09_MR	g4063760	BLASTX	332	6e-28	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1220	GM_61_A1_B12_MR	g2801679	BLASTN	594	2e-20	82	Glycine max telomere-associated sequence STAS8
1221	GM_61_A1_C03_MR	g1813979	BLASTX	232	9e-29	67	(Y10860) hypothetical protein [Musa acuminata]
1222	GM_61_A1_C03_T7	g3738337	BLASTX	296	4e-24	44	(AC005170) putative reverse transcriptase [Arabidopsis thaliana]
1223	GM_61_A1_C07_T7	g3377848	BLASTX	306	2e-26	52	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
1224	GM_61_A1_C10_T7	g2522228	BLASTX	359	4e-32	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
1225	GM_61_A1_D01_MR	g2522228	BLASTX	263	9e-22	79	(AB007466) reverse transcriptase-like protein [Vicia faba]
1226	GM_61_A1_D02_T7	g4159706	BLASTN	423	2e-20	68	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGL6, complete sequence [Arabidopsis thaliana]
1227	GM_61_A1_D05_MR	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1228	GM_61_A1_D08_MR	g4063760	BLASTX	309	2e-25	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1229	GM_61_A1_D09_MR	g18559	BLASTN	831	1e-30	78	G.max gene for catalase
1230	GM_61_A1_D10_MR	g18559	BLASTN	900	9e-34	75	G.max gene for catalase
1231	GM_61_A1_D10_T7	g2586082	BLASTX	118	1e-09	38	(U72725) retrofit [Oryza longistaminata]
1232	GM_61_A1_D11_MR	g3493149	BLASTX	259	1e-21	63	(AF084026) NBS type putative resistance protein [Phaseolus vulgaris]
1233	GM_61_A1_E01_T7	g3004545	BLASTX	153	9e-09	35	(AC003673) putative reverse transcriptase [Arabidopsis thaliana]
1234	GM_61_A1_E02_T7	g2688830	BLASTX	227	1e-23	96	(AF000952) putative sugar transporter [Prunus armeniaca]
1235	GM_61_A1_E04_MR	g1184075	BLASTX	202	4e-14	49	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
1236	GM_61_A1_E05_MR	g18559	BLASTN	749	6e-27	76	G.max gene for catalase
1237	GM_61_A1_E06_T7	g2995405	BLASTX	161	7e-10	45	(Y12432) polyprotein [Ananas comosus]
1238	GM_61_A1_F06_MR	g4063760	BLASTX	188	1e-12	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1239	GM_61_A1_F08_T7	g2443320	BLASTX	270	3e-21	53	(D85597) polyprotein [Oryza australiensis]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1240	GM_61_A1_F11_T7	g3252807	BLASTX	157	1e-09	38	(AC004705) hypothetical protein [Arabidopsis thaliana]
1241	GM_61_A1_F12_MR	g1769899	BLASTX	294	3e-25	73	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1242	GM_61_A1_G01_MR	g2760170	BLASTN	469	4e-14	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIO24, complete sequence [Arabidopsis thaliana]
1243	GM_61_A1_G02_MR	g3097320	BLASTN	486	7e-21	75	Glycine max gene for Bd 30K, complete cds
1244	GM_61_A1_G03_T7	g3810596	BLASTX	231	5e-22	43	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
1245	GM_61_A1_G07_MR	g4092471	BLASTN	473	3e-14	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
1246	GM_61_A1_G12_T7	g507910	BLASTN	344	6e-09	76	Glycine max BSR-101 satellite SB92 genomic sequence.
1247	GM_61_A1_H01_T7	g2129618	BLASTX	185	2e-12	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
1248	GM_61_A1_H06_MR	g4063760	BLASTX	188	1e-12	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1249	GM_61_A1_H08_MR	g3097320	BLASTN	740	2e-26	75	Glycine max gene for Bd 30K, complete cds
1250	GM_61_A1_H10_T7	g3777527	BLASTX	151	5e-18	44	(AF053008) gag-pol polyprotein [Glycine max]
1251	GM_61_A1_H12_MR	g4063760	BLASTX	243	2e-18	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1252	GM_61_A2_A10_MR	g99755	BLASTX	263	8e-30	50	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
1253	GM_61_A2_A12_T7	g2443320	BLASTX	242	3e-18	48	(D85597) polyprotein [Oryza australiensis]
1254	GM_61_A2_B02_T7	g3142328	BLASTN	1358	1e-54	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1255	GM_61_A2_B04_T7	g1167523	BLASTX	271	2e-21	38	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
1256	GM_61_A2_B05_T7	g2522228	BLASTX	362	2e-32	61	(AB007466) reverse transcriptase-like protein [Vicia faba]
1257	GM_61_A2_B08_MR	g1171591	BLASTN	434	1e-12	62	P.falciparum complete gene map of plastid-like DNA (IR-B)
1258	GM_61_A2_B10_MR	g3513745	BLASTX	222	5e-16	35	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
1259	GM_61_A2_C01_T7	g255578	BLASTN	525	1e-17	85	small auxin up RNA gene cluster: orf X10A [Glycine max=soybeans, cv. Wayne, Genomic, 666 nt]
1260	GM_61_A2_C02_T7	g3820757	BLASTN	436	6e-13	65	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
1261	GM_61_A2_C06_T7	g1658457	BLASTX	243	7e-20	60	(U75248) reverse transcriptase [Gossypium barbadense]
1262	GM_61_A2_C10_MR	g905361	BLASTX	369	1e-32	85	(U22103) gag-protease polyprotein [Glycine max]
1263	GM_61_A2_C12_T7	g2924341	BLASTN	441	4e-13	61	Saccharomyces cerevisiae mitochondrial Tyr-tRNA, Asn-tRNA and Met-tRNA genes
1264	GM_61_A2_D01_T7	g1076755	BLASTX	496	5e-49	76	protein kinase - rice gi 450300 (L27821) protein kinase [Oryza sativa]
1265	GM_61_A2_D08_T7	g507910	BLASTN	349	4e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
1266	GM_61_A2_F03_MR	g2735841	BLASTX	284	5e-23	43	(AF010283) No definition line found [Sorghum bicolor]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1267	GM_61_A2_F05_T7	g2522228	BLASTX	97	5e-17	52	(AB007466) reverse transcriptase-like protein [Vicia faba]
1268	GM_61_A2_F06_T7	g3142328	BLASTN	1087	3e-42	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1269	GM_61_A2_G01_T7	g4063760	BLASTX	477	2e-43	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1270	GM_61_A2_H07_MR	g114532	BLASTX	383	1e-34	80	ATP SYNTHASE ALPHA CHAIN gi 67824 pir PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast gi 11769 (V00162) alpha subunit of ATPase [Nicotiana tabacum] gi 11811 (Z00044) ATPase alpha subunit [Nicotiana tabacum] gi 225270 prf 1211235E ATPase alpha [Nicotiana tabacum]
1271	GM_61_A2_H07_T7	g117822	BLASTX	290	3e-39	87	CYTOCHROME B6 gi 65635 pir CBNT6 plastoquinol--plastocyanin reductase (EC 1.10.99.1) cytochrome b6 - common tobacco chloroplast gi 11858 (Z00044) cytochrome b6 [Nicotiana tabacum] gi 225226 prf 1211235BH cytochrome b6 [Nicotiana tabacum]
1272	GM_61_A2_H10_MR	g2244807	BLASTX	221	7e-18	55	(Z97336) hypothetical protein [Arabidopsis thaliana]
1273	GM_61_A2_H11_MR	g4063760	BLASTX	248	8e-20	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1274	GM_61_A2_H11_T7	g2586082	BLASTX	196	2e-13	38	(U72725) retrofit [Oryza longistaminata]
1275	GM_61_B1_A09_MR	g2522228	BLASTX	194	5e-14	76	(AB007466) reverse transcriptase-like protein [Vicia faba]
1276	GM_61_B1_B03_MR	g3319362	BLASTX	200	6e-14	41	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
1277	GM_61_B1_B03_T7	g100484	BLASTX	344	1e-29	50	hypothetical protein - garden snapdragon
1278	GM_61_B1_B06_T7	g3242700	BLASTN	357	4e-09	59	Arabidopsis thaliana chromosome II BAC F26B6 genomic sequence, complete sequence [Arabidopsis thaliana]
1279	GM_61_B1_B07_T7	g3402755	BLASTX	347	2e-29	43	(AL031187) putative transposable element [Arabidopsis thaliana]
1280	GM_61_B1_B09_MR	g507910	BLASTN	419	3e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
1281	GM_61_B1_B11_MR	g18559	BLASTN	1085	3e-42	89	G.max gene for catalase
1282	GM_61_B1_C07_T7	g728744	BLASTX	128	2e-09	42	AUXIN-INDUCED PROTEIN PCNT115 gi 100305 pir S16390 auxin-induced protein - common tobacco gi 19799 (X56267) auxin-induced protein [Nicotiana tabacum]
1283	GM_61_B1_D04_T7	g1326016	BLASTX	167	2e-10	40	TY3-2 orfB
1284	GM_61_B1_D05_MR	g507910	BLASTN	500	6e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1285	GM_61_B1_D06_MR	g507910	BLASTN	553	2e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
1286	GM_61_B1_D09_MR	g3097320	BLASTN	423	4e-12	79	Glycine max gene for Bd 30K, complete cds
1287	GM_61_B1_D11_MR	g984045	BLASTN	355	5e-09	74	A.thaliana ATK1 gene
1288	GM_61_B1_D12_T7	g3785980	BLASTX	323	1e-27	49	(AC005560) hypothetical protein [Arabidopsis thaliana]
1289	GM_61_B1_E03_MR	g3695395	BLASTX	171	4e-11	44	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1290	GM_61_B1_E03_T7	g130582	BLASTX	242	1e-33	50	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
1291	GM_61_B1_E04_T7	g2980757	BLASTN	406	3e-11	66	Arabidopsis thaliana DNA chromosome 4, BAC clone F6I18 (ESSAII project)
1292	GM_61_B1_E05_MR	g3599418	BLASTN	512	3e-16	72	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
1293	GM_61_B1_E09_T7	g2129618	BLASTX	197	1e-13	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
1294	GM_61_B1_E12_T7	g3777527	BLASTX	575	7e-62	94	(AF053008) gag-pol polyprotein [Glycine max]
1295	GM_61_B1_F05_MR	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
1296	GM_61_B1_F05_T7	g507910	BLASTN	578	2e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1297	GM_61_B1_F06_MR	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1298	GM_61_B1_F06_T7	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1299	GM_61_B1_F10_T7	g3777527	BLASTX	623	8e-59	93	(AF053008) gag-pol polyprotein [Glycine max]
1300	GM_61_B1_F11_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
1301	GM_61_B1_F12_T7	g4063760	BLASTX	539	4e-50	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1302	GM_61_B1_G05_T7	g2764526	BLASTN	412	1e-11	69	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
1303	GM_61_B1_G11_T7	g170029	BLASTN	371	9e-10	78	Glycine max cv. Dare nodulin 26 gene fragment.
1304	GM_61_B1_G12_MR	g507910	BLASTN	577	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
1305	GM_61_B1_H03_T7	g4063760	BLASTX	349	4e-55	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1306	GM_61_B1_H04_T7	g2654440	BLASTX	151	1e-18	53	(U70076) Lemir [Lycopersicon esculentum]
1307	GM_61_B1_H05_MR	g2522228	BLASTX	291	6e-25	61	(AB007466) reverse transcriptase-like protein [Vicia faba]
1308	GM_61_B1_H05_T7	g2853084	BLASTX	130	5e-12	58	(AL021768) putative protein [Arabidopsis thaliana]
1309	GM_61_B1_H07_MR	g507910	BLASTN	468	1e-14	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1310	GM_61_B1_H07_T7	g4063760	BLASTX	177	2e-11	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1311	GM_61_B1_H08_T7	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1312	GM_61_B1_H12_T7	g2522227	BLASTX	161	8e-11	45	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
1313	GM_61_B2_A02_T7	g4063760	BLASTX	450	4e-44	84	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1314	GM_61_B2_A05_MR	g505129	BLASTN	370	9e-10	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
1315	GM_61_B2_A06_T7	g3142379	BLASTX	255	1e-20	60	(AF053008) envelope-like [Glycine max]
1316	GM_61_B2_A07_T7	g2129651	BLASTX	114	4e-12	56	myosin heavy chain ATM2 - Arabidopsis thaliana (fragment) gi 499045 (Z34292) myosin [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1317	GM_61_B2_A08_MR	g2498732	BLASTX	386	5e-35	59	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2 gi 1362014 pir S57612 zeta-crystallin homolog - Arabidopsis thaliana gi 886430 (Z49268) zeta-crystallin homologue [Arabidopsis thaliana]
1318	GM_61_B2_A10_MR	g18559	BLASTN	362	2e-09	75	G.max gene for catalase
1319	GM_61_B2_A10_T7	g507910	BLASTN	559	1e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
1320	GM_61_B2_A11_MR	g3777527	BLASTX	652	7e-62	97	(AF053008) gag-pol polyprotein [Glycine max]
1321	GM_61_B2_A11_T7	g1167523	BLASTX	240	3e-32	43	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
1322	GM_61_B2_A12_MR	g2264308	BLASTN	364	5e-11	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIK22, complete sequence.
1323	GM_61_B2_B06_T7	g1916937	BLASTX	226	1e-16	40	(U90320) reverse transcriptase, gag, polyprotein [Volvox carteri f. nagariensis]
1324	GM_61_B2_B09_MR	g2443320	BLASTX	402	2e-35	71	(D85597) polyprotein [Oryza australiensis]
1325	GM_61_B2_B10_MR	g99922	BLASTX	166	5e-29	53	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
1326	GM_61_B2_C01_T7	g343537	BLASTN	377	5e-10	61	T.brucei mitochondrial maxicircle DNA encoding cytochrome c oxidase subunit I (COI), and NADH dehydrogenase subunits 4 and 5, complete cds.
1327	GM_61_B2_C02_T7	g3150006	BLASTN	393	1e-10	62	CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence [Arabidopsis thaliana]
1328	GM_61_B2_C03_T7	g3377834	BLASTX	156	2e-09	29	(AF075598) No definition line found [Arabidopsis thaliana]
1329	GM_61_B2_C09_MR	g2522228	BLASTX	405	5e-37	74	(AB007466) reverse transcriptase-like protein [Vicia faba]
1330	GM_61_B2_D04_MR	g507910	BLASTN	588	6e-20	85	Glycine max BSR-101 satellite SB92 genomic sequence.
1331	GM_61_B2_D04_T7	g507910	BLASTN	557	1e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
1332	GM_61_B2_D06_MR	g507910	BLASTN	504	4e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1333	GM_61_B2_D06_T7	g507910	BLASTN	569	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1334	GM_61_B2_D08_MR	g507910	BLASTN	451	9e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
1335	GM_61_B2_D09_T7	g3777527	BLASTX	692	3e-66	89	(AF053008) gag-pol polyprotein [Glycine max]
1336	GM_61_B2_D10_MR	g99922	BLASTX	180	7e-37	54	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
1337	GM_61_B2_E10_MR	g421955	BLASTX	131	1e-23	56	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
1338	GM_61_B2_E12_MR	g1480927	BLASTN	1255	5e-51	95	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
1339	GM_61_B2_E12_T7	g3377834	BLASTX	151	6e-09	30	(AF075598) No definition line found [Arabidopsis thaliana]
1340	GM_61_B2_F01_T7	g3845307	BLASTN	424	4e-12	59	Plasmodium falciparum chromosome 2, section 61 of 73 of the complete sequence
1341	GM_61_B2_F04_MR	g4063760	BLASTX	476	2e-43	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1342	GM_61_B2_F08_MR	g18559	BLASTN	801	3e-29	88	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1343	GM_61_B2_F08_T7	g1369955	BLASTN	382	3e-10	64	Caenorhabditis elegans cosmid B0564, complete sequence [Caenorhabditis elegans]
1344	GM_61_B2_F10_MR	g2865424	BLASTX	236	4e-20	52	(AF039371) polyprotein [Arabidopsis thaliana]
1345	GM_61_B2_F11_MR	g2129618	BLASTX	210	2e-16	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
1346	GM_61_B2_G02_T7	g3033375	BLASTX	161	1e-24	39	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]
1347	GM_61_B2_G03_MR	g4105782	BLASTX	138	1e-08	81	(AF049922) PGP169-12 [Petunia x hybrida]
1348	GM_61_B2_G05_MR	g3935164	BLASTX	205	3e-14	47	(AC004557) F17L21.7 [Arabidopsis thaliana]
1349	GM_61_B2_G05_T7	g409571	BLASTN	253	5e-11	65	Helicoverpa armigera mitochondrion D-loop, partial 12S rRNA gene, and partial tRNA-Met gene.
1350	GM_61_B2_G06_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1351	GM_61_B2_G10_T7	g3097320	BLASTN	384	2e-10	71	Glycine max gene for Bd 30K, complete cds
1352	GM_61_B2_G12_T7	g3097320	BLASTN	430	2e-12	68	Glycine max gene for Bd 30K, complete cds
1353	GM_61_B2_H01_MR	g1899158	BLASTN	351	5e-09	61	Saccharomyces cerevisiae synthetic green fluorescent protein (cox3::GFPm) gene, mitochondrial gene construct, complete cds
1354	GM_61_B2_H03_T7	g3097320	BLASTN	1184	1e-46	75	Glycine max gene for Bd 30K, complete cds
1355	GM_61_B2_H06_MR	g2443320	BLASTX	374	2e-32	51	(D85597) polyprotein [Oryza australiensis]
1356	GM_61_B2_H06_T7	g1769897	BLASTX	227	2e-17	38	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1357	GM_61_B2_H10_T7	g2920654	BLASTX	331	1e-28	60	(AF047697) putative high-pI laccase [Oryza sativa]
1358	GM_61_B2_H12_T7	g114734	BLASTX	189	4e-14	83	AUXIN-INDUCED PROTEIN AUX28 gi 81759 pir A28993 aux28 protein - soybean gi 169921 (J03919) auxin-regulated protein (Aux28) [Glycine max]
1359	GM_63_A1_A04_T7	g2764525	BLASTN	830	8e-31	69	Pisum sativum genomic DNA encoding truncated Ty3/Gypsy-like retroelement Cyclops-1
1360	GM_63_A1_A08_MR	g905361	BLASTX	163	3e-10	38	(U22103) gag-protease polyprotein [Glycine max]
1361	GM_63_A1_A08_T7	g100484	BLASTX	373	8e-33	55	hypothetical protein - garden snapdragon
1362	GM_63_A1_A09_MR	g3097320	BLASTN	941	1e-35	80	Glycine max gene for Bd 30K, complete cds
1363	GM_63_A1_A12_T7	g3097836	BLASTN	376	6e-10	62	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
1364	GM_63_A1_B04_MR	g4006833	BLASTX	218	2e-16	34	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
1365	GM_63_A1_C02_MR	g2129618	BLASTX	250	2e-19	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
1366	GM_63_A1_C04_MR	g4049647	BLASTN	410	2e-11	63	Melanoplus sanguinipes entomopoxvirus, complete genome
1367	GM_63_A1_C05_MR	g507910	BLASTN	594	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
1368	GM_63_A1_C05_T7	g507910	BLASTN	619	2e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1369	GM_63_A1_C07_MR	g3510505	BLASTX	145	3e-13	46	(AF030881) pol polyprotein [Fugu rubripes]
1370	GM_63_A1_C09_MR	g1480927	BLASTN	370	8e-10	87	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1371	GM_63_A1_C10_MR	g2213582	BLASTX	196	2e-13	36	(AC000348) T7N9.2 [Arabidopsis thaliana]
1372	GM_63_A1_D03_T7	g1703053	BLASTX	133	9e-11	40	ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD SUBUNIT) (A1 40 KD SUBUNIT) (RF-C 40 KD SUBUNIT) (RFC40) gi 2134397 pir I50704 replication factor C/activator 1 subunit - chicken gi 527669 (U12438) replication factor C/activator 1 subunit [Gallus gallus]
1373	GM_63_A1_D06_MR	g2979597	BLASTN	508	7e-16	64	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
1374	GM_63_A1_D08_MR	g3426334	BLASTN	623	3e-21	64	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
1375	GM_63_A1_D09_MR	g507910	BLASTN	373	3e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1376	GM_63_A1_D12_MR	g629693	BLASTX	224	2e-17	42	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
1377	GM_63_A1_E02_T7	g1817728	BLASTN	453	2e-13	65	Cloning vector pBeloBAC11
1378	GM_63_A1_E04_T7	g4063760	BLASTX	214	1e-23	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1379	GM_63_A1_E05_T7	g1167523	BLASTX	358	1e-30	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
1380	GM_63_A1_E08_T7	g4098647	BLASTX	228	1e-17	63	(U80668) homogentisate 1,2-dioxygenase [Arabidopsis thaliana]
1381	GM_63_A1_E12_T7	g507910	BLASTN	547	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1382	GM_63_A1_F02_MR	g507910	BLASTN	538	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1383	GM_63_A1_F02_T7	g507910	BLASTN	427	1e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
1384	GM_63_A1_F06_T7	g2292907	BLASTX	317	3e-26	45	(Y10099) P-glycoprotein homologue [Hordeum vulgare]
1385	GM_63_A1_G07_MR	g507910	BLASTN	594	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
1386	GM_63_A1_G07_T7	g4063760	BLASTX	285	6e-23	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1387	GM_63_A1_H03_MR	g3142328	BLASTN	840	4e-31	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1388	GM_63_A1_H11_T7	g3097320	BLASTN	418	7e-12	71	Glycine max gene for Bd 30K, complete cds
1389	GM_63_A2_A05_T7	g507910	BLASTN	388	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1390	GM_63_A2_A06_MR	g21430	BLASTN	382	3e-10	71	Potato DNA for copia-like transposable element
1391	GM_63_A2_A08_T7	g1532167	BLASTX	145	2e-09	38	(U63815) localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop codon could not be precisely determined [Arabidopsis thaliana]
1392	GM_63_A2_A09_MR	g1769898	BLASTX	204	9e-15	35	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1393	GM_63_A2_B01_MR	g507910	BLASTN	576	2e-19	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1394	GM_63_A2_B01_T7	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1395	GM_63_A2_B02_T7	g4063760	BLASTX	249	4e-19	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1396	GM_63_A2_B06_T7	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1397	GM_63_A2_C03_T7	g905361	BLASTX	190	3e-13	29	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1398	GM_63_A2_C05_T7	g2738248	BLASTX	261	9e-26	94	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]
1399	GM_63_A2_C12_MR	g3080666	BLASTN	364	2e-09	63	Homo sapiens PAC clone DJ0318J07 from 8q21, complete sequence [Homo sapiens]
1400	GM_63_A2_D02_T7	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
1401	GM_63_A2_D06_MR	g3402690	BLASTX	197	1e-25	46	(AC004697) hypothetical protein, 3' partial [Arabidopsis thaliana]
1402	GM_63_A2_D06_T7	g4102839	BLASTX	253	5e-20	43	(AF016713) LeOPT1 [Lycopersicon esculentum]
1403	GM_63_A2_D09_MR	g3033375	BLASTX	186	9e-24	77	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]
1404	GM_63_A2_D11_T7	g3687234	BLASTX	207	1e-14	49	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
1405	GM_63_A2_D12_MR	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
1406	GM_63_A2_D12_T7	g507910	BLASTN	395	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1407	GM_63_A2_E03_T7	g99922	BLASTX	347	7e-31	70	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
1408	GM_63_A2_E04_MR	g2970554	BLASTN	749	8e-27	78	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
1409	GM_63_A2_E07_MR	g508826	BLASTN	360	3e-09	62	Drosophila melanogaster Oregon-R mitochondrial A+T region.
1410	GM_63_A2_E07_T7	g100484	BLASTX	374	6e-33	53	hypothetical protein - garden snapdragon
1411	GM_63_A2_E11_MR	g1363492	BLASTX	243	1e-18	68	outer envelope membrane protein OEP75 precursor - garden pea gi 576507 (L36858) outer membrane protein [Pisum sativum] gi 633607 (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]
1412	GM_63_A2_F02_MR	g2462936	BLASTX	300	6e-26	42	(Y12321) open reading frame 2 [Brassica oleracea]
1413	GM_63_A2_F05_T7	g905361	BLASTX	413	2e-37	95	(U22103) gag-protease polyprotein [Glycine max]
1414	GM_63_A2_G01_MR	g3142328	BLASTN	1179	2e-46	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1415	GM_63_A2_G05_MR	g532706	BLASTN	432	3e-13	79	Glycine max clone GMFP6 isoprenylated protein mRNA, partial cds.
1416	GM_63_A2_G05_T7	g2443320	BLASTX	375	2e-32	49	(D85597) polyprotein [Oryza australiensis]
1417	GM_63_A2_G06_T7	g3777527	BLASTX	704	2e-67	94	(AF053008) gag-pol polyprotein [Glycine max]
1418	GM_63_A2_G07_MR	g507910	BLASTN	534	2e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
1419	GM_63_A2_G07_T7	g507910	BLASTN	555	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
1420	GM_63_A2_H01_MR	g3142328	BLASTN	1145	6e-45	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1421	GM_63_A2_H03_MR	g2970554	BLASTN	773	6e-28	73	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
1422	GM_63_A2_H04_T7	g507910	BLASTN	359	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1423	GM_63_A2_H08_T7	g2462134	BLASTX	163	2e-10	39	(Y13368) reverse transcriptase [Beta vulgaris]
1424	GM_63_A2_H11_T7	g507910	BLASTN	548	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1425	GM_63_A2_H12_T7	g2443320	BLASTX	243	2e-18	46	(D85597) polyprotein [Oryza australiensis]
1426	GM_63_B1_A05_MR	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1427	GM_63_B1_A05_T7	g507910	BLASTN	447	1e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
1428	GM_63_B1_A06_T7	g3367517	BLASTX	233	5e-18	51	(AC004392) Similar to F4I1.26 putative beta-glucosidase gi 3128187 from A. thaliana BAC gb AC004521. ESTs gb N97083, gb F19868 and gb F15482 come from this gene. [Arabidopsis thaliana]
1429	GM_63_B1_A07_MR	g99730	BLASTX	207	6e-20	43	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
1430	GM_63_B1_A08_MR	g1174613	BLASTX	201	1e-14	88	26S PROTEASE REGULATORY SUBUNIT S6A HOMOLOG (TAT-BINDING PROTEIN HOMOLOG 1) (TBP-1) gi 556560 gnl PID d1005143 (D17788) rice homologue of Tat binding protein [Oryza sativa]
1431	GM_63_B1_A10_MR	g3695395	BLASTX	192	1e-15	41	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
1432	GM_63_B1_B11_T7	g2191182	BLASTX	252	6e-20	59	(AF007271) similar to N. tabacum membrane-associated salt-inducible protein (PID:g473874) [Arabidopsis thaliana]
1433	GM_63_B1_B12_MR	g3777527	BLASTX	775	4e-75	95	(AF053008) gag-pol polyprotein [Glycine max]
1434	GM_63_B1_C01_T7	g668325	BLASTN	355	6e-10	62	Trypanosoma brucei EATRO 164 kinetoplast (CR4) mRNA, complete cds.
1435	GM_63_B1_C03_T7	g3777527	BLASTX	285	9e-23	43	(AF053008) gag-pol polyprotein [Glycine max]
1436	GM_63_B1_C04_MR	g3599418	BLASTN	366	1e-09	72	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
1437	GM_63_B1_C04_T7	g3367585	BLASTX	146	7e-09	35	(AL031135) putative polygalacturonase [Arabidopsis thaliana]
1438	GM_63_B1_C10_MR	g3777527	BLASTX	394	6e-42	87	(AF053008) gag-pol polyprotein [Glycine max]
1439	GM_63_B1_D01_MR	g2760830	BLASTX	465	2e-43	60	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]
1440	GM_63_B1_D02_MR	g1707020	BLASTX	181	2e-12	34	(U78721) hypothetical protein [Arabidopsis thaliana]
1441	GM_63_B1_D02_T7	g4097585	BLASTX	221	2e-17	67	(U64925) NTGP4 [Nicotiana tabacum]
1442	GM_63_B1_D03_MR	g2522230	BLASTX	243	8e-24	47	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
1443	GM_63_B1_D08_MR	g3337395	BLASTN	420	6e-12	63	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
1444	GM_63_B1_E02_T7	g1666236	BLASTX	244	6e-20	33	(U76261) unknown [Hordeum vulgare]
1445	GM_63_B1_E03_T7	g1769897	BLASTX	269	6e-22	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1446	GM_63_B1_E04_MR	g3386605	BLASTX	175	8e-12	35	(AC004665) hypothetical protein [Arabidopsis thaliana]
1447	GM_63_B1_E05_T7	g2522228	BLASTX	300	2e-46	63	(AB007466) reverse transcriptase-like protein [Vicia faba]
1448	GM_63_B1_E10_MR	g4063760	BLASTX	205	2e-14	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1449	GM_63_B1_F03_MR	g3142328	BLASTN	1125	5e-44	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1450	GM_63_B1_F04_MR	g3142328	BLASTN	786	1e-28	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1451	GM_63_B1_F06_T7	g4063760	BLASTX	230	4e-17	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1452	GM_63_B1_F07_T7	g1666236	BLASTX	165	4e-11	29	(U76261) unknown [Hordeum vulgare]
1453	GM_63_B1_F08_MR	g507910	BLASTN	696	8e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
1454	GM_63_B1_F11_T7	g1769898	BLASTX	227	3e-17	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1455	GM_63_B1_F12_T7	g18559	BLASTN	332	4e-11	71	G.max gene for catalase
1456	GM_63_B1_G01_MR	g2335061	BLASTN	328	3e-13	71	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence [Homo sapiens]
1457	GM_63_B1_G03_T7	g2970554	BLASTN	1094	2e-42	90	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
1458	GM_63_B1_G05_MR	g507910	BLASTN	579	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1459	GM_63_B1_G05_T7	g507910	BLASTN	589	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
1460	GM_63_B1_G06_MR	g3046704	BLASTX	240	4e-18	45	(AL022223) putative protein [Arabidopsis thaliana]
1461	GM_63_B1_G08_MR	g3097320	BLASTN	471	3e-14	76	Glycine max gene for Bd 30K, complete cds
1462	GM_63_B1_G10_T7	g3097320	BLASTN	536	3e-17	76	Glycine max gene for Bd 30K, complete cds
1463	GM_63_B1_H01_MR	g507910	BLASTN	566	6e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1464	GM_63_B1_H01_T7	g507910	BLASTN	345	6e-09	78	Glycine max BSR-101 satellite SB92 genomic sequence.
1465	GM_63_B1_H03_MR	g18695	BLASTN	475	1e-14	82	Soybean nodulin 22 gene
1466	GM_63_B1_H03_T7	g3810596	BLASTX	345	2e-29	49	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
1467	GM_63_B1_H05_MR	g3777527	BLASTX	493	6e-45	78	(AF053008) gag-pol polyprotein [Glycine max]
1468	GM_63_B1_H08_T7	g3600044	BLASTX	221	5e-16	36	(AF080119) contains similarity to proteases [Arabidopsis thaliana]
1469	GM_63_B1_H12_T7	g4104931	BLASTX	314	2e-26	52	(AF042196) auxin response factor 8 [Arabidopsis thaliana]
1470	GM_63_B2_A09_MR	g1052960	BLASTX	157	7e-24	87	(U37437) PNIL34 [Ipomoea nil]
1471	GM_63_B2_A10_MR	g4063760	BLASTX	229	5e-17	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1472	GM_63_B2_A11_MR	g3859610	BLASTN	641	6e-22	64	Arabidopsis thaliana BAC T9E19
1473	GM_63_B2_B07_MR	g2924733	BLASTN	382	3e-10	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUF9, complete sequence [Arabidopsis thaliana]
1474	GM_63_B2_B10_MR	g3142328	BLASTN	619	5e-21	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1475	GM_63_B2_B12_MR	g3097320	BLASTN	474	2e-14	71	Glycine max gene for Bd 30K, complete cds
1476	GM_63_B2_D03_MR	g3779030	BLASTX	201	2e-15	31	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
1477	GM_63_B2_D05_MR	g2462134	BLASTX	104	2e-11	33	(Y13368) reverse transcriptase [Beta vulgaris]
1478	GM_63_B2_D06_MR	g405321	BLASTX	117	1e-09	64	(S63758) metallothionein-I gene transcription activator [mice, L cells, Peptide, 102 aa] [Mus sp.]
1479	GM_63_B2_D07_MR	g3645899	BLASTX	428	2e-38	57	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1480	GM_63_B2_E05_MR	g4063760	BLASTX	482	5e-44	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1481	GM_63_B2_E08_MR	g2323254	BLASTN	391	1e-10	62	Human Chromosome X, complete sequence [Homo sapiens]
1482	GM_63_B2_G03_MR	g1184075	BLASTX	281	2e-22	45	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
1483	GM_63_B2_G07_MR	g166709	BLASTN	399	4e-11	64	Arabidopsis thaliana cytosolic glyceraldehyde-3-phosphate dehydrogenase (GapC) gene, exons 1-9, complete cds.
1484	GM_63_B2_G10_MR	g3777527	BLASTX	432	2e-38	82	(AF053008) gag-pol polyprotein [Glycine max]
1485	GM_63_B2_H07_MR	g507910	BLASTN	339	1e-08	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1486	GM_63_B2_H08_MR	g3645899	BLASTX	401	2e-35	54	(U68408) 5' end not determined experimentally [Zea mays]
1487	GM_63_B2_H09_MR	g130582	BLASTX	205	2e-14	34	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
1488	GM_64_A1_A11_T7	g2462058	BLASTX	140	8e-14	44	(Y13389) reverse transcriptase [Antirrhinum majus]
1489	GM_64_A1_B06_MR	g2121303	BLASTN	359	3e-09	61	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
1490	GM_64_A1_B06_T7	g3980412	BLASTX	313	2e-29	58	(AC004561) pumilio-like protein [Arabidopsis thaliana]
1491	GM_64_A1_B08_T7	g3142328	BLASTN	1925	1e-80	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1492	GM_64_A1_B09_MR	g3264565	BLASTN	353	7e-09	65	Homo sapiens chromosome 17, clone hRPC.1037_O_7, complete sequence [Homo sapiens]
1493	GM_64_A1_B10_MR	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1494	GM_64_A1_B10_T7	g4063760	BLASTX	220	5e-16	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1495	GM_64_A1_C04_MR	g3334661	BLASTX	205	5e-15	72	(Y10490) putative cytochrome P450 [Glycine max]
1496	GM_64_A1_C05_T7	g507910	BLASTN	632	6e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
1497	GM_64_A1_C09_T7	g2832623	BLASTX	112	5e-09	72	(AL021711) protein kinase - like protein [Arabidopsis thaliana]
1498	GM_64_A1_C10_T7	g3426334	BLASTN	595	6e-20	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
1499	GM_64_A1_C12_MR	g1769899	BLASTX	262	6e-22	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1500	GM_64_A1_C12_T7	g1769898	BLASTX	420	2e-38	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1501	GM_64_A1_D02_MR	g18559	BLASTN	1053	1e-40	74	G.max gene for catalase
1502	GM_64_A1_D04_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1503	GM_64_A1_D04_T7	g507910	BLASTN	375	2e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1504	GM_64_A1_D05_T7	g3377848	BLASTX	133	2e-11	31	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
1505	GM_64_A1_D06_MR	g18559	BLASTN	473	2e-14	69	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1506	GM_64_A1_D07_T7	g130582	BLASTX	159	2e-09	41	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
1507	GM_64_A1_D08_MR	g3914431	BLASTX	107	2e-11	86	PROTEASOME COMPONENT C8 (MACROPAIN SUBUNIT C8) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C8) >gi 2285802 gnl PID d1022501 (D78173) 26S proteasome alpha subunit [Spinacia oleracea]
1508	GM_64_A1_D08_T7	g2996647	BLASTN	507	7e-16	66	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
1509	GM_64_A1_D10_MR	g3810596	BLASTX	166	9e-25	57	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
1510	GM_64_A1_E05_MR	g2764526	BLASTN	486	6e-15	63	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
1511	GM_64_A1_E07_MR	g4063760	BLASTX	155	5e-09	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1512	GM_64_A1_E09_T7	g3777527	BLASTX	610	2e-57	92	(AF053008) gag-pol polyprotein [Glycine max]
1513	GM_64_A1_E12_T7	g170051	BLASTN	364	6e-10	74	Glycine max RNA polymerase II fifth largest subunit mRNA, complete cds.
1514	GM_64_A1_F05_MR	g3420052	BLASTX	187	5e-13	65	(AC004680) putative ubiqinone reductase [Arabidopsis thaliana]
1515	GM_64_A1_F07_T7	g3777527	BLASTX	673	3e-64	92	(AF053008) gag-pol polyprotein [Glycine max]
1516	GM_64_A1_F09_T7	g4063760	BLASTX	171	8e-11	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1517	GM_64_A1_F11_T7	g507910	BLASTN	414	4e-12	71	Glycine max BSR-101 satellite SB92 genomic sequence.
1518	GM_64_A1_G04_T7	g1769899	BLASTX	189	3e-16	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1519	GM_64_A1_G06_MR	g3097320	BLASTN	1585	9e-65	85	Glycine max gene for Bd 30K, complete cds
1520	GM_64_A1_G10_MR	g131289	BLASTX	761	8e-75	95	PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN) (CP43) gi 72709 pir F2NT44 photosystem II chlorophyll a-binding protein psbC - common tobacco chloroplast gi 225285 prf 1211235W photosystem II 44kD protein [Nicotiana tabacum]
1521	GM_64_A1_G10_T7	g131276	BLASTX	574	1e-60	92	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi 72704 pir QJNT6A photosystem II chlorophyll a-binding protein psbB - common tobacco chloroplast >gi 11856 (Z00044) PSII 47kD protein [Nicotiana tabacum] >gi 225224 prf 1211235BF photosystem II P680 apoprotein [Nicotiana tabacum]
1522	GM_64_A1_G11_T7	g421955	BLASTX	211	1e-21	50	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
1523	GM_64_A1_H10_MR	g905361	BLASTX	204	1e-14	33	(U22103) gag-protease polyprotein [Glycine max]
1524	GM_64_A2_A01_MR	g3777527	BLASTX	725	9e-70	91	(AF053008) gag-pol polyprotein [Glycine max]
1525	GM_64_A2_A07_T7	g3097320	BLASTN	350	8e-09	80	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1526	GM_64_A2_A08_T7	g507910	BLASTN	416	3e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1527	GM_64_A2_A10_MR	g3097320	BLASTN	1174	4e-46	80	Glycine max gene for Bd 30K, complete cds
1528	GM_64_A2_B01_T7	g629693	BLASTX	309	7e-27	44	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
1529	GM_64_A2_B04_T7	g1142702	BLASTN	363	7e-10	70	Glycine max satellite STR120-A.4.
1530	GM_64_A2_B05_T7	g1167523	BLASTX	218	7e-34	49	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
1531	GM_64_A2_B07_MR	g3319362	BLASTX	273	9e-22	39	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
1532	GM_64_A2_B10_T7	g2598579	BLASTX	246	2e-19	71	(Y15295) L-ascorbate oxidase [Medicago truncatula]
1533	GM_64_A2_C01_T7	g2464905	BLASTX	230	2e-18	57	(Z99708) minor allergen [Arabidopsis thaliana]
1534	GM_64_A2_C03_MR	g1769898	BLASTX	144	4e-14	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1535	GM_64_A2_C07_MR	g3645899	BLASTX	102	9e-09	41	(U68408) 5' end not determined experimentally [Zea mays]
1536	GM_64_A2_C08_MR	g549056	BLASTX	358	4e-34	70	T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) gi 631651 pir S43059 CCT (chaperonin containing TCP-1) beta chain - mouse gi 468546 (Z31553) CCT (chaperonin containing TCP-1) beta subunit [Mus musculus]
1537	GM_64_A2_C09_T7	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1538	GM_64_A2_C10_MR	g1840106	BLASTN	374	2e-10	64	Human fragile site locus (FRA16B) minisatellite repeat
1539	GM_64_A2_C11_T7	g2995405	BLASTX	340	5e-29	61	(Y12432) polyprotein [Ananas comosus]
1540	GM_64_A2_D01_MR	g2522228	BLASTX	220	3e-21	69	(AB007466) reverse transcriptase-like protein [Vicia faba]
1541	GM_64_A2_D02_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1542	GM_64_A2_D02_T7	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1543	GM_64_A2_D03_MR	g4151068	BLASTX	222	3e-26	84	(Y10862) ribonucleotide reductase [Nicotiana tabacum]
1544	GM_64_A2_E01_MR	g2522230	BLASTX	151	4e-10	27	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
1545	GM_64_A2_E01_T7	g4063760	BLASTX	598	2e-56	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1546	GM_64_A2_E08_MR	g4063760	BLASTX	265	8e-21	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1547	GM_64_A2_E09_MR	g3859610	BLASTN	416	9e-12	64	Arabidopsis thaliana BAC T9E19
1548	GM_64_A2_F02_MR	g505129	BLASTN	370	9e-10	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
1549	GM_64_A2_F02_T7	g1167523	BLASTX	212	7e-16	37	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
1550	GM_64_A2_F06_MR	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1551	GM_64_A2_F06_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
1552	GM_64_A2_F08_MR	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1553	GM_64_A2_F08_T7	g507910	BLASTN	561	1e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
1554	GM_64_A2_F09_T7	g3548819	BLASTX	161	3e-11	57	(AC005313) putative heterogeneous nuclear ribonucleoprotein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1555	GM_64_A2_F10_T7	g130582	BLASTX	172	8e-11	42	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
1556	GM_64_A2_G02_T7	g3935187	BLASTX	501	3e-47	64	(AC004557) F17L21.30 [Arabidopsis thaliana]
1557	GM_64_A2_G04_T7	g18559	BLASTN	519	2e-16	68	G.max gene for catalase
1558	GM_64_A2_G10_T7	g3097836	BLASTN	373	8e-10	63	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
1559	GM_64_A2_H01_MR	g1840106	BLASTN	400	9e-12	63	Human fragile site locus (FRA16B) minisatellite repeat
1560	GM_64_A2_H05_T7	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1561	GM_64_A2_H10_MR	g4063760	BLASTX	179	5e-13	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1562	GM_64_A2_H10_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1563	GM_64_A2_H11_T7	g4063760	BLASTX	237	8e-18	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1564	GM_64_B1_A02_MR	g1769898	BLASTX	119	9e-15	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1565	GM_64_B1_A03_MR	g3777527	BLASTX	487	3e-44	88	(AF053008) gag-pol polyprotein [Glycine max]
1566	GM_64_B1_A06_MR	g100484	BLASTX	267	2e-21	49	hypothetical protein - garden snapdragon
1567	GM_64_B1_A11_MR	g3845264	BLASTN	396	7e-11	62	Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence
1568	GM_64_B1_B05_MR	g18559	BLASTN	1242	3e-49	82	G.max gene for catalase
1569	GM_64_B1_B09_MR	g1711615	BLASTX	248	2e-19	58	HIGH AFFINITY SULPHATE TRANSPORTER 1 gi 1085847 pir S51763 high affinity sulphate transporter - Stylosanthes hamata gi 607184 (X82255) high affinity sulphate transporter [Stylosanthes hamata]
1570	GM_64_B1_B10_MR	g905361	BLASTX	212	1e-15	37	(U22103) gag-protease polyprotein [Glycine max]
1571	GM_64_B1_B12_MR	g136636	BLASTX	216	5e-17	95	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana gi 442594 pdb 1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) gi 2981894 pdb 2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana Ubiquitin Conjugation, Ligase Mol_id: 1; Molecule: Ubiquitin Conjugating Enzyme; Chain: Null; Synonym: Ubc1; Ec: 6.3.2.19; Engineered: Yes gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] gi 431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]
1572	GM_64_B1_C01_MR	g2052034	BLASTN	397	7e-11	62	Human DNA sequence from PAC 450C20 on chromosome X

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1573	GM_64_B1_C03_MR	g136636	BLASTX	168	6e-12	78	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana gi 442594 pdb 1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) gi 2981894 pdb 2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana Ubiquitin Conjugation, Ligase Mol_id: 1; Molecule: Ubiquitin Conjugating Enzyme; Chain: Null; Synonym: Ubc1; Ec: 6.3.2.19; Engineered: Yes gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] gi 431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]
1574	GM_64_B1_C04_T7	g507910	BLASTN	341	8e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1575	GM_64_B1_C07_MR	g3056593	BLASTX	144	7e-14	56	(AC004255) T1F9.14 [Arabidopsis thaliana]
1576	GM_64_B1_C08_T7	g3449327	BLASTN	477	2e-14	72	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]
1577	GM_64_B1_C12_T7	g3095075	BLASTX	139	7e-09	35	(AF031471) pollen allergen [Juniperus oxycedrus]
1578	GM_64_B1_D01_MR	g3777527	BLASTX	391	5e-34	92	(AF053008) gag-pol polyprotein [Glycine max]
1579	GM_64_B1_D05_MR	g3283026	BLASTX	106	2e-10	42	putative transposase [Arabidopsis thaliana]
1580	GM_64_B1_D06_T7	g130582	BLASTX	201	3e-27	67	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
1581	GM_64_B1_D07_MR	g2564050	BLASTN	376	6e-10	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]
1582	GM_64_B1_D12_T7	g2522228	BLASTX	147	7e-09	34	(AB007466) reverse transcriptase-like protein [Vicia faba]
1583	GM_64_B1_E02_MR	g629693	BLASTX	229	2e-24	49	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
1584	GM_64_B1_E03_MR	g587603	BLASTN	350	7e-09	61	P.falciparum gene for beta subunit RNA polymerase
1585	GM_64_B1_E03_T7	g3292816	BLASTX	174	9e-12	86	(AL031018) putative fizzy-related protein [Arabidopsis thaliana]
1586	GM_64_B1_E04_T7	g1167523	BLASTX	218	7e-34	49	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
1587	GM_64_B1_E05_MR	g3763934	BLASTX	309	4e-26	51	(AC004450) hypothetical protein [Arabidopsis thaliana]
1588	GM_64_B1_E06_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
1589	GM_64_B1_E07_MR	g2522228	BLASTX	387	4e-35	66	(AB007466) reverse transcriptase-like protein [Vicia faba]
1590	GM_64_B1_F03_T7	g2618698	BLASTX	128	1e-12	81	(AC002510) unknown protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1591	GM_64_B1_F10_T7	g2895630	BLASTN	375	3e-10	61	Phoebis sennae large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
1592	GM_64_B1_G03_T7	g3097320	BLASTN	966	1e-36	80	Glycine max gene for Bd 30K, complete cds
1593	GM_64_B1_G04_MR	g3913727	BLASTX	257	1e-20	72	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CYTOPLASMIC ISOFORM (G6PD) >gi 1174336 gnl PID e137420 (X84230) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
1594	GM_64_B1_H01_MR	g2129618	BLASTX	173	4e-11	32	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
1595	GM_64_B1_H01_T7	g2522228	BLASTX	149	4e-09	31	(AB007466) reverse transcriptase-like protein [Vicia faba]
1596	GM_64_B1_H03_MR	g4063770	BLASTX	258	3e-24	42	(AB004906) transposase [Ipomoea purpurea]
1597	GM_64_B1_H09_MR	g507910	BLASTN	550	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
1598	GM_64_B1_H10_MR	g1431738	BLASTN	353	5e-09	89	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
1599	GM_64_B1_H11_T7	g4006831	BLASTX	164	4e-10	47	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
1600	GM_64_B2_A02_T7	g2832901	BLASTN	1639	1e-73	78	Cajanus cajan copia-like retrotransposon,Panzee
1601	GM_64_B2_B03_T7	g3097320	BLASTN	560	3e-18	65	Glycine max gene for Bd 30K, complete cds
1602	GM_64_B2_B04_T7	g507910	BLASTN	404	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1603	GM_64_B2_B05_T7	g4038057	BLASTX	164	3e-10	37	(AC005897) hypothetical protein [Arabidopsis thaliana]
1604	GM_64_B2_B06_T7	g585565	BLASTX	165	1e-11	75	RIBOSOME RECYCLING FACTOR HOMOLOG (NUCLEAR LOCATED PROTEIN D2) gi 629661 pir S32716 nuclear protein - carrot gi 297891 (X72384) nuclear located protein [Daucus carota]
1605	GM_64_B2_B08_T7	g131274	BLASTX	174	9e-16	68	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi 12278 (X02945) P(680) apoprotein [Spinacia oleracea]
1606	GM_64_B2_C04_T7	g421955	BLASTX	192	7e-14	63	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
1607	GM_64_B2_C07_T7	g2924654	BLASTN	690	4e-24	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHK7, complete sequence [Arabidopsis thaliana]
1608	GM_64_B2_C09_T7	g3142328	BLASTN	1027	1e-39	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1609	GM_64_B2_D01_T7	g2576363	BLASTX	332	3e-29	48	(U39783) amino acid transport protein [Arabidopsis thaliana]
1610	GM_64_B2_D04_T7	g3645899	BLASTX	480	7e-44	52	(U68408) 5' end not determined experimentally [Zea mays]
1611	GM_64_B2_D06_T7	g2522230	BLASTX	206	6e-16	32	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1612	GM_64_B2_D10_T7	g559273	BLASTN	288	2e-11	67	Saccharomyces cerevisiae mitochondrion oxi3 gene, aapI gene, oli2 gene, ORF4, replication of origin (ori7 and ori2), and ORF5.
1613	GM_64_B2_D11_T7	g507910	BLASTN	538	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1614	GM_64_B2_E02_T7	g3461840	BLASTX	387	1e-33	46	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
1615	GM_64_B2_E03_T7	g18559	BLASTN	624	3e-21	68	G.max gene for catalase
1616	GM_64_B2_F02_T7	g3779021	BLASTX	179	1e-12	45	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]
1617	GM_64_B2_F03_T7	g18559	BLASTN	1046	2e-40	77	G.max gene for catalase
1618	GM_64_B2_F04_T7	g1171591	BLASTN	366	2e-09	61	P.falciparum complete gene map of plastid-like DNA (IR-B)
1619	GM_64_B2_F09_T7	g507910	BLASTN	591	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1620	GM_64_B2_G06_T7	g3777527	BLASTX	853	2e-88	97	(AF053008) gag-pol polyprotein [Glycine max]
1621	GM_64_B2_G07_T7	g493737	BLASTN	364	2e-09	61	Honey bee mitochondrial cytochrome oxidase subunit I and II genes, complete cds, and Trp-, Leu-, Asp-, and Lys-tRNAs.
1622	GM_64_B2_H04_T7	g100484	BLASTX	401	4e-44	50	hypothetical protein - garden snapdragon
1623	GM_64_B2_H08_T7	g2781364	BLASTX	124	2e-11	35	(AC003113) F24O1.20 [Arabidopsis thaliana]
1624	GM_64_B2_H09_T7	g2522228	BLASTX	625	1e-66	71	(AB007466) reverse transcriptase-like protein [Vicia faba]
1625	GM_65_A1_A04_T7	g3184508	BLASTN	450	3e-13	67	Homo sapiens chromosome 17, clone HRPC41C23, complete sequence [Homo sapiens]
1626	GM_65_A1_A09_MR	g4038056	BLASTX	291	9e-24	48	(AC005897) putative transposon [Arabidopsis thaliana]
1627	GM_65_A1_A11_T7	g3608481	BLASTX	216	4e-17	71	(AF088913) ribosomal protein L27a [Petunia x hybrida]
1628	GM_65_A1_A12_MR	g2995405	BLASTX	516	4e-48	65	(Y12432) polyprotein [Ananas comosus]
1629	GM_65_A1_B02_MR	g1666236	BLASTX	227	3e-18	30	(U76261) unknown [Hordeum vulgare]
1630	GM_65_A1_B02_T7	g3845070	BLASTN	349	9e-09	58	Plasmodium falciparum chromosome 2, section 3 of 73 of the complete sequence
1631	GM_65_A1_B03_T7	g1431738	BLASTN	598	3e-20	93	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
1632	GM_65_A1_B05_T7	g507910	BLASTN	417	3e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1633	GM_65_A1_B08_T7	g2443320	BLASTX	355	3e-30	56	(D85597) polyprotein [Oryza australiensis]
1634	GM_65_A1_B10_MR	g3021268	BLASTX	325	4e-27	50	(AL022347) putative protein [Arabidopsis thaliana]
1635	GM_65_A1_B12_T7	g4063760	BLASTX	387	8e-34	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1636	GM_65_A1_C04_MR	g3550435	BLASTN	534	4e-17	63	Hordeum vulgare Hotr1 gene
1637	GM_65_A1_C04_T7	g507910	BLASTN	660	3e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
1638	GM_65_A1_D02_T7	g3695395	BLASTX	177	8e-12	37	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
1639	GM_65_A1_D04_MR	g4092470	BLASTN	409	2e-11	59	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
1640	GM_65_A1_D05_T7	g507910	BLASTN	530	2e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
1641	GM_65_A1_D08_MR	g2344889	BLASTX	138	4e-14	47	(AC002388) unknown protein [Arabidopsis thaliana]
1642	GM_65_A1_D10_T7	g1769898	BLASTX	146	3e-10	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1643	GM_65_A1_D11_MR	g18559	BLASTN	598	4e-20	74	G.max gene for catalase
1644	GM_65_A1_D11_T7	g2104680	BLASTN	444	3e-13	76	V.faba mRNA for putative transciption factor (1556bp)
1645	GM_65_A1_D12_T7	g2842490	BLASTX	380	2e-34	55	(AL021749) heat-shock protein [Arabidopsis thaliana]
1646	GM_65_A1_E07_T7	g99730	BLASTX	182	9e-20	50	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
1647	GM_65_A1_E12_MR	g507910	BLASTN	556	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1648	GM_65_A1_F01_T7	g2252830	BLASTX	198	8e-15	79	(AF013293) weak similarity to receptor protein kinase [Arabidopsis thaliana]
1649	GM_65_A1_F08_MR	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
1650	GM_65_A1_F11_T7	g2462828	BLASTX	211	4e-15	41	(AF000657) hypothetical protein [Arabidopsis thaliana]
1651	GM_65_A1_G01_T7	g2129613	BLASTX	177	8e-18	47	homeotic protein BEL1 - Arabidopsis thaliana gi 1122533 (U39944) BELL1 [Arabidopsis thaliana]
1652	GM_65_A1_G03_MR	g2522227	BLASTX	213	1e-16	46	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
1653	GM_65_A1_G05_T7	g1142703	BLASTN	257	1e-13	73	Glycine max satellite STR120-B.1.
1654	GM_65_A1_G06_T7	g3212102	BLASTN	690	4e-24	68	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]
1655	GM_65_A1_G08_MR	g3777527	BLASTX	171	1e-10	33	(AF053008) gag-pol polyprotein [Glycine max]
1656	GM_65_A1_G08_T7	g535454	BLASTX	166	4e-11	43	(U13940) cysteine proteinase [Alnus glutinosa]
1657	GM_65_A1_H02_MR	g2961349	BLASTX	210	5e-15	52	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
1658	GM_65_A1_H02_T7	g2995405	BLASTX	155	3e-09	48	(Y12432) polyprotein [Ananas comosus]
1659	GM_65_A1_H04_T7	g3142328	BLASTN	1840	1e-76	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1660	GM_65_A1_H07_MR	g3142328	BLASTN	671	2e-23	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1661	GM_65_A1_H10_T7	g4115365	BLASTX	180	1e-11	41	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
1662	GM_65_A2_A03_MR	g1888357	BLASTX	191	5e-13	63	(X98130) alpha-mannosidase [Arabidopsis thaliana] gi 1890154 gnl PID e307744 (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]
1663	GM_65_A2_B05_MR	g132866	BLASTX	205	7e-16	89	CHLOROPLAST 50S RIBOSOMAL PROTEIN L2 gi 71086 pir R5NT2 ribosomal protein L2 - common tobacco chloroplast gi 435269 (Z00044) ribosomal protein L2 [Nicotiana tabacum] gi 1223691 (Z00044) ribosomal protein L2 [Nicotiana tabacum] gi 225238 prf 1211235BW ribosomal protein L2 [Nicotiana tabacum]
1664	GM_65_A2_B11_MR	g18559	BLASTN	1374	3e-55	82	G.max gene for catalase
1665	GM_65_A2_B12_MR	g3097320	BLASTN	467	4e-14	73	Glycine max gene for Bd 30K, complete cds
1666	GM_65_A2_C02_MR	g2052034	BLASTN	380	4e-10	68	Human DNA sequence from PAC 450C20 on chromosome X

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1667	GM_65_A2_D03_MR	g3738114	BLASTN	435	1e-12	65	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
1668	GM_65_A2_D06_T7	g2384671	BLASTX	128	1e-11	88	(AF012657) putative potassium transporter AtKT2p [Arabidopsis thaliana]
1669	GM_65_A2_D11_MR	g3779030	BLASTX	157	9e-11	37	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
1670	GM_65_A2_D12_T7	g3142328	BLASTN	842	4e-31	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1671	GM_65_A2_E04_T7	g3288442	BLASTN	408	2e-11	63	Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Ga...
1672	GM_65_A2_G12_T7	g2739374	BLASTX	190	2e-13	41	(AC002505) hypothetical protein [Arabidopsis thaliana]
1673	GM_65_A2_H02_MR	g3080384	BLASTX	290	7e-24	38	(AL022603) serine/threonine protein kinase [Arabidopsis thaliana] gi 3402759 gnl PID e1314603 (AL031187) serine/threonine protein kinase - like protein [Arabidopsis thaliana]
1674	GM_65_A2_H08_MR	g2522227	BLASTX	230	2e-18	41	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
1675	GM_65_A2_H09_MR	g2160144	BLASTX	214	7e-16	44	(AC000375) Strong similarity to Arabidopsis oligopeptide transporter (gb X77503). [Arabidopsis thaliana]
1676	GM_65_A2_H11_MR	g140419	BLASTX	146	1e-09	41	TRANSPOSON TY5-1 16.0 KD HYPOTHETICAL PROTEIN gi 83189 pir S19407 hypothetical protein YCL075w - yeast (Saccharomyces cerevisiae) gi 5284 gnl PID e264615 (X59720) YCL075w, len:146; not real ORF - included in pseudogene [Saccharomyces cerevisiae]
1677	GM_65_B1_A03_MR	g2129618	BLASTX	195	2e-13	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
1678	GM_65_B1_A04_MR	g507910	BLASTN	572	3e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1679	GM_65_B1_A04_T7	g507910	BLASTN	601	1e-20	84	Glycine max BSR-101 satellite SB92 genomic sequence.
1680	GM_65_B1_A08_MR	g3582347	BLASTN	353	7e-09	59	Homo sapiens chromosome Y, clone hCIT.144_J_1, complete sequence [Homo sapiens]
1681	GM_65_B1_A09_MR	g507910	BLASTN	557	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1682	GM_65_B1_A09_T7	g507910	BLASTN	511	2e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
1683	GM_65_B1_B03_T7	g2435519	BLASTX	206	3e-27	84	(AF024504) similar to mouse MEM3 (GB:U47024 and S. cerevisiae vacuolar sorting protein 35 (SW;P34110) [Arabidopsis thaliana]
1684	GM_65_B1_B07_T7	g4050011	BLASTN	420	6e-12	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
1685	GM_65_B1_B11_T7	g3142328	BLASTN	608	1e-20	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1686	GM_65_B1_C11_MR	g3097320	BLASTN	421	5e-12	79	Glycine max gene for Bd 30K, complete cds
1687	GM_65_B1_C12_MR	g905361	BLASTX	423	1e-38	95	(U22103) gag-protease polyprotein [Glycine max]
1688	GM_65_B1_D03_T7	g3319345	BLASTX	246	6e-19	40	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
1689	GM_65_B1_D04_MR	g3599418	BLASTN	497	2e-15	89	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
1690	GM_65_B1_D05_T7	g4063760	BLASTX	467	2e-42	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1691	GM_65_B1_D06_MR	g342963	BLASTN	390	5e-11	64	paramecium species 5,87 mt dna dimer: replication init. region.
1692	GM_65_B1_D08_T7	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1693	GM_65_B1_D09_MR	g18559	BLASTN	642	4e-22	78	G.max gene for catalase
1694	GM_65_B1_D10_MR	g1840106	BLASTN	405	5e-12	60	Human fragile site locus (FRA16B) minisatellite repeat
1695	GM_65_B1_D11_MR	g507910	BLASTN	747	4e-27	90	Glycine max BSR-101 satellite SB92 genomic sequence.
1696	GM_65_B1_D11_T7	g4063756	BLASTN	437	1e-12	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
1697	GM_65_B1_D12_MR	g2351067	BLASTN	384	1e-11	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12
1698	GM_65_B1_E03_MR	g2351067	BLASTN	398	4e-12	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPO12
1699	GM_65_B1_E04_MR	g1480927	BLASTN	1255	5e-51	81	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
1700	GM_65_B1_E04_T7	g99721	BLASTX	307	3e-25	37	retrovirus-related polyprotein - Arabidopsis thaliana retrotransposon Ta1-3 gi 16534 (X13291) polyprotein [Arabidopsis thaliana]
1701	GM_65_B1_E06_MR	g507910	BLASTN	401	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1702	GM_65_B1_E06_T7	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1703	GM_65_B1_E07_T7	g113497	BLASTX	88	2e-09	56	ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) gi 99880 pir S07472 alpha-galactosidase (EC 3.2.1.22) precursor - guar gi 18292 (X14619) alpha-galactosidase preproprotein [Cyamopsis tetragonoloba]
1704	GM_65_B1_E08_T7	g3426334	BLASTN	355	5e-09	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
1705	GM_65_B1_E09_T7	g3142328	BLASTN	2413	9e-104	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1706	GM_65_B1_E10_MR	g1769898	BLASTX	270	2e-32	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1707	GM_65_B1_E11_T7	g99922	BLASTX	424	5e-39	71	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
1708	GM_65_B1_E12_MR	g1769897	BLASTX	269	6e-22	71	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1709	GM_65_B1_F01_T7	g3142328	BLASTN	943	9e-36	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1710	GM_65_B1_F03_MR	g3319351	BLASTX	261	3e-20	52	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
1711	GM_65_B1_F04_T7	g421955	BLASTX	433	5e-40	53	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
1712	GM_65_B1_F05_MR	g4150930	BLASTN	548	1e-17	61	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
1713	GM_65_B1_F05_T7	g995751	BLASTN	354	4e-09	64	Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence
1714	GM_65_B1_G02_T7	g2970556	BLASTX	140	3e-18	78	(AF049708) aspartokinase-homoserine dehydrogenase [Glycine max]
1715	GM_65_B1_G06_T7	g18559	BLASTN	984	1e-37	76	G.max gene for catalase
1716	GM_65_B1_G07_T7	g995751	BLASTN	415	7e-12	61	Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence
1717	GM_65_B1_G09_MR	g905361	BLASTX	894	7e-92	92	(U22103) gag-protease polyprotein [Glycine max]
1718	GM_65_B1_G10_MR	g629693	BLASTX	165	2e-14	40	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
1719	GM_65_B1_G11_MR	g1806119	BLASTX	182	2e-13	43	(Y10603) L-lactate dehydrogenase [Lycopersicon esculentum]
1720	GM_65_B1_H01_T7	g4063760	BLASTX	332	2e-35	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1721	GM_65_B1_H03_T7	g3097320	BLASTN	383	3e-10	77	Glycine max gene for Bd 30K, complete cds
1722	GM_65_B1_H07_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1723	GM_65_B1_H07_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1724	GM_65_B1_H09_MR	g3377834	BLASTX	161	5e-10	27	(AF075598) No definition line found [Arabidopsis thaliana]
1725	GM_65_B1_H11_MR	g3097320	BLASTN	426	3e-12	62	Glycine max gene for Bd 30K, complete cds
1726	GM_65_B1_H11_T7	g4159699	BLASTN	461	8e-14	62	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16E1, complete sequence [Arabidopsis thaliana]
1727	GM_65_B2_A02_T7	g629693	BLASTX	147	5e-20	52	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
1728	GM_65_B2_A03_MR	g13533	BLASTN	369	8e-14	61	Yeast mitochondrial tRNA genes (several, map positions 3.5 to 8.6) encoding tRNAs for Lys, Arg, Gly, Asp, Ser, Arg, and Ala.
1729	GM_65_B2_A05_MR	g9837	BLASTN	395	7e-11	60	P.falciparum 3.8 gene for putative serine kinase (partial) and GBP130 gene for glycophorin binding protein (partial)
1730	GM_65_B2_B01_T7	g629693	BLASTX	254	6e-21	44	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
1731	GM_65_B2_B12_T7	g3645899	BLASTX	206	8e-28	59	(U68408) 5' end not determined experimentally [Zea mays]
1732	GM_65_B2_C02_T7	g4063760	BLASTX	217	4e-27	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1733	GM_65_B2_C03_T7	g2464880	BLASTX	355	9e-32	51	(Z99707) hypothetical protein [Arabidopsis thaliana]
1734	GM_65_B2_D01_MR	g4160362	BLASTN	384	3e-10	60	Saccharomyces cerevisiae complete mitochondrial genome
1735	GM_65_B2_D03_MR	g2708743	BLASTX	136	1e-13	38	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1736	GM_65_B2_D03_T7	g905361	BLASTX	226	5e-17	30	(U22103) gag-protease polyprotein [Glycine max]
1737	GM_65_B2_E02_MR	g2462134	BLASTX	170	3e-11	37	(Y13368) reverse transcriptase [Beta vulgaris]
1738	GM_65_B2_E03_T7	g3785975	BLASTX	194	1e-13	97	(AC005560) hypothetical protein [Arabidopsis thaliana]
1739	GM_65_B2_E04_MR	g4063756	BLASTN	359	3e-09	71	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
1740	GM_65_B2_E10_T7	g507910	BLASTN	398	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1741	GM_65_B2_F06_MR	g4006815	BLASTN	596	7e-20	72	Arabidopsis thaliana chromosome II BAC T6P5 genomic sequence, complete sequence [Arabidopsis thaliana]
1742	GM_65_B2_F07_T7	g100484	BLASTX	344	1e-29	59	hypothetical protein - garden snapdragon
1743	GM_65_B2_F09_MR	g3426334	BLASTN	494	2e-15	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
1744	GM_65_B2_F12_MR	g3777527	BLASTX	427	2e-40	65	(AF053008) gag-pol polyprotein [Glycine max]
1745	GM_65_B2_G03_MR	g3777527	BLASTX	306	5e-25	75	(AF053008) gag-pol polyprotein [Glycine max]
1746	GM_65_B2_G04_T7	g2995405	BLASTX	629	9e-61	59	(Y12432) polyprotein [Ananas comosus]
1747	GM_65_B2_G07_T7	g507910	BLASTN	388	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1748	GM_65_B2_G11_MR	g2982528	BLASTN	423	4e-12	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-01, complete sequence [Plasmodium falciparum]
1749	GM_65_B2_H02_T7	g905361	BLASTX	278	1e-22	35	(U22103) gag-protease polyprotein [Glycine max]
1750	GM_65_B2_H06_T7	g507910	BLASTN	528	3e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
1751	GM_65_B2_H07_MR	g3128140	BLASTN	352	7e-09	61	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE4, complete sequence.
1752	GM_65_B2_H09_T7	g2828185	BLASTN	494	3e-15	74	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]
1753	GM_66_A1_A01_T7	g18695	BLASTN	350	6e-09	66	Soybean nodulin 22 gene
1754	GM_66_A1_A04_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1755	GM_66_A1_A05_MR	g99922	BLASTX	147	5e-09	65	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
1756	GM_66_A1_A07_MR	g3319362	BLASTX	324	9e-31	54	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
1757	GM_66_A1_A08_T7	g507910	BLASTN	405	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1758	GM_66_A1_A09_T7	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
1759	GM_66_A1_A10_MR	g2522230	BLASTX	291	6e-25	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
1760	GM_66_A1_B03_T7	g2522230	BLASTX	151	4e-10	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
1761	GM_66_A1_B12_T7	g3097320	BLASTN	721	1e-25	83	Glycine max gene for Bd 30K, complete cds
1762	GM_66_A1_C03_MR	g4150930	BLASTN	373	8e-10	63	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
1763	GM_66_A1_C03_T7	g2995405	BLASTX	206	1e-14	44	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1764	GM_66_A1_C05_MR	g3777527	BLASTX	491	1e-44	78	(AF053008) gag-pol polyprotein [Glycine max]
1765	GM_66_A1_C12_MR	g3176726	BLASTX	211	3e-15	51	(AC002392) putative serine proteinase [Arabidopsis thaliana]
1766	GM_66_A1_D01_T7	g1906603	BLASTN	348	1e-08	70	Zea mays ACCase gene, intron containing colonist1 and colonist2 retrotransposons and reverse transcriptase pseudogene, complete sequence
1767	GM_66_A1_D02_T7	g18559	BLASTN	322	9e-10	75	G.max gene for catalase
1768	GM_66_A1_D03_T7	g4038592	BLASTX	208	8e-15	34	(Y10403) RNA-directed RNA polymerase [Lycopersicon esculentum]
1769	GM_66_A1_D04_MR	g3097836	BLASTN	371	1e-09	64	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
1770	GM_66_A1_D04_T7	g3805845	BLASTX	219	3e-21	80	(AL031986) putative protein [Arabidopsis thaliana]
1771	GM_66_A1_D06_T7	g4063760	BLASTX	552	2e-51	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1772	GM_66_A1_D09_MR	g4063760	BLASTX	366	2e-31	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1773	GM_66_A1_D12_MR	g3068704	BLASTX	325	2e-27	70	(AF049236) unknown [Arabidopsis thaliana]
1774	GM_66_A1_E01_T7	g3287288	BLASTN	372	8e-10	63	Vicia faba L. Kleine Thueringer
1775	GM_66_A1_E03_T7	g1171499	BLASTX	232	5e-30	69	(Z68913) reverse transcriptase [Beta vulgaris]
1776	GM_66_A1_E07_MR	g905361	BLASTX	218	3e-16	36	(U22103) gag-protease polyprotein [Glycine max]
1777	GM_66_A1_E10_MR	g3777527	BLASTX	742	2e-71	94	(AF053008) gag-pol polyprotein [Glycine max]
1778	GM_66_A1_F01_T7	g3142328	BLASTN	798	6e-55	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1779	GM_66_A1_F02_MR	g1142701	BLASTN	1364	3e-55	86	Glycine max satellite STR120-A.3.
1780	GM_66_A1_F02_T7	g3777527	BLASTX	599	3e-56	94	(AF053008) gag-pol polyprotein [Glycine max]
1781	GM_66_A1_F05_T7	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1782	GM_66_A1_F07_MR	g18559	BLASTN	1098	9e-43	77	G.max gene for catalase
1783	GM_66_A1_F10_MR	g3550435	BLASTN	530	6e-17	63	Hordeum vulgare Hotr1 gene
1784	GM_66_A1_F10_T7	g3337392	BLASTN	393	1e-10	64	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence [Homo sapiens]
1785	GM_66_A1_G01_MR	g2264318	BLASTN	415	1e-11	85	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]
1786	GM_66_A1_G02_MR	g4063760	BLASTX	194	3e-13	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1787	GM_66_A1_G03_T7	g3645899	BLASTX	154	5e-09	39	(U68408) 5' end not determined experimentally [Zea mays]
1788	GM_66_A1_G04_T7	g3513745	BLASTX	124	2e-11	36	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
1789	GM_66_A1_G05_MR	g3319362	BLASTX	253	1e-19	45	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
1790	GM_66_A1_G10_MR	g3873182	BLASTN	351	8e-09	60	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
1791	GM_66_A1_G11_MR	g2995405	BLASTX	317	1e-26	50	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1792	GM_66_A1_G12_MR	g342963	BLASTN	515	6e-17	66	paramecium species 5,87 mt dna dimer: replication init. region.
1793	GM_66_A1_H01_MR	g2262114	BLASTX	235	4e-19	53	(AC002343) cellulose synthase isolog [Arabidopsis thaliana]
1794	GM_66_A1_H03_T7	g3142328	BLASTN	1604	7e-66	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1795	GM_66_A1_H05_MR	g507910	BLASTN	585	8e-20	84	Glycine max BSR-101 satellite SB92 genomic sequence.
1796	GM_66_A1_H05_T7	g3810596	BLASTX	118	6e-09	36	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
1797	GM_66_A2_A02_T7	g4038056	BLASTX	171	6e-11	44	(AC005897) putative transposon [Arabidopsis thaliana]
1798	GM_66_A2_A03_T7	g3057150	BLASTX	163	2e-11	80	(AF059037) chaperonin 10 [Arabidopsis thaliana]
1799	GM_66_A2_A05_T7	g3777527	BLASTX	722	2e-69	91	(AF053008) gag-pol polyprotein [Glycine max]
1800	GM_66_A2_A07_MR	g3645899	BLASTX	182	5e-12	43	(U68408) 5' end not determined experimentally [Zea mays]
1801	GM_66_A2_A12_MR	g3142379	BLASTX	325	1e-28	67	(AF053008) envelope-like [Glycine max]
1802	GM_66_A2_A12_T7	g3142328	BLASTN	825	2e-30	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1803	GM_66_A2_B02_MR	g2213540	BLASTX	297	5e-24	54	(X98744) chloroplast DNA-binding protein PD3 [Pisum sativum]
1804	GM_66_A2_B02_T7	g2564048	BLASTN	566	2e-18	78	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]
1805	GM_66_A2_B05_MR	g4063770	BLASTX	103	4e-09	35	(AB004906) transposase [Ipomoea purpurea]
1806	GM_66_A2_B08_MR	g322663	BLASTX	288	1e-24	68	S-receptor kinase-related protein - Chinese kale gi 17917 (Z18884) S-receptor kinase related protein [Brassica oleracea]
1807	GM_66_A2_B09_MR	g3264565	BLASTN	430	2e-12	64	Homo sapiens chromosome 17, clone hRPC.1037_O_7, complete sequence [Homo sapiens]
1808	GM_66_A2_B10_MR	g1142699	BLASTN	247	2e-12	75	Glycine max satellite STR120-A.1.
1809	GM_66_A2_B10_T7	g4063770	BLASTX	180	6e-12	38	(AB004906) transposase [Ipomoea purpurea]
1810	GM_66_A2_B11_T7	g3142328	BLASTN	753	4e-27	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1811	GM_66_A2_C02_T7	g4063760	BLASTX	317	5e-45	79	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1812	GM_66_A2_C03_T7	g3810596	BLASTX	234	1e-17	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
1813	GM_66_A2_C05_MR	g507910	BLASTN	412	5e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
1814	GM_66_A2_C05_T7	g507910	BLASTN	348	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
1815	GM_66_A2_C08_MR	g3928116	BLASTN	391	1e-10	70	, complete sequence [Homo sapiens]
1816	GM_66_A2_C08_T7	g1431738	BLASTN	575	4e-19	77	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
1817	GM_66_A2_C10_MR	g905361	BLASTX	676	1e-65	98	(U22103) gag-protease polyprotein [Glycine max]
1818	GM_66_A2_C12_MR	g2880057	BLASTX	262	2e-22	51	(AC002340) putative RNA helicase A, 5' partial [Arabidopsis thaliana]
1819	GM_66_A2_D01_MR	g3820757	BLASTN	382	2e-10	60	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
1820	GM_66_A2_D03_MR	g3097320	BLASTN	1137	2e-44	82	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1821	GM_66_A2_D05_MR	g507910	BLASTN	556	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
1822	GM_66_A2_D05_T7	g507910	BLASTN	543	6e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1823	GM_66_A2_D06_MR	g304040	BLASTN	628	1e-21	81	Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene.
1824	GM_66_A2_E02_MR	g2914706	BLASTX	190	1e-22	74	(AC003974) putative homeobox protein [Arabidopsis thaliana]
1825	GM_66_A2_E04_MR	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1826	GM_66_A2_E04_T7	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1827	GM_66_A2_E09_MR	g905361	BLASTX	384	3e-34	89	(U22103) gag-protease polyprotein [Glycine max]
1828	GM_66_A2_E10_MR	g1870709	BLASTN	307	2e-10	62	Toxoplasma gondii chloroplast, complete genome
1829	GM_66_A2_F02_MR	g2522228	BLASTX	176	2e-16	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
1830	GM_66_A2_F03_MR	g2462058	BLASTX	196	7e-15	45	(Y13389) reverse transcriptase [Antirrhinum majus]
1831	GM_66_A2_F07_T7	g3650039	BLASTX	247	3e-19	40	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
1832	GM_66_A2_F09_MR	g18559	BLASTN	775	4e-28	75	G.max gene for catalase
1833	GM_66_A2_G04_MR	g3513747	BLASTX	181	1e-11	47	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
1834	GM_66_A2_G08_T7	g1769898	BLASTX	444	3e-41	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
1835	GM_66_A2_G10_T7	g4063760	BLASTX	226	1e-16	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1836	GM_66_A2_H01_MR	g505129	BLASTN	396	6e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
1837	GM_66_A2_H11_MR	g3777527	BLASTX	317	4e-26	43	(AF053008) gag-pol polyprotein [Glycine max]
1838	GM_66_B1_A01_MR	g2522230	BLASTX	202	2e-15	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
1839	GM_66_B1_A07_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1840	GM_66_B1_A11_T7	g18559	BLASTN	778	3e-28	76	G.max gene for catalase
1841	GM_66_B1_A12_T7	g422418	BLASTX	225	1e-16	42	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
1842	GM_66_B1_C08_T7	g421955	BLASTX	182	6e-26	38	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
1843	GM_66_B1_C09_T7	g2462134	BLASTX	438	2e-40	50	(Y13368) reverse transcriptase [Beta vulgaris]
1844	GM_66_B1_D01_MR	g3142328	BLASTN	459	9e-14	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1845	GM_66_B1_D01_T7	g3599418	BLASTN	647	3e-22	84	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
1846	GM_66_B1_D04_T7	g3142328	BLASTN	939	1e-35	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1847	GM_66_B1_D08_T7	g3033400	BLASTX	203	2e-31	78	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]
1848	GM_66_B1_E03_MR	g1666236	BLASTX	188	1e-13	37	(U76261) unknown [Hordeum vulgare]
1849	GM_66_B1_E09_T7	g3097320	BLASTN	892	2e-33	72	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1850	GM_66_B1_F01_MR	g3097320	BLASTN	441	6e-13	71	Glycine max gene for Bd 30K, complete cds
1851	GM_66_B1_F02_MR	g100484	BLASTX	408	1e-36	54	hypothetical protein - garden snapdragon
1852	GM_66_B1_F03_MR	g507910	BLASTN	402	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1853	GM_66_B1_F04_T7	g4063760	BLASTX	160	1e-13	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1854	GM_66_B1_F09_MR	g18559	BLASTN	620	4e-21	71	G.max gene for catalase
1855	GM_66_B1_G02_MR	g1732513	BLASTX	179	4e-13	64	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]
1856	GM_66_B1_G02_T7	g2852684	BLASTX	150	8e-09	43	(AF017751) resistance protein candidate [Lactuca sativa]
1857	GM_66_B1_G04_T7	g3142328	BLASTN	772	5e-28	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1858	GM_66_B1_H05_T7	g3885341	BLASTX	185	2e-12	34	(AC005623) unknown protein [Arabidopsis thaliana]
1859	GM_66_B1_H06_T7	g1706522	BLASTX	173	2e-26	69	DIHYDROFOLATE REDUCTASE / THYMIDYLATE SYNTHASE (DHFR-TS) gi 1362048 pir S55683 dihydrofolate reductase-thymidylate synthase - soybean gi 999190 bbs 166832 (S78087) dihydrofolate reductase-thymidylate synthase, DHFR-TS=bifunctional enzyme {EC 1.5.1.3} [Glycine max, seedling, Peptide, 530 aa] [Glycine max] gi 1096144 prf 2111237A dihydrofolate reductase-thymidylate synthase [Glycine max]
1860	GM_66_B1_H08_MR	g2765093	BLASTX	246	2e-19	60	(Y10983) putative cytochrome P450 [Glycine max]
1861	GM_66_B1_H12_T7	g77236	BLASTX	130	6e-11	28	pol polyprotein - mink cell focus-forming virus (fragment) >gi 50857 (X52622) integrase (409 AA) [Mus musculus]
1862	GM_66_B2_A02_T7	g99922	BLASTX	207	3e-24	76	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
1863	GM_66_B2_A07_MR	g2085783	BLASTN	360	3e-09	62	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
1864	GM_66_B2_A11_T7	g4063760	BLASTX	526	1e-48	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1865	GM_66_B2_B10_MR	g3152613	BLASTX	162	4e-10	53	(AC004482) hypothetical protein [Arabidopsis thaliana]
1866	GM_66_B2_B10_T7	g3242709	BLASTX	152	1e-24	50	(AC003040) putative guanine nucleotide-binding protein [Arabidopsis thaliana]
1867	GM_66_B2_C03_MR	g2160694	BLASTX	483	3e-45	92	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
1868	GM_66_B2_C05_T7	g3790154	BLASTN	365	2e-09	62	Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs ...
1869	GM_66_B2_C09_MR	g18559	BLASTN	444	4e-13	75	G.max gene for catalase
1870	GM_66_B2_D03_MR	g3738114	BLASTN	448	3e-13	65	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
1871	GM_66_B2_D05_MR	g1666236	BLASTX	224	7e-18	32	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1872	GM_66_B2_D06_MR	g2583130	BLASTX	134	1e-22	49	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
1873	GM_66_B2_D10_T7	g3142328	BLASTN	803	2e-29	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1874	GM_66_B2_D11_T7	g3810584	BLASTN	538	3e-17	67	Arabidopsis thaliana chromosome II BAC T6B13 genomic sequence, complete sequence [Arabidopsis thaliana]
1875	GM_66_B2_E02_T7	g3777527	BLASTX	108	1e-09	31	(AF053008) gag-pol polyprotein [Glycine max]
1876	GM_66_B2_E06_MR	g507910	BLASTN	451	9e-14	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1877	GM_66_B2_E07_MR	g2827715	BLASTX	127	9e-10	28	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
1878	GM_66_B2_E09_MR	g2924257	BLASTN	447	4e-13	69	Tobacco chloroplast genome DNA
1879	GM_66_B2_E10_MR	g3738114	BLASTN	374	7e-10	64	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
1880	GM_66_B2_E11_T7	g4063760	BLASTX	273	6e-35	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1881	GM_66_B2_F02_T7	g100484	BLASTX	346	6e-30	59	hypothetical protein - garden snapdragon
1882	GM_66_B2_F04_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1883	GM_66_B2_F05_T7	g4160362	BLASTN	390	1e-10	60	Saccharomyces cerevisiae complete mitochondrial genome
1884	GM_66_B2_F08_MR	g4063760	BLASTX	276	5e-22	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1885	GM_66_B2_F09_MR	g3142328	BLASTN	1303	4e-52	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1886	GM_66_B2_G03_T7	g3777527	BLASTX	697	1e-66	90	(AF053008) gag-pol polyprotein [Glycine max]
1887	GM_66_B2_G05_T7	g3080352	BLASTN	468	4e-14	64	Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSAII project).
1888	GM_66_B2_G08_MR	g2970554	BLASTN	547	1e-17	70	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
1889	GM_66_B2_G08_T7	g3777527	BLASTX	480	2e-43	87	(AF053008) gag-pol polyprotein [Glycine max]
1890	GM_66_B2_G11_T7	g100484	BLASTX	394	4e-35	58	hypothetical protein - garden snapdragon
1891	GM_66_B2_H09_T7	g3128142	BLASTN	259	3e-09	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQN23, complete sequence [Arabidopsis thaliana]
1892	GM_66_B2_H10_MR	g3426334	BLASTN	530	6e-17	64	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
1893	GM_66_B2_H11_MR	g100484	BLASTX	405	3e-36	54	hypothetical protein - garden snapdragon
1894	GM_66_B2_H11_T7	g4063760	BLASTX	232	3e-30	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1895	GM_67_A1_A02_T7	g1351995	BLASTX	119	4e-14	43	PROBABLE CALCIUM-TRANSPORTING ATPASE gi 2130357 pir S62557 hypothetical protein SPAC24B11.12c - fission yeast (Schizosaccharomyces pombe) gi 1061300 (Z67757) unknown [Schizosaccharomyces pombe]
1896	GM_67_A1_A04_T7	g3036804	BLASTX	153	2e-10	66	(AL022373) thaumatin-like protein [Arabidopsis thaliana]
1897	GM_67_A1_B07_T7	g510875	BLASTN	437	9e-13	77	P.vulgaris PvME1 gene
1898	GM_67_A1_B10_MR	g2245135	BLASTX	276	2e-23	68	(Z97344) hypothetical protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1899	GM_67_A1_C04_MR	g507910	BLASTN	428	1e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
1900	GM_67_A1_C04_T7	g3777527	BLASTX	234	2e-17	90	(AF053008) gag-pol polyprotein [Glycine max]
1901	GM_67_A1_C05_MR	g2245104	BLASTX	180	1e-11	31	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
1902	GM_67_A1_C08_MR	g170602	BLASTN	570	8e-20	63	Broad bean (V.faba) BamHI repetitive element, 900 bp family.
1903	GM_67_A1_C08_T7	g4160362	BLASTN	408	2e-11	66	Saccharomyces cerevisiae complete mitochondrial genome
1904	GM_67_A1_D02_MR	g1946279	BLASTX	176	8e-13	44	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
1905	GM_67_A1_D04_T7	g2266985	BLASTX	181	3e-12	77	(Y13943) MEtRS [Arabidopsis thaliana]
1906	GM_67_A1_D06_MR	g4097522	BLASTX	170	6e-26	59	(U63534) cinnamyl alcohol dehydrogenase [Fragaria x ananassa]
1907	GM_67_A1_D07_MR	g3097320	BLASTN	879	9e-33	74	Glycine max gene for Bd 30K, complete cds
1908	GM_67_A1_D07_T7	g629693	BLASTX	278	1e-23	55	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
1909	GM_67_A1_D11_MR	g3033389	BLASTX	205	1e-14	37	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
1910	GM_67_A1_E07_MR	g507910	BLASTN	591	4e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
1911	GM_67_A1_E10_MR	g18559	BLASTN	1050	1e-40	75	G.max gene for catalase
1912	GM_67_A1_E10_T7	g905361	BLASTX	176	1e-11	30	(U22103) gag-protease polyprotein [Glycine max]
1913	GM_67_A1_F04_MR	g3047068	BLASTX	157	2e-09	28	(AF058825) similar to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
1914	GM_67_A1_F07_T7	g3097320	BLASTN	606	2e-20	77	Glycine max gene for Bd 30K, complete cds
1915	GM_67_A1_G05_MR	g3645899	BLASTX	253	1e-19	41	(U68408) 5' end not determined experimentally [Zea mays]
1916	GM_67_A1_G12_MR	g3142328	BLASTN	625	3e-21	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1917	GM_67_A1_H04_MR	g3097320	BLASTN	469	3e-14	68	Glycine max gene for Bd 30K, complete cds
1918	GM_67_A1_H04_T7	g3097320	BLASTN	863	5e-32	72	Glycine max gene for Bd 30K, complete cds
1919	GM_67_A1_H05_MR	g507910	BLASTN	435	5e-13	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1920	GM_67_A1_H06_T7	g3777527	BLASTX	307	4e-25	62	(AF053008) gag-pol polyprotein [Glycine max]
1921	GM_67_A1_H07_MR	g2459437	BLASTX	210	2e-16	54	(AC002332) hypothetical protein [Arabidopsis thaliana]
1922	GM_67_A2_A02_T7	g465599	BLASTX	91	1e-08	50	HYPOTHETICAL 33.7 KD PROTEIN IN NFO-FRUA INTERGENIC REGION gi 405882 (U00007) yeiK [Escherichia coli] gi 1788486 (AE000305) hypothetical 33.7 kD protein in nfo-fruA intergenic region [Escherichia coli] gi 744197 prf 2014253BH yeiK gene [Escherichia coli]
1923	GM_67_A2_A03_T7	g507910	BLASTN	425	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
1924	GM_67_A2_A05_T7	g226407	BLASTX	256	1e-19	37	retrotransposon del1-46 [Lilium henryi]
1925	GM_67_A2_A12_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1926	GM_67_A2_B04_T7	g4063760	BLASTX	563	1e-52	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1927	GM_67_A2_B05_T7	g3142328	BLASTN	1215	4e-48	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1928	GM_67_A2_B06_T7	g2522228	BLASTX	157	6e-10	30	(AB007466) reverse transcriptase-like protein [Vicia faba]
1929	GM_67_A2_B07_T7	g4063760	BLASTX	624	3e-59	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1930	GM_67_A2_B09_MR	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
1931	GM_67_A2_B10_MR	g3097320	BLASTN	603	3e-20	81	Glycine max gene for Bd 30K, complete cds
1932	GM_67_A2_B12_MR	g4063760	BLASTX	185	3e-12	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1933	GM_67_A2_C06_MR	g1346735	BLASTX	182	2e-12	84	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) gi 1076562 pir S49647 phosphoglycerate mutase (EC 5.4.2.1) - castor bean gi 474170 (X70652) phosphoglycerate mutase [Ricinus communis]
1934	GM_67_A2_C08_MR	g3885336	BLASTX	299	1e-24	58	(AC005623) receptor-like protein kinase [Arabidopsis thaliana]
1935	GM_67_A2_C09_MR	g3859610	BLASTN	665	5e-23	65	Arabidopsis thaliana BAC T9E19
1936	GM_67_A2_C10_T7	g3789709	BLASTN	366	2e-09	63	Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence [Homo sapiens]
1937	GM_67_A2_D05_MR	g4063760	BLASTX	187	2e-12	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1938	GM_67_A2_D05_T7	g507910	BLASTN	724	4e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
1939	GM_67_A2_D12_MR	g3264767	BLASTX	190	3e-14	62	(AF071893) AP2 domain containing protein [Prunus armeniaca]
1940	GM_67_A2_D12_T7	g4160362	BLASTN	362	3e-09	60	Saccharomyces cerevisiae complete mitochondrial genome
1941	GM_67_A2_E02_T7	g231753	BLASTX	114	2e-15	69	60 KD CHAPERONIN 2 (PROTEIN CPN60 2) (GROEL PROTEIN 2) (HSP56) gi 80689 pir C41325 heat shock protein 56 - Streptomyces albus gi 153294 (M76658) open reading frame; GROEL1 encodes two gene products, related to a second GROEL-like gene (GROEL2) in S.albus [Streptomyces albus]
1942	GM_67_A2_E03_MR	g1732513	BLASTX	178	5e-13	66	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]
1943	GM_67_A2_E03_T7	g3777527	BLASTX	233	3e-17	35	(AF053008) gag-pol polyprotein [Glycine max]
1944	GM_67_A2_E04_MR	g992916	BLASTN	350	9e-09	75	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
1945	GM_67_A2_E07_MR	g2979597	BLASTN	612	1e-20	65	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
1946	GM_67_A2_E07_T7	g3688169	BLASTN	298	9e-14	69	Arabidopsis thaliana DNA chromosome 4, BAC clone F26P21 (ESSAII project)
1947	GM_67_A2_E08_MR	g505129	BLASTN	386	2e-10	61	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
1948	GM_67_A2_E08_T7	g4063756	BLASTN	382	3e-10	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
1949	GM_67_A2_E10_T7	g3097320	BLASTN	385	2e-10	77	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1950	GM_67_A2_F01_T7	g1666236	BLASTX	198	8e-15	29	(U76261) unknown [Hordeum vulgare]
1951	GM_67_A2_F06_T7	g170080	BLASTN	1010	7e-39	90	Soybean seed lectin gene transposable element tgm1.
1952	GM_67_A2_F11_T7	g3894383	BLASTX	159	1e-09	43	(AF053993) disease resistance protein [Lycopersicon esculentum]
1953	GM_67_A2_G02_MR	g2230823	BLASTN	363	2e-09	64	D.discoideum mRNA for stat protein, first finger stage
1954	GM_67_A2_G02_T7	g3097320	BLASTN	778	6e-36	76	Glycine max gene for Bd 30K, complete cds
1955	GM_67_A2_G06_T7	g3319362	BLASTX	153	5e-09	44	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
1956	GM_67_A2_G12_MR	g3642874	BLASTN	360	8e-10	71	Pisum sativum putative IAA-related protein gene, partial cds
1957	GM_67_A2_H01_T7	g3659406	BLASTN	365	2e-09	65	Homo sapiens Xp22 bins 29-30 BAC GSHB-227L7 (Genome Systems Human BAC Library) complete sequence [Homo sapiens]
1958	GM_67_A2_H02_MR	g3550044	BLASTN	420	6e-12	68	Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) ...
1959	GM_67_A2_H09_T7	g1167523	BLASTX	219	8e-16	35	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
1960	GM_67_A2_H10_T7	g3142328	BLASTN	799	3e-29	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1961	GM_67_A2_H12_T7	g130582	BLASTX	434	9e-39	66	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
1962	GM_67_B1_A02_MR	g4039114	BLASTN	370	9e-10	68	Glycine max alcohol-dehydrogenase (Adh-2) gene, partial cds
1963	GM_67_B1_A08_T7	g2522228	BLASTX	229	6e-18	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
1964	GM_67_B1_B04_T7	g2995405	BLASTX	339	6e-29	62	(Y12432) polyprotein [Ananas comosus]
1965	GM_67_B1_B07_MR	g2498329	BLASTX	250	4e-19	76	PATTERN FORMATION PROTEIN EMB30 gi 2129665 pir S65571 pattern-formation protein GNOM - Arabidopsis thaliana gi 1209633 (U36433) GNOM gene product [Arabidopsis thaliana] gi 1335997 (U56140) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana] gi 1335999 (U56141) similar to the Saccharomyces cerevisiae Sec7 protein, GenBank Accession Number J03918 [Arabidopsis thaliana]
1966	GM_67_B1_B09_T7	g1167523	BLASTX	275	8e-22	41	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
1967	GM_67_B1_C04_T7	g18768	BLASTN	361	6e-10	73	Soybean Tgm6 transposable element 3' end
1968	GM_67_B1_C08_MR	g3142328	BLASTN	1285	3e-51	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
1969	GM_67_B1_C08_T7	g507910	BLASTN	378	2e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
1970	GM_67_B1_D05_MR	g1769897	BLASTX	201	2e-14	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1971	GM_67_B1_D06_T7	g2769655	BLASTN	547	1e-17	66	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
1972	GM_67_B1_D07_T7	g3650039	BLASTX	275	3e-22	44	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
1973	GM_67_B1_D10_MR	g2842478	BLASTX	133	6e-10	58	(AL021749) receptor protein kinase like protein [Arabidopsis thaliana]
1974	GM_67_B1_D11_MR	g2104945	BLASTN	396	7e-11	78	Glycine max copia-like retrotransposon Tgmr, complete sequence
1975	GM_67_B1_E07_T7	g4063756	BLASTN	492	3e-15	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
1976	GM_67_B1_E10_MR	g294042	BLASTN	474	2e-14	64	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
1977	GM_67_B1_F01_T7	g3176776	BLASTN	346	2e-09	66	Homo sapiens allele 4 fragile site locus (FRA10B) minisatellite, 5' sequence
1978	GM_67_B1_F03_MR	g507910	BLASTN	562	9e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
1979	GM_67_B1_F04_T7	g4063760	BLASTX	285	9e-28	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
1980	GM_67_B1_F07_MR	g507910	BLASTN	364	8e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
1981	GM_67_B1_F07_T7	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
1982	GM_67_B1_G01_MR	g1786115	BLASTX	152	3e-09	54	(U85250) phosphoinositide-specific phospholipase C [Vigna unguiculata]
1983	GM_67_B1_G03_T7	g2191194	BLASTX	261	8e-22	49	(AF007271) contains weak to the SAPB protein (TR:E236624) [Arabidopsis thaliana]
1984	GM_67_B1_G11_MR	g2995405	BLASTX	182	4e-12	43	(Y12432) polyprotein [Ananas comosus]
1985	GM_67_B2_A02_T7	g2129618	BLASTX	158	2e-09	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
1986	GM_67_B2_A04_MR	g18559	BLASTN	999	3e-38	77	G.max gene for catalase
1987	GM_67_B2_A12_MR	g4038056	BLASTX	314	3e-26	55	(AC005897) putative transposon [Arabidopsis thaliana]
1988	GM_67_B2_A12_T7	g2443320	BLASTX	245	1e-18	55	(D85597) polyprotein [Oryza australiensis]
1989	GM_67_B2_B06_T7	g905361	BLASTX	345	6e-30	95	(U22103) gag-protease polyprotein [Glycine max]
1990	GM_67_B2_B07_MR	g4006855	BLASTX	322	4e-27	78	(Z99707) Cu2+-transporting ATPase-like protein [Arabidopsis thaliana]
1991	GM_67_B2_B12_MR	g3777527	BLASTX	535	2e-49	97	(AF053008) gag-pol polyprotein [Glycine max]
1992	GM_67_B2_C04_T7	g905360	BLASTN	849	1e-31	92	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
1993	GM_67_B2_C07_MR	g100484	BLASTX	276	2e-22	45	hypothetical protein - garden snapdragon
1994	GM_67_B2_D04_MR	g4038056	BLASTX	263	9e-21	53	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
1995	GM_67_B2_D09_MR	g4092471	BLASTN	509	6e-16	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
1996	GM_67_B2_D11_MR	g3135969	BLASTN	404	3e-11	60	Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family prot...
1997	GM_67_B2_D11_T7	g18559	BLASTN	826	2e-30	82	G.max gene for catalase
1998	GM_67_B2_E01_T7	g3193306	BLASTX	244	1e-18	54	(AF069300) contains similarity to Arabidopsis membrane-associated salt-inducible-like protein (GB:AL021637) [Arabidopsis thaliana]
1999	GM_67_B2_E06_T7	g100484	BLASTX	199	4e-14	56	hypothetical protein - garden snapdragon
2000	GM_67_B2_E11_MR	g3935200	BLASTN	522	1e-16	68	Homo sapiens Chromosome 22q11.2 PAC Clone p201m18 In DGCR Region, complete sequence [Homo sapiens]
2001	GM_67_B2_E12_MR	g18559	BLASTN	602	3e-20	71	G.max gene for catalase
2002	GM_67_B2_F05_MR	g2462134	BLASTX	184	1e-12	30	(Y13368) reverse transcriptase [Beta vulgaris]
2003	GM_67_B2_F06_T7	g4063760	BLASTX	187	2e-12	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2004	GM_67_B2_F11_MR	g3650035	BLASTX	207	1e-14	39	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
2005	GM_67_B2_G06_MR	g4063760	BLASTX	112	5e-09	81	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2006	GM_68_A1_A03_MR	g3695387	BLASTX	148	3e-13	68	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
2007	GM_68_A1_A08_MR	g3641838	BLASTX	246	4e-42	59	(AL023094) putative protein (fragment) [Arabidopsis thaliana]
2008	GM_68_A1_B04_MR	g507910	BLASTN	394	3e-11	78	Glycine max BSR-101 satellite SB92 genomic sequence.
2009	GM_68_A1_B05_MR	g905361	BLASTX	202	2e-14	29	(U22103) gag-protease polyprotein [Glycine max]
2010	GM_68_A1_B09_MR	g3193282	BLASTN	321	3e-14	62	Arabidopsis thaliana BAC T14P8
2011	GM_68_A1_B09_T7	g3738298	BLASTX	233	8e-18	80	(AC005309) unknown protein [Arabidopsis thaliana]
2012	GM_68_A1_B10_MR	g3738325	BLASTX	493	2e-46	58	(AC005170) putative CaMB-channel protein [Arabidopsis thaliana]
2013	GM_68_A1_B10_T7	g3766106	BLASTN	429	2e-12	70	Arabidopsis thaliana chromosome 1 BAC F9K20 sequence, complete sequence [Arabidopsis thaliana]
2014	GM_68_A1_C03_MR	g507910	BLASTN	580	1e-19	84	Glycine max BSR-101 satellite SB92 genomic sequence.
2015	GM_68_A1_C03_T7	g507910	BLASTN	494	1e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
2016	GM_68_A1_C05_T7	g18559	BLASTN	378	4e-10	69	G.max gene for catalase
2017	GM_68_A1_C10_T7	g1144553	BLASTN	391	1e-11	62	Anopheles melas 12S ribosomal RNA, D-loop, and tRNA-Ile mitochondrial genes, partial sequence.
2018	GM_68_A1_D04_MR	g4063760	BLASTX	473	5e-43	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2019	GM_68_A1_D07_T7	g1666236	BLASTX	210	3e-16	31	(U76261) unknown [Hordeum vulgare]
2020	GM_68_A1_D11_MR	g18683	BLASTN	717	1e-25	77	G.max N-20t gene
2021	GM_68_A1_E02_T7	g3492803	BLASTX	263	2e-20	50	(AJ002479) ENBP1 [Medicago truncatula]
2022	GM_68_A1_E03_T7	g3283026	BLASTX	198	6e-14	35	putative transposase [Arabidopsis thaliana]
2023	GM_68_A1_E04_MR	g507910	BLASTN	404	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2024	GM_68_A1_E04_T7	g507910	BLASTN	395	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2025	GM_68_A1_E05_T7	g505129	BLASTN	417	7e-12	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
2026	GM_68_A1_E07_MR	g130582	BLASTX	272	6e-28	51	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
2027	GM_68_A1_E10_MR	g2522227	BLASTX	293	4e-25	40	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
2028	GM_68_A1_E12_T7	g3097320	BLASTN	570	9e-19	71	Glycine max gene for Bd 30K, complete cds
2029	GM_68_A1_F03_T7	g18683	BLASTN	518	6e-25	81	G.max N-20t gene
2030	GM_68_A1_F08_T7	g170296	BLASTN	550	6e-18	65	Nicotiana plumbaginifolia plasma-membrane H+ ATPase (pma3) gene, exons 1-9.
2031	GM_68_A1_G02_T7	g629693	BLASTX	147	6e-09	33	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
2032	GM_68_A1_G06_MR	g1946279	BLASTX	155	1e-10	45	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
2033	GM_68_A1_G12_MR	g547683	BLASTX	330	3e-28	68	HEAT SHOCK COGNATE PROTEIN 80 gi 170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] gi 445601 prf 1909348A heat shock protein hsp80 [Lycopersicon esculentum]
2034	GM_68_A1_H01_T7	g3777527	BLASTX	239	7e-18	85	(AF053008) gag-pol polyprotein [Glycine max]
2035	GM_68_A1_H03_MR	g3097320	BLASTN	1565	7e-64	82	Glycine max gene for Bd 30K, complete cds
2036	GM_68_A1_H03_T7	g3097320	BLASTN	502	1e-15	81	Glycine max gene for Bd 30K, complete cds
2037	GM_68_A1_H06_T7	g3779026	BLASTX	468	2e-42	65	(AC005171) putative retrotransposon [Arabidopsis thaliana]
2038	GM_68_A1_H10_MR	g507910	BLASTN	358	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2039	GM_68_A1_H10_T7	g3142330	BLASTX	595	3e-57	88	(U96295) envelope-like [Glycine max]
2040	GM_68_A1_H11_T7	g3059060	BLASTN	452	2e-13	66	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
2041	GM_68_A2_A03_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2042	GM_68_A2_A07_MR	g2760331	BLASTX	229	3e-17	39	(AC002130) F1N21.16 [Arabidopsis thaliana]
2043	GM_68_A2_A08_MR	g3334667	BLASTX	215	4e-16	39	(Y10493) putative cytochrome P450 [Glycine max]
2044	GM_68_A2_B01_MR	g18559	BLASTN	827	2e-30	74	G.max gene for catalase
2045	GM_68_A2_B06_MR	g3461840	BLASTX	302	1e-24	44	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
2046	GM_68_A2_C02_MR	g4063760	BLASTX	207	1e-14	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2047	GM_68_A2_D06_MR	g507910	BLASTN	575	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2048	GM_68_A2_D12_MR	g507910	BLASTN	544	6e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2049	GM_68_A2_E05_MR	g507910	BLASTN	381	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2050	GM_68_A2_E11_MR	g99730	BLASTX	337	8e-30	50	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
2051	GM_68_A2_F02_MR	g3560029	BLASTN	439	6e-13	65	Schistosoma intercalatum ribosomal intergenic spacer DNA (2169 bp)
2052	GM_68_A2_F03_MR	g170080	BLASTN	291	2e-14	96	Soybean seed lectin gene transposable element tgm1.
2053	GM_68_A2_F09_MR	g3845197	BLASTN	536	3e-17	66	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
2054	GM_68_A2_F10_MR	g421955	BLASTX	314	2e-27	50	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
2055	GM_68_A2_G05_MR	g2129618	BLASTX	223	2e-16	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2056	GM_68_A2_H09_MR	g507910	BLASTN	350	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2057	GM_68_B1_A02_T7	g4063760	BLASTX	402	2e-35	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2058	GM_68_B1_A03_T7	g2827516	BLASTX	518	7e-48	67	(AL021633) DNA topoisomerase like- protein [Arabidopsis thaliana]
2059	GM_68_B1_A07_T7	g2367418	BLASTX	191	2e-13	57	(AF000392) peptide transporter [Lotus japonicus]
2060	GM_68_B1_A09_T7	g18559	BLASTN	623	3e-21	69	G.max gene for catalase
2061	GM_68_B1_B05_T7	g3097320	BLASTN	463	6e-14	73	Glycine max gene for Bd 30K, complete cds
2062	GM_68_B1_B06_T7	g3777527	BLASTX	375	2e-32	93	(AF053008) gag-pol polyprotein [Glycine max]
2063	GM_68_B1_B09_T7	g507910	BLASTN	412	5e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2064	GM_68_B1_C08_T7	g507910	BLASTN	651	8e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
2065	GM_68_B1_C09_T7	g395293	BLASTN	393	9e-11	62	T.repens pseudogene for alcohol dehydrogenase
2066	GM_68_B1_E09_T7	g629693	BLASTX	200	9e-15	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
2067	GM_68_B1_E11_T7	g3319362	BLASTX	262	1e-20	47	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
2068	GM_68_B1_F02_T7	g18559	BLASTN	356	4e-09	65	G.max gene for catalase
2069	GM_68_B1_F05_T7	g2498731	BLASTX	168	2e-11	55	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 gi 1362013 pir S57611 zeta-crystallin homolog - Arabidopsis thaliana gi 886428 (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]
2070	GM_68_B1_F06_T7	g1040875	BLASTX	524	1e-49	84	(U30382) expansin S1 precursor [Cucumis sativus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2071	GM_68_B1_F10_T7	g114532	BLASTX	287	5e-24	65	ATP SYNTHASE ALPHA CHAIN gi 67824 pir PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast gi 11769 (V00162) alpha subunit of ATPase [Nicotiana tabacum] gi 11811 (Z00044) ATPase alpha subunit [Nicotiana tabacum] gi 225270 prf 1211235E ATPase alpha [Nicotiana tabacum]
2072	GM_68_B1_G01_T7	g3142328	BLASTN	484	6e-15	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2073	GM_68_B1_G03_T7	g507910	BLASTN	593	3e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
2074	GM_68_B1_H11_T7	g2827516	BLASTX	121	3e-09	43	(AL021633) DNA topoisomerase like- protein [Arabidopsis thaliana]
2075	GM_68_B2_A03_T7	g905361	BLASTX	413	1e-37	91	(U22103) gag-protease polyprotein [Glycine max]
2076	GM_68_B2_A10_MR	g3142328	BLASTN	1755	9e-73	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2077	GM_68_B2_B05_T7	g99726	BLASTX	121	2e-11	47	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976) orf 3 [Arabidopsis thaliana]
2078	GM_68_B2_B10_T7	g975703	BLASTN	569	1e-18	71	P.sativum GR gene
2079	GM_68_B2_C01_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2080	GM_68_B2_C02_MR	g507910	BLASTN	397	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2081	GM_68_B2_C02_T7	g507910	BLASTN	377	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2082	GM_68_B2_C06_T7	g1663537	BLASTX	339	4e-30	71	(U55803) disease resistance protein homolog [Glycine max]
2083	GM_68_B2_C07_MR	g130405	BLASTX	224	2e-16	39	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 17.6) gi 74642 pir GNFF17 retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) transposon 17.6 gi 1335613 gnl PID e1849 (X01472) ORF 2, pot. reverse transcriptase [Drosophila melanogaster] gi 224319 prf 1101404B ORF 2 [Drosophila melanogaster]
2084	GM_68_B2_C12_MR	g3097320	BLASTN	699	1e-24	83	Glycine max gene for Bd 30K, complete cds
2085	GM_68_B2_D07_MR	g1335861	BLASTN	562	2e-18	85	Glycine max clathrin heavy chain mRNA, complete cds
2086	GM_68_B2_E01_T7	g3461840	BLASTX	222	4e-16	39	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
2087	GM_68_B2_E07_MR	g4063760	BLASTX	183	7e-14	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2088	GM_68_B2_E08_MR	g18695	BLASTN	494	2e-15	76	Soybean nodulin 22 gene
2089	GM_68_B2_E10_MR	g4063756	BLASTN	456	1e-13	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
2090	GM_68_B2_E12_T7	g3645899	BLASTX	304	5e-25	59	(U68408) 5' end not determined experimentally [Zea mays]
2091	GM_68_B2_F06_MR	g3319362	BLASTX	251	2e-19	45	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2092	GM_68_B2_G02_T7	g507910	BLASTN	376	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2093	GM_68_B2_G05_T7	g18559	BLASTN	1166	7e-46	87	G.max gene for catalase
2094	GM_68_B2_G08_MR	g3777527	BLASTX	200	9e-14	34	(AF053008) gag-pol polyprotein [Glycine max]
2095	GM_68_B2_G12_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2096	GM_68_B2_G12_T7	g507910	BLASTN	350	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2097	GM_68_B2_H04_MR	g3132472	BLASTX	163	4e-10	34	(AC003096) unknown protein [Arabidopsis thaliana]
2098	GM_68_B2_H05_MR	g3097320	BLASTN	463	6e-14	71	Glycine max gene for Bd 30K, complete cds
2099	GM_68_B2_H05_T7	g18695	BLASTN	568	6e-19	79	Soybean nodulin 22 gene
2100	GM_68_B2_H10_MR	g2498732	BLASTX	271	7e-23	80	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P2 gi 1362014 pir S57612 zeta-crystallin homolog - Arabidopsis thaliana gi 886430 (Z49268) zeta-crystallin homologue [Arabidopsis thaliana]
2101	GM_69_A1_A02_T7	g505129	BLASTN	417	7e-12	69	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
2102	GM_69_A1_A05_T7	g101042	BLASTX	178	1e-11	31	hypothetical protein Tf1 - fission yeast (Schizosaccharomyces pombe) gi 173477 (M38526) Tf1 protein [Schizosaccharomyces pombe]
2103	GM_69_A1_A08_T7	g507910	BLASTN	478	5e-15	81	Glycine max BSR-101 satellite SB92 genomic sequence.
2104	GM_69_A1_A12_T7	g3426334	BLASTN	378	4e-10	65	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
2105	GM_69_A1_B02_T7	g2052034	BLASTN	349	1e-08	62	Human DNA sequence from PAC 450C20 on chromosome X
2106	GM_69_A1_B09_T7	g1769898	BLASTX	380	7e-34	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2107	GM_69_A1_B11_T7	g99755	BLASTX	417	3e-38	55	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
2108	GM_69_A1_C01_T7	g1172441	BLASTX	363	1e-32	56	POSSIBLE TRANSCRIPTION FACTOR POSF21 gi 99685 pir S21883 DNA-binding protein POSF21 - Arabidopsis thaliana gi 16429 (X61031) posF21 gene product [Arabidopsis thaliana]
2109	GM_69_A1_D04_T7	g3522943	BLASTX	166	3e-10	68	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]
2110	GM_69_A1_D06_T7	g507910	BLASTN	444	2e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
2111	GM_69_A1_E02_T7	g1167523	BLASTX	232	4e-34	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
2112	GM_69_A1_E04_T7	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2113	GM_69_A1_E06_T7	g2764526	BLASTN	448	3e-13	65	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
2114	GM_69_A1_E10_T7	g2462134	BLASTX	189	3e-13	34	(Y13368) reverse transcriptase [Beta vulgaris]
2115	GM_69_A1_F10_T7	g3142303	BLASTX	472	8e-43	66	(AC002411) Strong similarity to MRP-like ABC transporter gb U92650 from A. thaliana and canalicular multi-drug resistance protein gb L49379 from Rattus norvegicus. [Arabidopsis thaliana]
2116	GM_69_A1_G02_T7	g2739359	BLASTN	436	1e-12	67	Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2117	GM_69_A1_G04_T7	g3142328	BLASTN	1090	2e-42	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2118	GM_69_A1_H04_T7	g629693	BLASTX	381	2e-34	55	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
2119	GM_69_A1_H10_T7	g2129618	BLASTX	229	4e-17	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2120	GM_69_B1_A01_MR	g3097320	BLASTN	889	3e-33	80	Glycine max gene for Bd 30K, complete cds
2121	GM_69_B1_B02_MR	g507910	BLASTN	372	3e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2122	GM_69_B1_B02_T7	g507910	BLASTN	354	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2123	GM_69_B1_B08_MR	g3777527	BLASTX	187	3e-13	41	(AF053008) gag-pol polyprotein [Glycine max]
2124	GM_69_B1_B10_T7	g1142702	BLASTN	448	9e-14	73	Glycine max satellite STR120-A.4.
2125	GM_69_B1_B11_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2126	GM_69_B1_C09_MR	g1872521	BLASTX	155	1e-10	74	(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] gi 1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana]
2127	GM_69_B1_D01_MR	g1769898	BLASTX	472	4e-44	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2128	GM_69_B1_D02_MR	g3097320	BLASTN	875	1e-32	76	Glycine max gene for Bd 30K, complete cds
2129	GM_69_B1_D06_MR	g2894591	BLASTN	400	5e-11	65	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K21 (ESSAII project).
2130	GM_69_B1_D07_T7	g905361	BLASTX	358	4e-36	94	(U22103) gag-protease polyprotein [Glycine max]
2131	GM_69_B1_D11_MR	g3786011	BLASTX	129	6e-10	61	(AC005499) putative elongation factor [Arabidopsis thaliana]
2132	GM_69_B1_E01_MR	g3080400	BLASTX	418	2e-38	89	(AL022603) putative protein [Arabidopsis thaliana]
2133	GM_69_B1_E02_MR	g1945277	BLASTX	153	2e-09	72	(Z94180) branched chain alpha-keto acid dehydrogenase E1-alpha subunit [Lycopersicon esculentum]
2134	GM_69_B1_E04_MR	g507910	BLASTN	711	2e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
2135	GM_69_B1_H08_T7	g3097320	BLASTN	709	5e-25	83	Glycine max gene for Bd 30K, complete cds
2136	GM_70_A1_A07_T7	g1142701	BLASTN	251	5e-19	75	Glycine max satellite STR120-A.3.
2137	GM_70_A1_A08_MR	g1518540	BLASTX	686	8e-67	95	(U53418) UDP-glucose dehydrogenase [Glycine max]
2138	GM_70_A1_A11_T7	g3367585	BLASTX	151	2e-09	35	(AL031135) putative polygalacturonase [Arabidopsis thaliana]
2139	GM_70_A1_B04_MR	g2191187	BLASTX	289	5e-28	59	(AF007271) contains similarity to a DNAJ-like domain [Arabidopsis thaliana]
2140	GM_70_A1_B07_T7	g4063770	BLASTX	220	3e-16	40	(AB004906) transposase [Ipomoea purpurea]
2141	GM_70_A1_B10_MR	g3645899	BLASTX	246	9e-33	57	(U68408) 5' end not determined experimentally [Zea mays]
2142	GM_70_A1_B11_MR	g2522230	BLASTX	292	5e-25	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
2143	GM_70_A1_C03_T7	g2129618	BLASTX	220	4e-16	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2144	GM_70_A1_C04_T7	g1167523	BLASTX	286	3e-25	40	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2145	GM_70_A1_C11_MR	g2764526	BLASTN	634	1e-21	63	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
2146	GM_70_A1_D02_T7	g1769897	BLASTX	189	6e-16	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2147	GM_70_A1_D04_T7	g3142328	BLASTN	1880	2e-78	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2148	GM_70_A1_D07_T7	g585416	BLASTX	122	9e-14	82	LIPOXYGENASE gi 467565 (X71344) lipoxygenase [Lens culinaris]
2149	GM_70_A1_D12_MR	g507910	BLASTN	575	2e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
2150	GM_70_A1_D12_T7	g507910	BLASTN	520	7e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2151	GM_70_A1_E05_MR	g3097320	BLASTN	1229	1e-48	82	Glycine max gene for Bd 30K, complete cds
2152	GM_70_A1_E08_T7	g507910	BLASTN	340	9e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
2153	GM_70_A1_F02_MR	g3845336	BLASTN	362	3e-09	61	Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence
2154	GM_70_A1_F03_MR	g1666236	BLASTX	197	1e-14	29	(U76261) unknown [Hordeum vulgare]
2155	GM_70_A1_F06_MR	g1663549	BLASTX	464	3e-43	78	(U55809) disease resistance protein homolog [Glycine max]
2156	GM_70_A1_F07_MR	g507910	BLASTN	568	5e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
2157	GM_70_A1_F09_MR	g507910	BLASTN	480	4e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
2158	GM_70_A1_F09_T7	g4092471	BLASTN	446	4e-13	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
2159	GM_70_A1_F10_MR	g1666236	BLASTX	215	9e-17	29	(U76261) unknown [Hordeum vulgare]
2160	GM_70_A1_F10_T7	g18559	BLASTN	953	3e-36	73	G.max gene for catalase
2161	GM_70_A1_F11_MR	g3810596	BLASTX	224	1e-23	46	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
2162	GM_70_A1_G01_MR	g2244976	BLASTX	177	4e-16	65	(Z97340) hypothetical protein [Arabidopsis thaliana]
2163	GM_70_A1_G02_T7	g2323254	BLASTN	422	5e-12	64	Human Chromosome X, complete sequence [Homo sapiens]
2164	GM_70_A1_G07_MR	g2462058	BLASTX	196	3e-17	55	(Y13389) reverse transcriptase [Antirrhinum majus]
2165	GM_70_A1_G07_T7	g3930515	BLASTX	121	2e-12	47	(AF059674) putative gag protein [Nicotiana tabacum]
2166	GM_70_A1_G11_T7	g4063760	BLASTX	456	4e-41	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2167	GM_70_A1_H01_T7	g3859610	BLASTN	552	6e-18	63	Arabidopsis thaliana BAC T9E19
2168	GM_70_A1_H09_T7	g4038056	BLASTX	199	5e-17	44	(AC005897) putative transposon [Arabidopsis thaliana]
2169	GM_70_A1_H11_MR	g3319362	BLASTX	290	1e-23	47	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
2170	GM_70_A2_A02_MR	g4115383	BLASTX	204	1e-14	55	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]
2171	GM_70_A2_A03_MR	g1666236	BLASTX	193	3e-14	31	(U76261) unknown [Hordeum vulgare]
2172	GM_70_A2_A03_T7	g343537	BLASTN	389	1e-10	63	T.brucei mitochondrial maxicircle DNA encoding cytochrome c oxidase subunit I (COI), and NADH dehydrogenase subunits 4 and 5, complete cds.
2173	GM_70_A2_A07_T7	g507910	BLASTN	426	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2174	GM_70_A2_A08_MR	g3241916	BLASTN	375	7e-10	61	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]
2175	GM_70_A2_A09_T7	g4038056	BLASTX	292	6e-27	43	(AC005897) putative transposon [Arabidopsis thaliana]
2176	GM_70_A2_B02_MR	g4063760	BLASTX	199	7e-15	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2177	GM_70_A2_B04_T7	g4038029	BLASTN	394	9e-11	59	Arabidopsis thaliana chromosome II BAC F5O4 genomic sequence, complete sequence [Arabidopsis thaliana]
2178	GM_70_A2_B05_MR	g1771162	BLASTX	494	6e-46	60	(X98930) SBT2 [Lycopersicon esculentum] gi 3687307 gnl PID e1299612 (AJ006379) subtilisin-like protease [Lycopersicon esculentum]
2179	GM_70_A2_B05_T7	g18559	BLASTN	737	2e-26	74	G.max gene for catalase
2180	GM_70_A2_B08_MR	g18559	BLASTN	800	3e-29	74	G.max gene for catalase
2181	GM_70_A2_B08_T7	g18559	BLASTN	417	7e-12	66	G.max gene for catalase
2182	GM_70_A2_B10_T7	g3738232	BLASTX	167	3e-11	50	(AB007791) DREB2B [Arabidopsis thaliana]
2183	GM_70_A2_B12_MR	g1171591	BLASTN	313	4e-10	61	P.falciparum complete gene map of plastid-like DNA (IR-B)
2184	GM_70_A2_C01_T7	g687867	BLASTN	370	1e-09	60	Caenorhabditis elegans cosmid C45G9
2185	GM_70_A2_C04_T7	g2160155	BLASTN	351	8e-09	65	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
2186	GM_70_A2_C09_MR	g3810596	BLASTX	176	1e-23	41	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
2187	GM_70_A2_C09_T7	g3510505	BLASTX	380	5e-33	44	(AF030881) pol polyprotein [Fugu rubripes]
2188	GM_70_A2_C11_T7	g4038056	BLASTX	152	1e-10	59	(AC005897) putative transposon [Arabidopsis thaliana]
2189	GM_70_A2_D01_MR	g4038056	BLASTX	308	1e-25	41	(AC005897) putative transposon [Arabidopsis thaliana]
2190	GM_70_A2_D02_T7	g2443320	BLASTX	320	1e-27	42	(D85597) polyprotein [Oryza australiensis]
2191	GM_70_A2_D04_MR	g4038056	BLASTX	417	3e-37	54	(AC005897) putative transposon [Arabidopsis thaliana]
2192	GM_70_A2_D08_MR	g3845197	BLASTN	360	3e-09	59	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
2193	GM_70_A2_D08_T7	g18559	BLASTN	488	4e-15	75	G.max gene for catalase
2194	GM_70_A2_D10_MR	g2827658	BLASTX	341	3e-30	60	(AL021637) putative protein [Arabidopsis thaliana]
2195	GM_70_A2_E02_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
2196	GM_70_A2_E04_MR	g3142328	BLASTN	1415	3e-57	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2197	GM_70_A2_E05_MR	g4115365	BLASTX	170	8e-12	53	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
2198	GM_70_A2_E06_MR	g576758	BLASTN	244	1e-08	64	Myrmecia pilosula HI87-135 mitochondrion cytochrome b gene, partial cds.
2199	GM_70_A2_E06_T7	g421955	BLASTX	190	1e-13	42	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
2200	GM_70_A2_E07_T7	g421955	BLASTX	368	9e-37	51	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2201	GM_70_A2_E08_MR	g130398	BLASTX	175	8e-17	48	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 297) gi 85089 pir B24872 retrovirus-related pol polyprotein homolog - fruit fly (Drosophila melanogaster) transposon 297
2202	GM_70_A2_E10_MR	g2129677	BLASTX	512	2e-48	68	probablel N-acetyltransferase hookless 1 - Arabidopsis thaliana gi 1277090 (U50399) putative N-acetyltransferase hookless1 [Arabidopsis thaliana] gi 1277092 (U50400) putative N-acetyltransferase hookless1 [Arabidopsis thaliana]
2203	GM_70_A2_E10_T7	g467843	BLASTN	367	1e-09	60	Prototheca wickerhamii 263-11 complete mitochondrial DNA.
2204	GM_70_A2_E12_MR	g507910	BLASTN	443	2e-13	79	Glycine max BSR-101 satellite SB92 genomic sequence.
2205	GM_70_A2_F02_T7	g2829888	BLASTX	284	1e-28	54	(AC002396) Hypothetical protein [Arabidopsis thaliana]
2206	GM_70_A2_F04_MR	g4159708	BLASTN	425	4e-12	66	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MKP6, complete sequence [Arabidopsis thaliana]
2207	GM_70_A2_F04_T7	g3985934	BLASTN	432	2e-12	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJE7, complete sequence [Arabidopsis thaliana]
2208	GM_70_A2_F08_MR	g3779021	BLASTX	161	1e-09	42	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]
2209	GM_70_A2_F11_MR	g2739309	BLASTX	128	5e-09	58	(Y15990) P-glycoprotein-like protein [Arabidopsis thaliana]
2210	GM_70_A2_F12_T7	g840618	BLASTN	566	5e-19	61	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
2211	GM_70_A2_G02_MR	g3426334	BLASTN	540	2e-17	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
2212	GM_70_A2_G03_MR	g3777527	BLASTX	326	3e-40	53	(AF053008) gag-pol polyprotein [Glycine max]
2213	GM_70_A2_G06_MR	g4063760	BLASTX	125	2e-09	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2214	GM_70_A2_G08_MR	g3142328	BLASTN	2044	4e-86	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2215	GM_70_A2_G09_T7	g3645899	BLASTX	294	6e-24	55	(U68408) 5' end not determined experimentally [Zea mays]
2216	GM_70_A2_G11_MR	g3810596	BLASTX	317	2e-26	47	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
2217	GM_70_A2_H02_MR	g3021697	BLASTN	362	2e-10	60	Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, complete sequence [Homo sapiens]
2218	GM_70_A2_H04_MR	g2982576	BLASTN	437	1e-12	58	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-105, complete sequence [Plasmodium falciparum]
2219	GM_70_A2_H04_T7	g4115536	BLASTX	144	6e-09	42	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]
2220	GM_70_A2_H06_MR	g11575	BLASTN	1398	7e-57	98	G.max chloroplast DNA for tRNA (Arg)

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2221	GM_70_A2_H06_T7	g128771	BLASTX	220	9e-18	82	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST gi 100110 pir S08494 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - fava bean chloroplast gi 11555 (X14804) ndhF gene product (AA 1-746) [Vicia faba] gi 12390 (X51471) NADH dehydrogenase [Vicia faba] gi 552971 (M36832) NADH dehydrogenase (ndhF) [Vicia faba]
2222	GM_70_A2_H07_MR	g3869176	BLASTX	216	4e-22	80	(AB019518) cyclophilin [Trichophyton mentagrophytes]
2223	GM_70_A2_H07_T7	g479124	BLASTN	369	8e-10	62	C.parapsilosos mitochondrial DNA for right telomeric region and ATP6 gene
2224	GM_70_A2_H09_MR	g3758836	BLASTN	412	1e-11	60	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
2225	GM_70_A2_H10_MR	g1363488	BLASTX	226	5e-18	66	IAA8 protein - Arabidopsis thaliana gi 972919 (U18410) IAA8 [Arabidopsis thaliana]
2226	GM_70_A2_H12_MR	g100484	BLASTX	321	3e-27	41	hypothetical protein - garden snapdragon
2227	GM_70_B1_A02_MR	g2522227	BLASTX	215	7e-17	53	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
2228	GM_70_B1_A02_T7	g2623300	BLASTX	170	2e-11	60	(AC002409) putative protein phosphatase 2C [Arabidopsis thaliana]
2229	GM_70_B1_A03_MR	g18559	BLASTN	1014	6e-39	74	G.max gene for catalase
2230	GM_70_B1_A04_MR	g3319372	BLASTX	192	5e-13	34	(AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]
2231	GM_70_B1_A06_MR	g100484	BLASTX	290	8e-24	55	hypothetical protein - garden snapdragon
2232	GM_70_B1_A09_MR	g3513747	BLASTX	353	5e-30	51	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
2233	GM_70_B1_A10_MR	g4063770	BLASTX	161	6e-10	45	(AB004906) transposase [Ipomoea purpurea]
2234	GM_70_B1_B02_MR	g18559	BLASTN	1041	3e-40	75	G.max gene for catalase
2235	GM_70_B1_B04_MR	g100484	BLASTX	260	1e-20	57	hypothetical protein - garden snapdragon
2236	GM_70_B1_B04_T7	g3142328	BLASTN	1754	1e-72	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2237	GM_70_B1_B06_MR	g2245073	BLASTN	359	3e-09	64	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8
2238	GM_70_B1_B09_MR	g2506938	BLASTX	149	9e-14	64	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4, CHLOROPLAST
2239	GM_70_B1_C01_MR	g3097320	BLASTN	1236	6e-49	78	Glycine max gene for Bd 30K, complete cds
2240	GM_70_B1_C03_T7	g1769898	BLASTX	402	5e-43	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2241	GM_70_B1_C06_T7	g226407	BLASTX	448	3e-40	63	retrotransposon del1-46 [Lilium henryi]
2242	GM_70_B1_C08_T7	g4063760	BLASTX	179	2e-19	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2243	GM_70_B1_D01_T7	g531389	BLASTX	190	7e-24	43	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2244	GM_70_B1_D02_MR	g2811096	BLASTN	354	6e-09	63	Homo sapiens Xp22 BAC GSHB-257G1 (Genome Systems BAC Library) complete sequence [Homo sapiens]
2245	GM_70_B1_D02_T7	g13767	BLASTN	404	4e-12	68	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
2246	GM_70_B1_D03_MR	g3676069	BLASTX	192	8e-14	71	(Y17899) ERG protein [Antirrhinum majus]
2247	GM_70_B1_D07_MR	g3924609	BLASTX	245	1e-18	48	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
2248	GM_70_B1_D07_T7	g3935164	BLASTX	218	1e-16	47	(AC004557) F17L21.7 [Arabidopsis thaliana]
2249	GM_70_B1_D09_MR	g2642431	BLASTX	374	3e-32	52	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
2250	GM_70_B1_D09_T7	g2443320	BLASTX	252	1e-30	49	(D85597) polyprotein [Oryza australiensis]
2251	GM_70_B1_E01_T7	g3777527	BLASTX	656	2e-62	94	(AF053008) gag-pol polyprotein [Glycine max]
2252	GM_70_B1_E03_MR	g3097320	BLASTN	894	2e-33	77	Glycine max gene for Bd 30K, complete cds
2253	GM_70_B1_E05_T7	g2660675	BLASTX	200	3e-14	83	T19K24.15; similar to DNA-damage-inducible protein P
2254	GM_70_B1_E10_T7	g905361	BLASTX	417	6e-38	92	(U22103) gag-protease polyprotein [Glycine max]
2255	GM_70_B1_F04_MR	g3097320	BLASTN	435	1e-12	74	Glycine max gene for Bd 30K, complete cds
2256	GM_70_B1_F06_MR	g4063760	BLASTX	168	3e-14	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2257	GM_70_B1_F06_T7	g507910	BLASTN	356	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2258	GM_70_B1_F11_T7	g2982431	BLASTX	325	3e-27	49	(AL022224) leucine rich repeat-like protein [Arabidopsis thaliana]
2259	GM_70_B1_G01_MR	g225268	BLASTX	242	9e-20	88	NADH dehydrogenase 2-like ORF 180 [Nicotiana tabacum]
2260	GM_70_B1_G02_MR	g2760836	BLASTX	175	1e-11	73	(AC003105) putative Ser/Thr protein kinase [Arabidopsis thaliana]
2261	GM_70_B1_G02_T7	g4150930	BLASTN	558	4e-18	66	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
2262	GM_70_B1_G04_MR	g2769655	BLASTN	357	4e-09	62	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
2263	GM_70_B1_G06_MR	g3171875	BLASTN	357	4e-09	62	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.1...
2264	GM_70_B1_G07_MR	g4063760	BLASTX	238	4e-23	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2265	GM_70_B1_G09_MR	g170606	BLASTN	718	6e-26	67	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
2266	GM_70_B1_H01_T7	g225242	BLASTX	251	1e-26	76	ORF 1708 [Nicotiana tabacum]
2267	GM_70_B1_H02_T7	g170080	BLASTN	360	3e-09	78	Soybean seed lectin gene transposable element tgm1.
2268	GM_70_B1_H03_MR	g1769897	BLASTX	154	2e-09	29	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2269	GM_70_B1_H09_MR	g2160128	BLASTN	495	2e-15	69	Genomic sequence from Human 17, complete sequence [Homo sapiens]
2270	GM_70_B2_A11_MR	g507910	BLASTN	498	7e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
2271	GM_70_B2_A12_MR	g2832901	BLASTN	1142	2e-50	76	Cajanus cajan copia-like retrotransposon,Panzee
2272	GM_70_B2_B03_MR	g2462134	BLASTX	156	1e-09	31	(Y13368) reverse transcriptase [Beta vulgaris]
2273	GM_70_B2_B04_MR	g507910	BLASTN	454	7e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2274	GM_70_B2_B04_T7	g507910	BLASTN	382	1e-10	76	Glycine max BSR-101 satellite SB92 genomic sequence.
2275	GM_70_B2_B06_MR	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2276	GM_70_B2_B06_T7	g507910	BLASTN	398	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2277	GM_70_B2_C02_MR	g1769898	BLASTX	227	3e-17	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2278	GM_70_B2_C11_T7	g3096949	BLASTX	193	2e-13	53	(Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]
2279	GM_70_B2_C12_MR	g3142328	BLASTN	542	2e-17	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2280	GM_70_B2_D03_T7	g2522228	BLASTX	236	1e-18	70	(AB007466) reverse transcriptase-like protein [Vicia faba]
2281	GM_70_B2_D06_T7	g4063760	BLASTX	303	7e-25	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2282	GM_70_B2_D08_T7	g507910	BLASTN	410	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2283	GM_70_B2_D11_MR	g170029	BLASTN	352	7e-09	77	Glycine max cv. Dare nodulin 26 gene fragment.
2284	GM_70_B2_D11_T7	g3513745	BLASTX	161	1e-09	43	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
2285	GM_70_B2_E01_MR	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
2286	GM_70_B2_E04_MR	g2702268	BLASTX	157	1e-17	69	(AC003033) putative cellulase [Arabidopsis thaliana]
2287	GM_70_B2_E06_T7	g507910	BLASTN	380	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2288	GM_70_B2_E07_T7	g2829911	BLASTX	203	3e-15	74	(AC002291) Unknown protein [Arabidopsis thaliana]
2289	GM_70_B2_E10_T7	g3097320	BLASTN	452	2e-13	69	Glycine max gene for Bd 30K, complete cds
2290	GM_70_B2_E11_MR	g4063760	BLASTX	209	8e-15	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2291	GM_70_B2_F01_MR	g3297863	BLASTN	426	3e-12	62	Homo sapiens DNA sequence from PAC 3E5 on chromosome 20q12-13.12. Contains protein tyrosine phosphatase (RPTP-rho) EST, STS, GSS, complete sequence [Homo sapiens]
2292	GM_70_B2_F02_T7	g2194136	BLASTX	210	6e-18	60	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
2293	GM_70_B2_F03_MR	g2264313	BLASTN	419	7e-12	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence [Arabidopsis thaliana]
2294	GM_70_B2_F04_MR	g4126312	BLASTN	366	2e-09	61	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
2295	GM_70_B2_F07_T7	g18559	BLASTN	819	4e-30	76	G.max gene for catalase
2296	GM_70_B2_F09_MR	g342952	BLASTN	344	2e-09	62	paramecium species 1,168 mt dna dimer: replication init. region.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2297	GM_70_B2_G07_MR	g4140398	BLASTX	169	6e-12	45	(AF081794) sterol-C5(6)-desaturase [Nicotiana tabacum]
2298	GM_70_B2_G08_T7	g2564750	BLASTN	404	3e-11	60	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
2299	GM_70_B2_G09_MR	g2522227	BLASTX	220	2e-17	56	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
2300	GM_70_B2_H07_MR	g130582	BLASTX	245	1e-18	38	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
2301	GM_70_B2_H09_MR	g507910	BLASTN	392	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2302	GM_70_B2_H10_MR	g3810596	BLASTX	232	2e-17	38	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
2303	GM_71_A1_A04_MR	g343946	BLASTN	382	4e-11	60	Yeast (S.cerevisiae) mitochondrial var1 gene, 3' flank.
2304	GM_71_A1_A05_T7	g507910	BLASTN	540	8e-18	83	Glycine max BSR-101 satellite SB92 genomic sequence.
2305	GM_71_A1_A09_MR	g3777527	BLASTX	156	2e-14	50	(AF053008) gag-pol polyprotein [Glycine max]
2306	GM_71_A1_A10_MR	g4063760	BLASTX	500	6e-46	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2307	GM_71_A1_A10_T7	g130582	BLASTX	241	2e-24	40	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
2308	GM_71_A1_B04_T7	g18559	BLASTN	438	8e-13	79	G.max gene for catalase
2309	GM_71_A1_B06_MR	g3738114	BLASTN	430	2e-12	62	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
2310	GM_71_A1_B06_T7	g2880057	BLASTX	338	1e-28	50	(AC002340) putative RNA helicase A, 5' partial [Arabidopsis thaliana]
2311	GM_71_A1_B08_T7	g18559	BLASTN	857	8e-32	85	G.max gene for catalase
2312	GM_71_A1_B09_MR	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2313	GM_71_A1_B09_T7	g507910	BLASTN	377	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2314	GM_71_A1_B12_MR	g2367675	BLASTX	172	4e-14	51	(AF017040) Pol [Dictyostelium discoideum]
2315	GM_71_A1_C02_MR	g507910	BLASTN	467	2e-14	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2316	GM_71_A1_C02_T7	g4063760	BLASTX	263	1e-20	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2317	GM_71_A1_C05_MR	g2213608	BLASTX	188	1e-12	34	(AC000103) F21J9.2 [Arabidopsis thaliana]
2318	GM_71_A1_C07_MR	g3142379	BLASTX	266	6e-22	63	(AF053008) envelope-like [Glycine max]
2319	GM_71_A1_C08_MR	g1705929	BLASTX	221	1e-17	53	ATP-DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT 1 (ENDOPEPTIDASE CLP 1) gi 755165 (U16135) ClpP [Synechococcus sp.]
2320	GM_71_A1_C08_T7	g3810596	BLASTX	232	2e-17	34	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2321	GM_71_A1_C09_MR	g170080	BLASTN	380	3e-10	70	Soybean seed lectin gene transposable element tgm1.
2322	GM_71_A1_D03_MR	g3645899	BLASTX	180	2e-17	52	(U68408) 5' end not determined experimentally [Zea mays]
2323	GM_71_A1_D03_T7	g3097320	BLASTN	358	4e-09	64	Glycine max gene for Bd 30K, complete cds
2324	GM_71_A1_E01_MR	g1431738	BLASTN	389	1e-10	89	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
2325	GM_71_A1_E02_T7	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
2326	GM_71_A1_E03_MR	g20861	BLASTN	366	1e-09	68	P.sativum retrotransposon
2327	GM_71_A1_E04_MR	g2160189	BLASTX	218	6e-16	37	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this gene. [Arabidopsis thaliana]
2328	GM_71_A1_E05_T7	g3319362	BLASTX	155	3e-09	31	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
2329	GM_71_A1_E06_MR	g99922	BLASTX	209	4e-16	52	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
2330	GM_71_A1_E06_T7	g13584	BLASTN	382	1e-10	63	Yeast mitochondrial oxi3 gene exon 1 for cytochrome c oxidase subunit I
2331	GM_71_A1_E07_MR	g2522228	BLASTX	383	1e-34	56	(AB007466) reverse transcriptase-like protein [Vicia faba]
2332	GM_71_A1_E11_MR	g3142328	BLASTN	654	1e-22	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2333	GM_71_A1_F05_MR	g18559	BLASTN	1094	1e-42	75	G.max gene for catalase
2334	GM_71_A1_F09_MR	g3777527	BLASTX	198	6e-14	46	(AF053008) gag-pol polyprotein [Glycine max]
2335	GM_71_A1_G03_T7	g905361	BLASTX	190	3e-13	29	(U22103) gag-protease polyprotein [Glycine max]
2336	GM_71_A1_G04_MR	g3241926	BLASTN	363	2e-09	60	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]
2337	GM_71_A1_G09_T7	g507910	BLASTN	532	2e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
2338	GM_71_A1_G11_T7	g3695395	BLASTX	245	4e-19	41	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
2339	GM_71_A1_H01_T7	g18767	BLASTN	334	9e-09	68	Soybean Tgm6 transposable element 5' end
2340	GM_71_A1_H03_MR	g3097320	BLASTN	1158	2e-45	80	Glycine max gene for Bd 30K, complete cds
2341	GM_71_A1_H05_T7	g3763929	BLASTX	198	4e-14	61	(AC004450) hypothetical protein [Arabidopsis thaliana]
2342	GM_71_A1_H07_T7	g639722	BLASTX	504	2e-47	78	(L27484) calcium-dependent protein kinase [Zea mays]
2343	GM_71_A1_H09_T7	g3860277	BLASTX	139	8e-09	77	(AC005824) putative ribosomal protein L10 [Arabidopsis thaliana]
2344	GM_71_A1_H10_T7	g4063760	BLASTX	513	3e-47	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2345	GM_71_A1_H11_T7	g507910	BLASTN	543	6e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2346	GM_71_A2_A02_MR	g2792220	BLASTX	323	1e-30	50	(AF032688) NBS-LRR type resistance protein [Oryza sativa]
2347	GM_71_A2_A11_MR	g905361	BLASTX	432	1e-39	97	(U22103) gag-protease polyprotein [Glycine max]
2348	GM_71_A2_A12_MR	g629693	BLASTX	270	1e-22	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2349	GM_71_A2_B04_MR	g3377834	BLASTX	170	5e-11	29	(AF075598) No definition line found [Arabidopsis thaliana]
2350	GM_71_A2_B06_MR	g4049609	BLASTN	465	6e-14	59	Oryzias latipes gene for membrane guanylyl cyclase OlGC1, complete cds
2351	GM_71_A2_C01_MR	g1142701	BLASTN	1332	7e-54	88	Glycine max satellite STR120-A.3.
2352	GM_71_A2_C02_MR	g522302	BLASTX	144	1e-21	55	(L35053) endonuclease [Magnaporthe grisea]
2353	GM_71_A2_C03_MR	g1147568	BLASTN	386	2e-10	64	H.sapiens genes for semenogelin I and semenogelin II
2354	GM_71_A2_C05_MR	g3152594	BLASTX	232	8e-18	43	(AC002986) Contains repeats similar to RECA protein gb L26100 from Acinetobacter calcoaceticus. [Arabidopsis thaliana]
2355	GM_71_A2_C07_MR	g507910	BLASTN	598	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
2356	GM_71_A2_C10_MR	g3152594	BLASTX	133	5e-12	46	(AC002986) Contains repeats similar to RECA protein gb L26100 from Acinetobacter calcoaceticus. [Arabidopsis thaliana]
2357	GM_71_A2_C11_MR	g2522230	BLASTX	183	2e-13	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
2358	GM_71_A2_D01_MR	g3283026	BLASTX	193	2e-13	40	putative transposase [Arabidopsis thaliana]
2359	GM_71_A2_D04_MR	g99922	BLASTX	996	1e-99	93	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
2360	GM_71_A2_D06_MR	g4049332	BLASTN	502	1e-15	63	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)
2361	GM_71_A2_D09_MR	g3785977	BLASTX	213	2e-17	40	(AC005560) putative growth regulator protein [Arabidopsis thaliana]
2362	GM_71_A2_D12_MR	g2098713	BLASTX	355	1e-31	72	(U82977) pectinesterase [Citrus sinensis]
2363	GM_71_A2_E06_MR	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
2364	GM_71_A2_E09_MR	g2191130	BLASTX	216	4e-16	36	(AF007269) A_IG002N01.7 gene product [Arabidopsis thaliana]
2365	GM_71_A2_F04_MR	g2995405	BLASTX	171	3e-15	42	(Y12432) polyprotein [Ananas comosus]
2366	GM_71_A2_F06_MR	g1769898	BLASTX	478	8e-45	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2367	GM_71_A2_F07_MR	g1173223	BLASTX	142	4e-09	75	40S RIBOSOMAL PROTEIN S11 gi 454848 (L28831) ribosomal protein S11 [Glycine max]
2368	GM_71_A2_F12_MR	g130582	BLASTX	303	2e-46	61	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
2369	GM_71_A2_G01_MR	g1769898	BLASTX	553	1e-52	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2370	GM_71_A2_G06_MR	g3097320	BLASTN	701	1e-24	71	Glycine max gene for Bd 30K, complete cds
2371	GM_71_A2_G07_MR	g1666236	BLASTX	217	5e-17	29	(U76261) unknown [Hordeum vulgare]
2372	GM_71_A2_G10_MR	g507910	BLASTN	405	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2373	GM_71_A2_G11_MR	g1666236	BLASTX	300	6e-26	33	(U76261) unknown [Hordeum vulgare]
2374	GM_71_A2_H02_MR	g3142328	BLASTN	441	6e-13	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2375	GM_71_A2_H07_MR	g100484	BLASTX	211	2e-15	38	hypothetical protein - garden snapdragon
2376	GM_71_A2_H11_MR	g100484	BLASTX	491	7e-46	48	hypothetical protein - garden snapdragon
2377	GM_71_A2_H12_MR	g1399306	BLASTN	363	1e-13	90	Glycine max phosphoinositide-specific phospholipase C P25 mRNA, complete cds.
2378	GM_71_B1_A02_MR	g2586082	BLASTX	327	3e-27	53	(U72725) retrofit [Oryza longistaminata]
2379	GM_71_B1_A03_MR	g1532163	BLASTX	233	7e-19	68	(U63815) similar to glutaredoxin encoded by GenBank Accession Number Z49699; localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop c...
2380	GM_71_B1_A04_T7	g507910	BLASTN	347	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2381	GM_71_B1_A07_MR	g3935164	BLASTX	192	7e-13	50	(AC004557) F17L21.7 [Arabidopsis thaliana]
2382	GM_71_B1_A09_T7	g18559	BLASTN	803	2e-29	76	G.max gene for catalase
2383	GM_71_B1_A12_MR	g3894156	BLASTN	391	1e-10	62	Arabidopsis thaliana chromosome II BAC T16F16 genomic sequence, complete sequence [Arabidopsis thaliana]
2384	GM_71_B1_B04_T7	g1039432	BLASTN	445	4e-16	70	Glycine max cellulase gene, partial cds.
2385	GM_71_B1_C02_T7	g531596	BLASTN	350	6e-09	62	M.capricolum DNA for CONTIG MC002
2386	GM_71_B1_C03_T7	g2462058	BLASTX	102	9e-13	48	(Y13389) reverse transcriptase [Antirrhinum majus]
2387	GM_71_B1_C05_T7	g4063760	BLASTX	231	3e-17	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2388	GM_71_B1_C07_MR	g1769897	BLASTX	155	1e-09	29	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2389	GM_71_B1_C09_MR	g1769898	BLASTX	264	4e-21	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2390	GM_71_B1_C10_T7	g2618698	BLASTX	160	7e-10	73	(AC002510) unknown protein [Arabidopsis thaliana]
2391	GM_71_B1_C12_T7	g18559	BLASTN	490	4e-15	78	G.max gene for catalase
2392	GM_71_B1_E01_T7	g3845089	BLASTN	410	2e-11	61	Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence
2393	GM_71_B1_E02_MR	g507910	BLASTN	622	2e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
2394	GM_71_B1_E02_T7	g507910	BLASTN	570	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2395	GM_71_B1_E05_MR	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2396	GM_71_B1_E11_T7	g3894194	BLASTX	205	2e-15	50	(AC005662) putative strictosidine synthase [Arabidopsis thaliana]
2397	GM_71_B1_F01_MR	g2522228	BLASTX	421	1e-38	59	(AB007466) reverse transcriptase-like protein [Vicia faba]
2398	GM_71_B1_F03_T7	g905361	BLASTX	216	5e-16	33	(U22103) gag-protease polyprotein [Glycine max]
2399	GM_71_B1_F04_T7	g2995405	BLASTX	154	4e-09	59	(Y12432) polyprotein [Ananas comosus]
2400	GM_71_B1_F05_MR	g469153	BLASTN	381	3e-10	68	P.sativum (Birte) Lox1:Ps:2 gene.
2401	GM_71_B1_F06_T7	g22635	BLASTN	579	3e-24	78	P.vulgaris mRNA for 70 kD heat shock protein
2402	GM_71_B1_G01_T7	g1785736	BLASTX	97	5e-11	54	(Y08502) orf119 [Arabidopsis thaliana]
2403	GM_71_B1_G04_MR	g629693	BLASTX	417	3e-38	57	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2404	GM_71_B1_G04_T7	g4126312	BLASTN	373	8e-10	63	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
2405	GM_71_B1_G05_MR	g505129	BLASTN	358	1e-11	73	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
2406	GM_71_B1_G07_MR	g507910	BLASTN	455	6e-14	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2407	GM_71_B1_G10_T7	g99922	BLASTX	472	4e-44	81	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
2408	GM_71_B1_G12_T7	g1142702	BLASTN	398	2e-11	86	Glycine max satellite STR120-A.4.
2409	GM_71_B1_H11_MR	g1532162	BLASTN	356	5e-09	71	Arabidopsis thaliana AT.I.24-1, AT.I.24-2, AT.I.24-3, AT.I.24-4, AT.I.24-5, AT.I.24-6, AT.I.24-9 and AT.I.24-14 genes, partial cds, AT.I.24-7, ascorbate peroxidase (ATHAPX1), EF-1alpha-A1, -A2 and -A3 (EF-1alpha) and AT.I....
2410	GM_71_B2_A03_MR	g3860271	BLASTX	161	7e-10	36	(AC005824) putative selenium-binding protein [Arabidopsis thaliana]
2411	GM_71_B2_A05_T7	g3810596	BLASTX	269	2e-21	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
2412	GM_71_B2_A07_T7	g498931	BLASTX	177	7e-13	43	(Z12825) ORF167; homologous to reverse transcriptases from retroviral-like transposons TNT 1-94 from tobacco and COPIA from Drosophila [Beta vulgaris]
2413	GM_71_B2_B01_MR	g905361	BLASTX	193	2e-13	33	(U22103) gag-protease polyprotein [Glycine max]
2414	GM_71_B2_B01_T7	g535454	BLASTX	179	1e-12	56	(U13940) cysteine proteinase [Alnus glutinosa]
2415	GM_71_B2_B04_MR	g4063770	BLASTX	166	2e-10	37	(AB004906) transposase [Ipomoea purpurea]
2416	GM_71_B2_B09_MR	g170606	BLASTN	727	2e-26	66	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
2417	GM_71_B2_C01_T7	g2895616	BLASTN	371	4e-10	60	Colias alexandra edwardsii large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
2418	GM_71_B2_C02_T7	g130398	BLASTX	207	1e-14	38	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 297) gi 85089 pir B24872 retrovirus-related pol polyprotein homolog - fruit fly (Drosophila melanogaster) transposon 297
2419	GM_71_B2_C05_T7	g18559	BLASTN	501	1e-15	68	G.max gene for catalase
2420	GM_71_B2_C07_T7	g3142328	BLASTN	568	1e-18	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2421	GM_71_B2_D02_T7	g507910	BLASTN	388	6e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
2422	GM_71_B2_D07_MR	g99922	BLASTX	317	1e-27	85	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2423	GM_71_B2_D09_MR	g2129559	BLASTX	150	6e-09	47	cellulase homolog OR16pep - Arabidopsis thaliana gi 1022807 (U37702) cellulase [Arabidopsis thaliana] gi 3493633 (AF074092) cellulase [Arabidopsis thaliana] gi 3598956 (AF074375) cellulase [Arabidopsis thaliana]
2424	GM_71_B2_E01_MR	g2654868	BLASTX	154	4e-18	61	(AF015301) RbohAp108 [Arabidopsis thaliana]
2425	GM_71_B2_E01_T7	g2252836	BLASTX	416	2e-37	71	(AF013293) contains weak similarity to S. cerevisiae BOB1 protein (PIR:S45444) [Arabidopsis thaliana]
2426	GM_71_B2_E02_MR	g4150930	BLASTN	384	3e-10	61	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
2427	GM_71_B2_E04_T7	g507910	BLASTN	405	1e-11	82	Glycine max BSR-101 satellite SB92 genomic sequence.
2428	GM_71_B2_E09_T7	g3738114	BLASTN	349	1e-08	64	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
2429	GM_71_B2_E10_MR	g2522228	BLASTX	165	8e-16	48	(AB007466) reverse transcriptase-like protein [Vicia faba]
2430	GM_71_B2_E12_MR	g3882356	BLASTX	158	3e-10	52	(U92460) pdr2 [Arabidopsis thaliana]
2431	GM_71_B2_F04_T7	g3645899	BLASTX	301	1e-24	56	(U68408) 5' end not determined experimentally [Zea mays]
2432	GM_71_B2_F11_T7	g2522230	BLASTX	229	2e-18	35	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
2433	GM_71_B2_G04_T7	g170029	BLASTN	394	8e-11	83	Glycine max cv. Dare nodulin 26 gene fragment.
2434	GM_71_B2_G07_T7	g905361	BLASTX	577	3e-55	91	(U22103) gag-protease polyprotein [Glycine max]
2435	GM_71_B2_G10_T7	g507910	BLASTN	451	9e-14	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2436	GM_71_B2_H05_T7	g507910	BLASTN	410	6e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
2437	GM_71_B2_H06_MR	g1142701	BLASTN	1366	2e-55	87	Glycine max satellite STR120-A.3.
2438	GM_71_B2_H06_T7	g226407	BLASTX	182	7e-12	40	retrotransposon del1-46 [Lilium henryi]
2439	GM_72_A1_A06_MR	g3097320	BLASTN	989	9e-38	80	Glycine max gene for Bd 30K, complete cds
2440	GM_72_A1_A08_MR	g2522228	BLASTX	151	3e-09	31	(AB007466) reverse transcriptase-like protein [Vicia faba]
2441	GM_72_A1_A10_T7	g2522228	BLASTX	358	5e-32	78	(AB007466) reverse transcriptase-like protein [Vicia faba]
2442	GM_72_A1_B08_T7	g4063760	BLASTX	239	5e-18	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2443	GM_72_A1_B10_MR	g2586082	BLASTX	258	6e-20	45	(U72725) retrofit [Oryza longistaminata]
2444	GM_72_A1_B12_T7	g2982550	BLASTN	1120	1e-43	74	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-65, complete sequence [Plasmodium falciparum]
2445	GM_72_A1_C02_MR	g3860271	BLASTX	305	3e-25	43	(AC005824) putative selenium-binding protein [Arabidopsis thaliana]
2446	GM_72_A1_C04_T7	g905361	BLASTX	198	5e-14	36	(U22103) gag-protease polyprotein [Glycine max]
2447	GM_72_A1_C05_T7	g3845143	BLASTN	402	4e-11	60	Plasmodium falciparum chromosome 2, section 22 of 73 of the complete sequence
2448	GM_72_A1_C08_MR	g3777527	BLASTX	615	6e-58	93	(AF053008) gag-pol polyprotein [Glycine max]
2449	GM_72_A1_D02_MR	g169980	BLASTN	2015	1e-85	94	Soybean heat-shock protein (Gmhsp26-A) gene, complete cds.
2450	GM_72_A1_D03_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2451	GM_72_A1_D05_MR	g3695294	BLASTN	417	7e-12	84	Glycine max nodule-specific glutamine synthetase gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2452	GM_72_A1_D07_T7	g905361	BLASTX	311	5e-33	93	(U22103) gag-protease polyprotein [Glycine max]
2453	GM_72_A1_D11_MR	g4063760	BLASTX	358	1e-30	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2454	GM_72_A1_D11_T7	g507910	BLASTN	353	2e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2455	GM_72_A1_E06_MR	g3142328	BLASTN	397	6e-11	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2456	GM_72_A1_E06_T7	g1946279	BLASTX	153	2e-10	48	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
2457	GM_72_A1_E09_T7	g4140712	BLASTX	338	1e-32	58	(AF110183) putative integrase [Oryza sativa]
2458	GM_72_A1_E10_MR	g507910	BLASTN	522	6e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
2459	GM_72_A1_E10_T7	g507910	BLASTN	549	3e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2460	GM_72_A1_F05_T7	g3513301	BLASTN	371	1e-09	63	Homo sapiens chromosome 19, cosmid R26894, complete sequence [Homo sapiens]
2461	GM_72_A1_F06_T7	g3142328	BLASTN	656	1e-22	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2462	GM_72_A1_F07_MR	g3645899	BLASTX	107	5e-09	45	(U68408) 5' end not determined experimentally [Zea mays]
2463	GM_72_A1_F09_T7	g2995405	BLASTX	237	5e-18	68	(Y12432) polyprotein [Ananas comosus]
2464	GM_72_A1_G04_MR	g3702738	BLASTN	422	5e-12	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWJ3, complete sequence [Arabidopsis thaliana]
2465	GM_72_A1_G04_T7	g2924653	BLASTN	433	2e-12	76	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]
2466	GM_72_A1_G05_MR	g3540207	BLASTX	184	2e-12	54	(AC004260) Putative protein kinase [Arabidopsis thaliana]
2467	GM_72_A1_G08_MR	g3142328	BLASTN	1809	3e-75	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2468	GM_72_A1_G10_T7	g3395441	BLASTX	187	6e-14	52	(AC004683) unknown protein [Arabidopsis thaliana]
2469	GM_72_A1_H05_T7	g507910	BLASTN	597	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
2470	GM_72_A2_A03_MR	g2961370	BLASTN	585	2e-19	70	Arabidopsis thaliana DNA chromosome 4, BAC clone F23E13 (ESSAII project)
2471	GM_72_A2_A03_T7	g3461832	BLASTX	103	2e-10	40	(AC004138) putative reverse transcriptase [Arabidopsis thaliana]
2472	GM_72_A2_A08_MR	g18559	BLASTN	958	2e-36	75	G.max gene for catalase
2473	GM_72_A2_A09_MR	g507910	BLASTN	350	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2474	GM_72_A2_A12_MR	g3142328	BLASTN	433	1e-12	68	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2475	GM_72_A2_B02_MR	g4006838	BLASTN	352	7e-09	61	Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence [Homo sapiens]
2476	GM_72_A2_B04_MR	g2961349	BLASTX	249	4e-19	42	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
2477	GM_72_A2_B07_MR	g1171583	BLASTN	480	1e-14	61	P.falciparum complete gene map of plastid-like DNA (IR-A)
2478	GM_72_A2_B07_T7	g3080412	BLASTX	282	2e-22	62	(AL022604) putative protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2479	GM_72_A2_B09_MR	g3142328	BLASTN	404	3e-11	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2480	GM_72_A2_B09_T7	g1946279	BLASTX	176	8e-13	41	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
2481	GM_72_A2_B11_MR	g100484	BLASTX	226	6e-17	40	hypothetical protein - garden snapdragon
2482	GM_72_A2_C06_MR	g507910	BLASTN	669	1e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
2483	GM_72_A2_C06_T7	g507910	BLASTN	546	5e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2484	GM_72_A2_C08_MR	g507910	BLASTN	397	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2485	GM_72_A2_C08_T7	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
2486	GM_72_A2_C11_T7	g2073447	BLASTN	475	2e-14	68	L.japonicus gln1, pge1 & krm genes
2487	GM_72_A2_D02_T7	g2244803	BLASTX	202	2e-15	42	(Z97336) reverse transcriptase-like protein [Arabidopsis thaliana]
2488	GM_72_A2_D08_MR	g99922	BLASTX	406	1e-65	77	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
2489	GM_72_A2_D08_T7	g170080	BLASTN	610	1e-20	73	Soybean seed lectin gene transposable element tgm1.
2490	GM_72_A2_D10_MR	g3264565	BLASTN	382	3e-10	62	Homo sapiens chromosome 17, clone hRPC.1037_O_7, complete sequence [Homo sapiens]
2491	GM_72_A2_D10_T7	g2129618	BLASTX	194	2e-13	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2492	GM_72_A2_E04_T7	g130582	BLASTX	192	6e-13	41	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
2493	GM_72_A2_E06_MR	g507910	BLASTN	384	9e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.
2494	GM_72_A2_E08_T7	g3928116	BLASTN	364	2e-09	60	, complete sequence [Homo sapiens]
2495	GM_72_A2_E11_MR	g507910	BLASTN	347	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2496	GM_72_A2_E11_T7	g507910	BLASTN	395	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2497	GM_72_A2_F04_MR	g2522230	BLASTX	267	2e-22	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
2498	GM_72_A2_F04_T7	g2194136	BLASTX	212	4e-15	44	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
2499	GM_72_A2_F08_MR	g2522227	BLASTX	185	1e-13	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
2500	GM_72_A2_F10_MR	g507910	BLASTN	382	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2501	GM_72_A2_F10_T7	g507910	BLASTN	377	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2502	GM_72_A2_G01_T7	g18559	BLASTN	850	2e-31	80	G.max gene for catalase
2503	GM_72_A2_G02_MR	g3142328	BLASTN	907	4e-34	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2504	GM_72_A2_G05_MR	g3850962	BLASTX	109	4e-09	55	(AF060421) ATP synthase beta subunit [Panopsis ferruginea]
2505	GM_72_A2_G06_T7	g18559	BLASTN	972	5e-37	76	G.max gene for catalase
2506	GM_72_A2_G07_T7	g3097320	BLASTN	694	2e-24	79	Glycine max gene for Bd 30K, complete cds
2507	GM_72_A2_G08_MR	g18559	BLASTN	504	8e-16	78	G.max gene for catalase
2508	GM_72_A2_G09_T7	g2997694	BLASTX	142	5e-09	27	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
2509	GM_72_A2_H02_MR	g398966	BLASTX	666	9e-65	93	4-COUMARATE--COA LIGASE 2 (4CL) (CLONE 4CL16) gi 541937 pir PQ0772 4-coumarate--CoA ligase (EC 6.2.1.12) (clone GM4CL1B) - soybean (fragment) gi 18520 (X69955) 4-coumarate--CoA ligase [Glycine max]
2510	GM_72_A2_H03_T7	g1785729	BLASTN	443	6e-13	65	A.thaliana mitochondrial genome, part B
2511	GM_72_A2_H04_T7	g3641780	BLASTN	382	3e-10	62	Homo sapiens PAC clone DJ1159C10 from 7q34-q36, complete sequence [Homo sapiens]
2512	GM_72_A2_H09_T7	g131254	BLASTX	546	5e-52	82	PHOTOSYSTEM Q(B) PROTEIN (32 KD THYLAKOID MEMBRANE PROTEIN) (PHOTOSYSTEM II PROTEIN D1) >gi 99477 pir S15957 photosystem II protein D1 - shore pine chloroplast >gi 320208 pir S29327 photosystem II protein D1 - Japanese black pine chloroplast >gi 12082 (X53721) D1 protein of photosystem II [Pinus contorta] >gi 12084 (X53722) D1 protein of photosystem II [Pinus contorta] >gi 12091 (X57097) D1 protein of photosystem II [Pinus contorta] >gi 12093 (X57097) D1 protein of photosystem II [Pinus contorta] >gi 344012 gnl PID d1002506 (D11467) photosystem II D1 protein [Pinus thunbergii] >gi 1262747 gnl PID d1004987 (D17510) PSII 32kDa protein [Pinus thunbergii]
2513	GM_73_A1_A08_T7	g4063760	BLASTX	137	9e-09	32	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2514	GM_73_A1_B03_T7	g2764526	BLASTN	494	3e-15	65	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
2515	GM_73_A1_B08_T7	g905361	BLASTX	646	2e-62	95	(U22103) gag-protease polyprotein [Glycine max]
2516	GM_73_A1_B09_T7	g3777527	BLASTX	169	2e-10	90	(AF053008) gag-pol polyprotein [Glycine max]
2517	GM_73_A1_B11_T7	g4038056	BLASTX	252	1e-19	42	(AC005897) putative transposon [Arabidopsis thaliana]
2518	GM_73_A1_C07_T7	g4063760	BLASTX	297	3e-24	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2519	GM_73_A1_C10_MR	g2522226	BLASTN	645	3e-22	69	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
2520	GM_73_A1_D07_MR	g4038056	BLASTX	218	6e-16	40	(AC005897) putative transposon [Arabidopsis thaliana]
2521	GM_73_A1_D09_T7	g2506277	BLASTX	272	2e-32	88	RUBISCO SUBUNIT BINDING-PROTEIN BETA SUBUNIT PRECURSOR (60 KD CHAPERONIN BETA SUBUNIT) (CPN-60 BETA) gi 806808 (U21139) chaperonin precursor [Pisum sativum]
2522	GM_73_A1_E04_MR	g3560028	BLASTN	358	3e-09	62	Schistosoma intercalatum ribosomal intergenic spacer DNA

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2523	GM_73_A1_E10_T7	g3687234	BLASTX	109	9e-09	25	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
2524	GM_73_A1_F01_MR	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2525	GM_73_A1_F04_MR	g3599418	BLASTN	1086	3e-42	88	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
2526	GM_73_A1_F12_T7	g3687234	BLASTX	168	2e-10	36	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
2527	GM_73_A1_G07_T7	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
2528	GM_73_A1_G11_MR	g905361	BLASTX	172	3e-11	34	(U22103) gag-protease polyprotein [Glycine max]
2529	GM_73_A1_H01_MR	g3319362	BLASTX	186	2e-12	37	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
2530	GM_73_A1_H03_T7	g3212869	BLASTX	323	1e-27	80	(AC004005) unknown protein [Arabidopsis thaliana]
2531	GM_73_A1_H04_T7	g22738	BLASTN	1512	2e-61	95	G.max mitochondrial atpA.
2532	GM_73_A1_H06_MR	g3859610	BLASTN	413	1e-11	68	Arabidopsis thaliana BAC T9E19
2533	GM_73_A2_A02_MR	g4038056	BLASTX	379	3e-34	50	(AC005897) putative transposon [Arabidopsis thaliana]
2534	GM_73_A2_A07_MR	g3142379	BLASTX	234	2e-18	57	(AF053008) envelope-like [Glycine max]
2535	GM_73_A2_A08_T7	g2801681	BLASTN	671	5e-24	72	Glycine max telomere-associated sequence STAS10
2536	GM_73_A2_A10_MR	g4063760	BLASTX	233	1e-20	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2537	GM_73_A2_B02_MR	g507910	BLASTN	368	5e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2538	GM_73_A2_B02_T7	g507910	BLASTN	343	7e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
2539	GM_73_A2_B03_MR	g3859610	BLASTN	514	3e-16	65	Arabidopsis thaliana BAC T9E19
2540	GM_73_A2_B03_T7	g905361	BLASTX	269	1e-21	39	(U22103) gag-protease polyprotein [Glycine max]
2541	GM_73_A2_B04_MR	g1769898	BLASTX	297	9e-25	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2542	GM_73_A2_B04_T7	g2462058	BLASTX	304	2e-26	47	(Y13389) reverse transcriptase [Antirrhinum majus]
2543	GM_73_A2_B09_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2544	GM_73_A2_B09_T7	g507910	BLASTN	358	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2545	GM_73_A2_C03_T7	g99721	BLASTX	401	3e-35	50	retrovirus-related polyprotein - Arabidopsis thaliana retrotransposon Ta1-3 gi 16534 (X13291) polyprotein [Arabidopsis thaliana]
2546	GM_73_A2_C06_T7	g3650026	BLASTN	369	1e-09	64	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]
2547	GM_73_A2_D02_T7	g1785736	BLASTX	171	1e-14	57	(Y08502) orf119 [Arabidopsis thaliana]
2548	GM_73_A2_D04_T7	g4063760	BLASTX	249	4e-19	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2549	GM_73_A2_D09_T7	g2462936	BLASTX	277	2e-23	44	(Y12321) open reading frame 2 [Brassica oleracea]
2550	GM_73_A2_E01_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2551	GM_73_A2_E01_T7	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2552	GM_73_A2_E02_MR	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2553	GM_73_A2_E02_T7	g507910	BLASTN	339	1e-08	69	Glycine max BSR-101 satellite SB92 genomic sequence.
2554	GM_73_A2_E07_MR	g18695	BLASTN	349	7e-09	67	Soybean nodulin 22 gene

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2555	GM_73_A2_E08_MR	g3142328	BLASTN	708	4e-25	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2556	GM_73_A2_E10_T7	g3273387	BLASTN	455	2e-13	64	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
2557	GM_73_A2_E12_MR	g507910	BLASTN	431	7e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
2558	GM_73_A2_E12_T7	g507910	BLASTN	384	9e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2559	GM_73_A2_F03_T7	g1769897	BLASTX	355	2e-31	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2560	GM_73_A2_F04_T7	g4115536	BLASTX	169	7e-12	34	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]
2561	GM_73_A2_F08_T7	g18559	BLASTN	433	1e-12	73	G.max gene for catalase
2562	GM_73_A2_F09_T7	g22738	BLASTN	1661	3e-68	91	G.max mitochondrial atpA.
2563	GM_73_A2_F10_MR	g4063760	BLASTX	467	2e-42	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2564	GM_73_A2_F11_T7	g2642431	BLASTX	192	2e-20	47	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
2565	GM_73_A2_F12_MR	g507910	BLASTN	539	1e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
2566	GM_73_A2_G03_T7	g3097320	BLASTN	795	6e-29	75	Glycine max gene for Bd 30K, complete cds
2567	GM_73_A2_G11_T7	g3097320	BLASTN	393	9e-11	68	Glycine max gene for Bd 30K, complete cds
2568	GM_73_A2_G12_MR	g130582	BLASTX	200	7e-14	35	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
2569	GM_73_A2_H03_MR	g1666236	BLASTX	197	1e-14	29	(U76261) unknown [Hordeum vulgare]
2570	GM_73_A2_H04_T7	g2522230	BLASTX	272	6e-23	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
2571	GM_73_A2_H06_T7	g3004564	BLASTX	148	5e-09	49	(AC003673) putative receptor Ser/Thr protein kinase [Arabidopsis thaliana]
2572	GM_73_A2_H09_T7	g3845197	BLASTN	379	4e-10	58	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
2573	GM_73_A2_H10_MR	g4063760	BLASTX	203	3e-14	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2574	GM_74_A1_A02_MR	g3582333	BLASTX	150	4e-09	82	(AC005496) hypothetical protein [Arabidopsis thaliana]
2575	GM_74_A1_A05_T7	g2244950	BLASTN	332	2e-13	65	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 5
2576	GM_74_A1_B01_T7	g1666236	BLASTX	212	2e-16	32	(U76261) unknown [Hordeum vulgare]
2577	GM_74_A1_B03_T7	g905361	BLASTX	422	2e-38	93	(U22103) gag-protease polyprotein [Glycine max]
2578	GM_74_A1_B08_T7	g2129618	BLASTX	177	1e-11	31	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2579	GM_74_A1_B12_MR	g2995405	BLASTX	304	3e-25	60	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2580	GM_74_A1_B12_T7	g3097320	BLASTN	1116	2e-43	78	Glycine max gene for Bd 30K, complete cds
2581	GM_74_A1_C07_T7	g2769655	BLASTN	367	1e-09	60	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
2582	GM_74_A1_D04_MR	g3641780	BLASTN	375	7e-10	60	Homo sapiens PAC clone DJ1159C10 from 7q34-q36, complete sequence [Homo sapiens]
2583	GM_74_A1_D10_MR	g3645899	BLASTX	193	4e-15	43	(U68408) 5' end not determined experimentally [Zea mays]
2584	GM_74_A1_D11_MR	g1167523	BLASTX	464	5e-42	56	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
2585	GM_74_A1_E01_MR	g2764526	BLASTN	483	8e-15	59	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
2586	GM_74_A1_E06_MR	g18559	BLASTN	819	4e-30	72	G.max gene for catalase
2587	GM_74_A1_E09_MR	g507910	BLASTN	415	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2588	GM_74_A1_E11_MR	g3777527	BLASTX	619	2e-58	81	(AF053008) gag-pol polyprotein [Glycine max]
2589	GM_74_A1_F04_MR	g507910	BLASTN	347	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
2590	GM_74_A1_F04_T7	g507910	BLASTN	385	9e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2591	GM_74_A1_F05_T7	g387902	BLASTX	179	9e-19	48	(L23524) ORF [Hordeum vulgare]
2592	GM_74_A1_F06_MR	g505129	BLASTN	347	1e-08	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
2593	GM_74_A1_F06_T7	g531389	BLASTX	170	1e-10	53	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
2594	GM_74_A1_F12_MR	g2995405	BLASTX	231	7e-21	51	(Y12432) polyprotein [Ananas comosus]
2595	GM_74_A1_G02_T7	g3378661	BLASTX	181	8e-13	35	(Y13048) putative outward rectifying potassium channel StKCO1 [Solanum tuberosum]
2596	GM_74_A1_G08_MR	g18559	BLASTN	488	4e-15	69	G.max gene for catalase
2597	GM_74_A1_G11_MR	g3513747	BLASTX	170	2e-10	44	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
2598	GM_74_A1_H02_T7	g2921210	BLASTN	425	2e-12	76	Perilla frutescens beta-ketoacyl-ACP synthase II (KAS II) mRNA, complete cds
2599	GM_74_A1_H07_T7	g4038056	BLASTX	243	1e-18	43	(AC005897) putative transposon [Arabidopsis thaliana]
2600	GM_74_A1_H09_MR	g4063760	BLASTX	235	5e-39	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2601	GM_74_A2_A03_MR	g441205	BLASTN	610	1e-20	72	Soybean lox1gm4 gene encoding lipxygenase L-4
2602	GM_74_A2_A03_T7	g3786500	BLASTN	358	4e-09	69	Caenorhabditis elegans cosmid T06A4
2603	GM_74_A2_A04_T7	g507910	BLASTN	553	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2604	GM_74_A2_A07_MR	g1142703	BLASTN	271	9e-15	73	Glycine max satellite STR120-B.1.
2605	GM_74_A2_A07_T7	g905361	BLASTX	421	2e-38	92	(U22103) gag-protease polyprotein [Glycine max]
2606	GM_74_A2_A09_T7	g3777527	BLASTX	170	1e-10	32	(AF053008) gag-pol polyprotein [Glycine max]
2607	GM_74_A2_A10_MR	g3377834	BLASTX	154	3e-09	29	(AF075598) No definition line found [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2608	GM_74_A2_A10_T7	g3142328	BLASTN	454	1e-13	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2609	GM_74_A2_B01_MR	g170080	BLASTN	359	3e-09	63	Soybean seed lectin gene transposable element tgm1.
2610	GM_74_A2_B05_MR	g3097320	BLASTN	632	1e-21	79	Glycine max gene for Bd 30K, complete cds
2611	GM_74_A2_B10_MR	g3097320	BLASTN	891	3e-33	78	Glycine max gene for Bd 30K, complete cds
2612	GM_74_A2_C09_T7	g4038056	BLASTX	155	3e-09	35	(AC005897) putative transposon [Arabidopsis thaliana]
2613	GM_74_A2_C11_T7	g2129677	BLASTX	180	1e-12	55	probablel N-acetyltransferase hookless 1 - Arabidopsis thaliana gi 1277090 (U50399) putative N-acetyltransferase hookless1 [Arabidopsis thaliana] gi 1277092 (U50400) putative N-acetyltransferase hookless1 [Arabidopsis thaliana]
2614	GM_74_A2_C12_T7	g3097320	BLASTN	1125	6e-44	83	Glycine max gene for Bd 30K, complete cds
2615	GM_74_A2_D01_MR	g1167523	BLASTX	176	1e-12	44	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
2616	GM_74_A2_D02_MR	g507910	BLASTN	579	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2617	GM_74_A2_D03_MR	g3549681	BLASTX	152	2e-09	54	(AL031394) male sterility 2-like protein [Arabidopsis thaliana]
2618	GM_74_A2_D03_T7	g1360141	BLASTX	177	4e-12	60	(X97980) protein kinase [Solanum berthaultii]
2619	GM_74_A2_D06_MR	g507910	BLASTN	399	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2620	GM_74_A2_D06_T7	g507910	BLASTN	359	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2621	GM_74_A2_D07_MR	g2522230	BLASTX	252	8e-21	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
2622	GM_74_A2_D09_MR	g18559	BLASTN	753	4e-27	77	G.max gene for catalase
2623	GM_74_A2_D10_MR	g3645899	BLASTX	319	8e-29	48	(U68408) 5' end not determined experimentally [Zea mays]
2624	GM_74_A2_D10_T7	g3142328	BLASTN	450	2e-13	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2625	GM_74_A2_E02_T7	g4063760	BLASTX	157	3e-09	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2626	GM_74_A2_E04_MR	g2995405	BLASTX	192	3e-13	52	(Y12432) polyprotein [Ananas comosus]
2627	GM_74_A2_E08_MR	g4063760	BLASTX	259	4e-20	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2628	GM_74_A2_E09_MR	g629693	BLASTX	183	7e-13	45	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
2629	GM_74_A2_E11_T7	g4063760	BLASTX	241	3e-18	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2630	GM_74_A2_F01_MR	g1666236	BLASTX	129	4e-12	39	(U76261) unknown [Hordeum vulgare]
2631	GM_74_A2_F04_MR	g4063760	BLASTX	191	7e-13	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2632	GM_74_A2_F05_MR	g100484	BLASTX	260	1e-20	57	hypothetical protein - garden snapdragon
2633	GM_74_A2_F05_T7	g3142328	BLASTN	861	5e-32	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2634	GM_74_A2_F07_T7	g3193290	BLASTX	173	3e-11	38	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabido...

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2635	GM_74_A2_G01_T7	g4063770	BLASTX	197	8e-14	42	(AB004906) transposase [Ipomoea purpurea]
2636	GM_74_A2_G04_T7	g3777527	BLASTX	691	4e-66	92	(AF053008) gag-pol polyprotein [Glycine max]
2637	GM_74_A2_G05_T7	g1785693	BLASTX	123	2e-10	47	(Y08501) orf111a [Arabidopsis thaliana]
2638	GM_74_A2_G10_MR	g2997694	BLASTX	101	2e-13	36	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
2639	GM_74_A2_G10_T7	g4063760	BLASTX	162	8e-10	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2640	GM_74_A2_H03_MR	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2641	GM_74_A2_H03_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2642	GM_74_A2_H11_T7	g2982540	BLASTN	374	7e-10	66	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-30, complete sequence [Plasmodium falciparum]
2643	GM_74_B1_A03_T7	g4115365	BLASTX	126	1e-15	38	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
2644	GM_74_B1_A09_MR	g4063760	BLASTX	485	2e-44	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2645	GM_74_B1_A10_MR	g158813	BLASTN	363	6e-10	64	Drosophila hydei Y chromosome lampbrush loop transcribed repeats.
2646	GM_74_B1_A11_T7	g3777526	BLASTN	736	3e-26	79	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
2647	GM_74_B1_B01_T7	g3777526	BLASTN	1135	2e-44	93	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
2648	GM_74_B1_B03_MR	g3928116	BLASTN	397	7e-11	60	, complete sequence [Homo sapiens]
2649	GM_74_B1_B04_MR	g3650039	BLASTX	175	1e-11	34	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
2650	GM_74_B1_B05_MR	g3777527	BLASTX	650	9e-62	96	(AF053008) gag-pol polyprotein [Glycine max]
2651	GM_74_B1_B06_MR	g1666236	BLASTX	115	1e-09	41	(U76261) unknown [Hordeum vulgare]
2652	GM_74_B1_B07_T7	g3687234	BLASTX	170	1e-10	45	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
2653	GM_74_B1_B09_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2654	GM_74_B1_C01_T7	g905361	BLASTX	437	3e-40	96	(U22103) gag-protease polyprotein [Glycine max]
2655	GM_74_B1_C02_MR	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2656	GM_74_B1_C02_T7	g507910	BLASTN	360	1e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
2657	GM_74_B1_C05_MR	g505129	BLASTN	362	2e-09	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
2658	GM_74_B1_C05_T7	g2129618	BLASTX	184	2e-12	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2659	GM_74_B1_C07_MR	g4049647	BLASTN	421	6e-12	65	Melanoplus sanguinipes entomopoxvirus, complete genome
2660	GM_74_B1_C07_T7	g4160441	BLASTX	161	2e-10	37	(AF098674) lateral suppressor protein [Lycopersicon esculentum]
2661	GM_74_B1_C10_MR	g3142328	BLASTN	1167	6e-46	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2662	GM_74_B1_C12_MR	g629693	BLASTX	273	5e-23	61	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
2663	GM_74_B1_D02_T7	g2149640	BLASTX	227	8e-17	75	(U91995) Argonaute protein [Arabidopsis thaliana]
2664	GM_74_B1_D03_T7	g730526	BLASTX	235	2e-38	80	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis thaliana gi 404166 (X75162) BBC1 protein [Arabidopsis thaliana]
2665	GM_74_B1_D04_MR	g507910	BLASTN	345	6e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2666	GM_74_B1_D09_T7	g3097320	BLASTN	480	1e-14	71	Glycine max gene for Bd 30K, complete cds
2667	GM_74_B1_E04_MR	g507910	BLASTN	401	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2668	GM_74_B1_E04_T7	g507910	BLASTN	385	9e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2669	GM_74_B1_E10_MR	g905361	BLASTX	150	5e-12	27	(U22103) gag-protease polyprotein [Glycine max]
2670	GM_74_B1_F01_T7	g4038056	BLASTX	386	6e-34	53	(AC005897) putative transposon [Arabidopsis thaliana]
2671	GM_74_B1_F05_MR	g3449334	BLASTN	395	8e-11	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]
2672	GM_74_B1_F07_T7	g905361	BLASTX	239	2e-18	34	(U22103) gag-protease polyprotein [Glycine max]
2673	GM_74_B1_F08_MR	g99922	BLASTX	464	3e-43	58	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
2674	GM_74_B1_F09_MR	g507910	BLASTN	386	8e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2675	GM_74_B1_F11_T7	g547683	BLASTX	133	4e-16	77	HEAT SHOCK COGNATE PROTEIN 80 gi 170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] gi 445601 prf 1909348A heat shock protein hsp80 [Lycopersicon esculentum]
2676	GM_74_B1_F12_T7	g3097320	BLASTN	1421	2e-57	82	Glycine max gene for Bd 30K, complete cds
2677	GM_74_B1_G01_T7	g2323254	BLASTN	405	3e-11	64	Human Chromosome X, complete sequence [Homo sapiens]
2678	GM_74_B1_G02_MR	g4160362	BLASTN	388	2e-10	61	Saccharomyces cerevisiae complete mitochondrial genome
2679	GM_74_B1_G04_MR	g3548805	BLASTX	147	3e-12	65	(AC005313) unknown protein [Arabidopsis thaliana]
2680	GM_74_B1_G08_MR	g1346736	BLASTX	162	4e-11	43	POLLEN-SPECIFIC MEMBRANE INTEGRAL PROTEIN gi 665948 (U20490) putative membrane integral protein [Nicotiana alata]
2681	GM_74_B1_G09_MR	g4063760	BLASTX	495	2e-45	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2682	GM_74_B1_G11_T7	g3928116	BLASTN	509	6e-16	65	, complete sequence [Homo sapiens]
2683	GM_74_B1_H07_MR	g3269291	BLASTX	132	4e-14	60	(AL030978) putative receptor protein kinase [Arabidopsis thaliana]
2684	GM_74_B1_H11_T7	g4063760	BLASTX	495	2e-45	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2685	GM_74_B1_H12_T7	g2522227	BLASTX	184	3e-17	40	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
2686	GM_74_B2_A01_T7	g3650039	BLASTX	277	1e-22	41	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
2687	GM_74_B2_A03_T7	g2982540	BLASTN	349	1e-08	66	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-30, complete sequence [Plasmodium falciparum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2688	GM_74_B2_A04_T7	g13096	BLASTN	362	2e-09	67	Leishmania tarentolae maxicircle DNA fragment
2689	GM_74_B2_B02_T7	g507910	BLASTN	396	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2690	GM_74_B2_B05_T7	g4063760	BLASTX	348	1e-41	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2691	GM_74_B2_B08_MR	g18559	BLASTN	583	2e-19	71	G.max gene for catalase
2692	GM_74_B2_B11_MR	g4063760	BLASTX	342	5e-29	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2693	GM_74_B2_B12_T7	g1877523	BLASTN	483	9e-15	70	Arabidopsis thaliana BAC T7I23, complete sequence [Arabidopsis thaliana]
2694	GM_74_B2_C04_T7	g3097320	BLASTN	1168	7e-46	77	Glycine max gene for Bd 30K, complete cds
2695	GM_74_B2_C06_MR	g3243214	BLASTN	428	3e-12	72	Arabidopsis thaliana BAC T19B17 from chromsome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]
2696	GM_74_B2_D03_T7	g3097320	BLASTN	454	2e-13	65	Glycine max gene for Bd 30K, complete cds
2697	GM_74_B2_D05_T7	g3777527	BLASTX	306	5e-25	46	(AF053008) gag-pol polyprotein [Glycine max]
2698	GM_74_B2_D09_T7	g507910	BLASTN	405	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2699	GM_74_B2_D11_T7	g2522227	BLASTX	216	5e-17	53	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
2700	GM_74_B2_E01_MR	g1658457	BLASTX	226	4e-18	66	(U75248) reverse transcriptase [Gossypium barbadense]
2701	GM_74_B2_E10_T7	g422418	BLASTX	210	2e-26	45	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
2702	GM_74_B2_E11_MR	g507910	BLASTN	372	3e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2703	GM_74_B2_F02_T7	g3097320	BLASTN	1167	8e-46	75	Glycine max gene for Bd 30K, complete cds
2704	GM_74_B2_F08_T7	g2443320	BLASTX	213	1e-26	51	(D85597) polyprotein [Oryza australiensis]
2705	GM_74_B2_G07_MR	g4056494	BLASTX	293	2e-25	69	(AC005896) putative protein translocase [Arabidopsis thaliana]
2706	GM_74_B2_G07_T7	g3785975	BLASTX	208	5e-15	76	(AC005560) hypothetical protein [Arabidopsis thaliana]
2707	GM_74_B2_G09_T7	g2443320	BLASTX	216	2e-32	52	(D85597) polyprotein [Oryza australiensis]
2708	GM_74_B2_H01_MR	g2961346	BLASTX	174	1e-11	59	(AL022140) pectinesterase like protein [Arabidopsis thaliana]
2709	GM_74_B2_H02_MR	g313189	BLASTN	367	1e-09	70	A.thaliana TMKL1 mRNA
2710	GM_74_B2_H06_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2711	GM_74_B2_H06_T7	g507910	BLASTN	378	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2712	GM_74_B2_H07_MR	g507910	BLASTN	463	3e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
2713	GM_75_A1_A08_MR	g507910	BLASTN	414	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2714	GM_75_A1_A08_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2715	GM_75_A1_B02_T7	g2244747	BLASTN	361	3e-09	75	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 0
2716	GM_75_A1_B04_T7	g2464864	BLASTX	158	1e-09	52	(Z99707) selenium-binding protein homolog [Arabidopsis thaliana]
2717	GM_75_A1_B05_T7	g99755	BLASTX	378	8e-34	54	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2718	GM_75_A1_B10_MR	g8540	BLASTN	391	2e-11	61	Drosophila satellite DNA fragment 1.672-614 >gi 158379 gb M29744 DROSAT02 Drosophila satellite DNA fragment 1.672-614.
2719	GM_75_A1_C04_T7	g3810595	BLASTX	232	3e-17	56	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
2720	GM_75_A1_C12_MR	g100484	BLASTX	169	1e-19	44	hypothetical protein - garden snapdragon
2721	GM_75_A1_D01_MR	g3777527	BLASTX	507	2e-46	80	(AF053008) gag-pol polyprotein [Glycine max]
2722	GM_75_A1_D05_T7	g409571	BLASTN	392	1e-11	65	Helicoverpa armigera mitochondrion D-loop, partial 12S rRNA gene, and partial tRNA-Met gene.
2723	GM_75_A1_D09_T7	g2995405	BLASTX	200	4e-14	66	(Y12432) polyprotein [Ananas comosus]
2724	GM_75_A1_E02_T7	g3645899	BLASTX	346	2e-29	50	(U68408) 5' end not determined experimentally [Zea mays]
2725	GM_75_A1_E03_MR	g3097320	BLASTN	558	3e-18	83	Glycine max gene for Bd 30K, complete cds
2726	GM_75_A1_E05_MR	g4063760	BLASTX	513	3e-47	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2727	GM_75_A1_E11_MR	g18559	BLASTN	416	8e-12	87	G.max gene for catalase
2728	GM_75_A1_G01_T7	g114661	BLASTX	182	2e-13	76	ATP SYNTHASE A CHAIN PRECURSOR (SUBUNIT IV) gi 67924 pir LWNT6 H+-transporting ATP synthase (EC 3.6.1.34) chain a - common tobacco chloroplast gi 11813 (Z00044) ATPase sunthase IV subunit [Nicotiana tabacum] gi 225273 prf 1211235H ATPase a [Nicotiana tabacum]
2729	GM_75_A1_G02_MR	g507910	BLASTN	351	3e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2730	GM_75_A1_G07_T7	g2351061	BLASTN	457	1e-13	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19
2731	GM_75_A1_G11_MR	g3241927	BLASTN	528	8e-17	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence [Arabidopsis thaliana]
2732	GM_75_A1_H02_MR	g3600044	BLASTX	202	5e-14	42	(AF080119) contains similarity to proteases [Arabidopsis thaliana]
2733	GM_75_A1_H08_MR	g2443320	BLASTX	314	6e-26	46	(D85597) polyprotein [Oryza australiensis]
2734	GM_75_A1_H08_T7	g1769898	BLASTX	187	7e-13	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2735	GM_75_A1_H12_T7	g507910	BLASTN	500	6e-16	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2736	GM_76_A1_A07_MR	g3688328	BLASTX	223	3e-26	61	(AJ228325) reverse transcriptase [Ginkgo biloba]
2737	GM_76_A1_A10_MR	g4063760	BLASTX	279	3e-22	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2738	GM_76_A1_A12_T7	g3746069	BLASTX	254	1e-19	45	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
2739	GM_76_A1_B04_T7	g3777527	BLASTX	233	2e-26	91	(AF053008) gag-pol polyprotein [Glycine max]
2740	GM_76_A1_B07_T7	g2522228	BLASTX	460	7e-43	73	(AB007466) reverse transcriptase-like protein [Vicia faba]
2741	GM_76_A1_B09_MR	g992916	BLASTN	505	8e-16	68	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
2742	GM_76_A1_B10_T7	g18559	BLASTN	1180	2e-46	76	G.max gene for catalase
2743	GM_76_A1_C03_MR	g3779030	BLASTX	217	4e-17	30	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
2744	GM_76_A1_C08_MR	g434060	BLASTN	509	4e-16	71	Soybean DNA for basic 7S globulin, complete cds
2745	GM_76_A1_C10_MR	g1666236	BLASTX	209	4e-16	32	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2746	GM_76_A1_C10_T7	g2264320	BLASTN	724	1e-25	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
2747	GM_76_A1_D03_T7	g99922	BLASTX	519	4e-49	62	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
2748	GM_76_A1_D04_MR	g2264367	BLASTN	391	1e-10	63	Arabidopsis thaliana BAC F6P23 from chromosome IV, top arm, complete sequence.
2749	GM_76_A1_D05_MR	g507910	BLASTN	357	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
2750	GM_76_A1_D06_T7	g170080	BLASTN	424	3e-12	89	Soybean seed lectin gene transposable element tgm1.
2751	GM_76_A1_D09_T7	g4063760	BLASTX	160	1e-09	33	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2752	GM_76_A1_D10_T7	g3776466	BLASTN	359	3e-09	61	Homo sapiens immunoglobulin-like transcript 10 protein gene, exons 7 and 8 and complete cds
2753	GM_76_A1_E03_T7	g507910	BLASTN	424	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2754	GM_76_A1_F01_T7	g2895615	BLASTN	419	3e-12	63	Colias croceus large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
2755	GM_76_A1_F02_T7	g1076570	BLASTX	172	2e-12	74	homeotic protein CHB6 - carrot
2756	GM_76_A1_F06_MR	g4063760	BLASTX	274	7e-32	81	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2757	GM_76_A1_F06_T7	g3097320	BLASTN	441	6e-13	70	Glycine max gene for Bd 30K, complete cds
2758	GM_76_A1_F08_MR	g3763921	BLASTX	297	1e-25	63	(AC004450) putative pirin protein [Arabidopsis thaliana]
2759	GM_76_A1_F08_T7	g3763915	BLASTN	395	8e-11	65	Arabidopsis thaliana chromosome II BAC F14B2 genomic sequence, complete sequence [Arabidopsis thaliana]
2760	GM_76_A1_F12_MR	g3097320	BLASTN	711	4e-41	76	Glycine max gene for Bd 30K, complete cds
2761	GM_76_A1_G07_MR	g4050011	BLASTN	418	7e-12	64	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
2762	GM_76_A1_G10_MR	g507910	BLASTN	420	2e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2763	GM_76_A1_G10_T7	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2764	GM_76_A1_G11_MR	g507910	BLASTN	620	2e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
2765	GM_76_A1_G11_T7	g507910	BLASTN	549	3e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
2766	GM_76_A1_H08_MR	g2507455	BLASTX	376	2e-33	75	FORMATE--TETRAHYDROFOLATE LIGASE (FORMYLTETRAHYDROFOLATE SYNTHETASE) (FHS) (FTHFS) gi 322401 pir A43350 formate--tetrahydrofolate ligase (EC 6.3.4.3) - spinach gi 170145 (M83940) 10-formyltetrahydrofolate synthetase [Spinacia oleracea]
2767	GM_76_A1_H11_MR	g507910	BLASTN	389	6e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2768	GM_76_A1_H11_T7	g507910	BLASTN	423	2e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2769	GM_76_A1_H12_MR	g1769898	BLASTX	189	2e-27	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2770	GM_76_A2_A03_MR	g3859610	BLASTN	716	3e-25	64	Arabidopsis thaliana BAC T9E19

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2771	GM_76_A2_A04_T7	g2627181	BLASTX	216	2e-29	83	(D89619) cycloartenol synthase [Pisum sativum]
2772	GM_76_A2_A06_MR	g2583130	BLASTX	185	3e-12	35	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
2773	GM_76_A2_B06_T7	g3319362	BLASTX	204	1e-21	47	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
2774	GM_76_A2_B07_T7	g507910	BLASTN	581	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2775	GM_76_A2_B10_MR	g507910	BLASTN	383	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2776	GM_76_A2_C03_MR	g3319362	BLASTX	260	2e-20	40	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
2777	GM_76_A2_C05_MR	g2760839	BLASTX	306	1e-25	70	(AC003105) putative receptor kinase [Arabidopsis thaliana]
2778	GM_76_A2_C12_T7	g3641780	BLASTN	398	6e-11	64	Homo sapiens PAC clone DJ1159C10 from 7q34-q36, complete sequence [Homo sapiens]
2779	GM_76_A2_D01_T7	g3924609	BLASTX	251	3e-19	47	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
2780	GM_76_A2_D04_MR	g507910	BLASTN	583	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
2781	GM_76_A2_D06_MR	g3777527	BLASTX	509	1e-46	90	(AF053008) gag-pol polyprotein [Glycine max]
2782	GM_76_A2_D07_MR	g3021268	BLASTX	309	2e-25	57	(AL022347) putative protein [Arabidopsis thaliana]
2783	GM_76_A2_D09_MR	g130582	BLASTX	180	1e-11	36	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
2784	GM_76_A2_D12_MR	g3033375	BLASTX	489	6e-46	64	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]
2785	GM_76_A2_E02_MR	g742344	BLASTX	169	5e-23	78	S receptor kinase [Brassica oleracea]
2786	GM_76_A2_E04_MR	g343938	BLASTN	302	5e-12	70	Yeast (S.cerevisiae) mitochondrial Ser-tRNA and ATPase proteolipid genes.
2787	GM_76_A2_E04_T7	g507910	BLASTN	549	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
2788	GM_76_A2_E06_MR	g3777527	BLASTX	827	1e-80	95	(AF053008) gag-pol polyprotein [Glycine max]
2789	GM_76_A2_F01_T7	g1504063	BLASTX	107	3e-13	77	(Y07597) shaggy-like kinase kappa [Arabidopsis thaliana]
2790	GM_76_A2_F02_MR	g3777527	BLASTX	345	4e-29	57	(AF053008) gag-pol polyprotein [Glycine max]
2791	GM_76_A2_F05_MR	g3777527	BLASTX	230	4e-18	42	(AF053008) gag-pol polyprotein [Glycine max]
2792	GM_76_A2_F06_T7	g2245136	BLASTX	283	5e-23	77	(Z97344) trehalose-6-phosphate synthase homolog [Arabidopsis thaliana]
2793	GM_76_A2_G02_T7	g1769898	BLASTX	179	2e-24	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2794	GM_76_A2_G06_MR	g4050011	BLASTN	408	2e-11	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
2795	GM_76_A2_H04_MR	g818849	BLASTX	244	2e-19	63	(U25430) nucleotide pyrophosphatase precursor [Oryza sativa]
2796	GM_76_A2_H06_MR	g100484	BLASTX	395	3e-35	52	hypothetical protein - garden snapdragon

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2797	GM_76_A2_H06_T7	g3176795	BLASTN	466	6e-15	64	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
2798	GM_76_A2_H08_MR	g4063760	BLASTX	299	2e-24	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2799	GM_76_A2_H08_T7	g3777527	BLASTX	554	2e-51	92	(AF053008) gag-pol polyprotein [Glycine max]
2800	GM_76_A2_H11_MR	g507910	BLASTN	409	7e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2801	GM_76_A2_H12_T7	g3097320	BLASTN	564	2e-18	75	Glycine max gene for Bd 30K, complete cds
2802	GM_76_B1_A01_T7	g507910	BLASTN	738	1e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
2803	GM_76_B1_A03_MR	g465535	BLASTX	148	2e-09	41	HYPOTHETICAL 32.7 KD PROTEIN IN NTH2-COQ1 INTERGENIC REGION gi 626491 pir S44561 hypothetical protein YBR002c - yeast (Saccharomyces cerevisiae) gi 403317 (Z26494) unknown [Saccharomyces cerevisiae] gi 536188 (Z35871) ORF YBR002c [Saccharomyces cerevisiae] gi 1582565 prf 2118405F ORF YBR0107 [Saccharomyces cerevisiae]
2804	GM_76_B1_A06_MR	g507910	BLASTN	339	1e-08	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2805	GM_76_B1_A06_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2806	GM_76_B1_A07_MR	g2129618	BLASTX	154	3e-13	47	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2807	GM_76_B1_A09_T7	g1666236	BLASTX	209	4e-16	33	(U76261) unknown [Hordeum vulgare]
2808	GM_76_B1_A10_MR	g2696018	BLASTN	382	3e-10	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9
2809	GM_76_B1_A10_T7	g4092471	BLASTN	420	6e-12	62	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
2810	GM_76_B1_B01_MR	g1840106	BLASTN	276	8e-10	62	Human fragile site locus (FRA16B) minisatellite repeat
2811	GM_76_B1_B01_T7	g1001478	BLASTX	208	1e-15	51	(D63999) hypothetical protein [Synechocystis sp.]
2812	GM_76_B1_B03_MR	g3810596	BLASTX	301	8e-25	53	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
2813	GM_76_B1_B12_MR	g3930515	BLASTX	112	1e-10	45	(AF059674) putative gag protein [Nicotiana tabacum]
2814	GM_76_B1_C01_T7	g507910	BLASTN	404	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2815	GM_76_B1_C03_T7	g1504063	BLASTX	173	4e-23	93	(Y07597) shaggy-like kinase kappa [Arabidopsis thaliana]
2816	GM_76_B1_C05_T7	g417073	BLASTX	184	8e-12	91	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) gi 484529 pir JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa gi 166412 (L01660) NADH-glutamate synthase [Medicago sativa]
2817	GM_76_B1_C10_T7	g18559	BLASTN	793	6e-29	74	G.max gene for catalase
2818	GM_76_B1_D01_T7	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
2819	GM_76_B1_D02_T7	g3924609	BLASTX	236	6e-19	47	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
2820	GM_76_B1_D03_T7	g99922	BLASTX	532	2e-50	63	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2821	GM_76_B1_D06_T7	g3142328	BLASTN	1203	1e-47	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2822	GM_76_B1_D12_T7	g1769897	BLASTX	189	3e-13	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2823	GM_76_B1_E03_MR	g507910	BLASTN	386	8e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2824	GM_76_B1_E03_T7	g507910	BLASTN	387	7e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2825	GM_76_B1_E04_MR	g2791289	BLASTX	186	2e-12	36	(AJ000387) protease [Drosophila melanogaster]
2826	GM_76_B1_E05_T7	g4063760	BLASTX	488	1e-44	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2827	GM_76_B1_F02_T7	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2828	GM_76_B1_F05_T7	g1769898	BLASTX	142	3e-28	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2829	GM_76_B1_F06_T7	g905360	BLASTN	1100	2e-43	93	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
2830	GM_76_B1_F09_T7	g1778843	BLASTN	424	3e-12	66	Dictyostelium discoideum LimA (limA) mRNA, partial cds
2831	GM_76_B1_G01_T7	g2921208	BLASTN	384	2e-10	63	Perilla frutescens beta-ketoacyl-ACP synthase I (KAS I) mRNA, complete cds
2832	GM_76_B1_G02_MR	g1769898	BLASTX	341	1e-29	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2833	GM_76_B1_G04_T7	g2443320	BLASTX	326	3e-27	42	(D85597) polyprotein [Oryza australiensis]
2834	GM_76_B1_G09_MR	g2129618	BLASTX	167	2e-10	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2835	GM_76_B1_G10_MR	g1369835	BLASTN	368	1e-09	66	Homo sapiens chromosome-19 36.3-kbp cosmid F7501, with 3 regions of similarity to olfactory receptor protein genes.
2836	GM_76_B1_G10_T7	g2642433	BLASTX	149	1e-08	33	(AC002391) putative receptor protein kinase [Arabidopsis thaliana]
2837	GM_76_B1_G12_MR	g507910	BLASTN	647	1e-22	86	Glycine max BSR-101 satellite SB92 genomic sequence.
2838	GM_76_B1_G12_T7	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
2839	GM_76_B1_H01_T7	g18559	BLASTN	1063	3e-41	81	G.max gene for catalase
2840	GM_76_B1_H08_T7	g905361	BLASTX	416	7e-38	92	(U22103) gag-protease polyprotein [Glycine max]
2841	GM_76_B1_H11_MR	g1030731	BLASTX	228	6e-17	37	(X14037) polyprotein [Drosophila melanogaster]
2842	GM_76_B2_A02_MR	g1335862	BLASTX	163	7e-23	75	(U42608) clathrin heavy chain [Glycine max]
2843	GM_76_B2_A07_MR	g4160362	BLASTN	357	4e-09	62	Saccharomyces cerevisiae complete mitochondrial genome
2844	GM_76_B2_A10_T7	g4063760	BLASTX	247	7e-19	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2845	GM_76_B2_B04_MR	g3645899	BLASTX	229	4e-26	46	(U68408) 5' end not determined experimentally [Zea mays]
2846	GM_76_B2_B07_T7	g905361	BLASTX	370	9e-33	89	(U22103) gag-protease polyprotein [Glycine max]
2847	GM_76_B2_B08_T7	g3979928	BLASTN	349	1e-08	61	Caenorhabditis elegans cosmid Y18D10A, complete sequence [Caenorhabditis elegans]
2848	GM_76_B2_B09_MR	g3097320	BLASTN	1320	9e-53	83	Glycine max gene for Bd 30K, complete cds
2849	GM_76_B2_C08_MR	g387902	BLASTX	183	2e-13	44	(L23524) ORF [Hordeum vulgare]
2850	GM_76_B2_C08_T7	g4006831	BLASTX	191	7e-13	40	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
2851	GM_76_B2_C12_MR	g2129618	BLASTX	241	2e-18	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2852	GM_76_B2_D06_T7	g3779020	BLASTN	397	7e-11	63	Arabidopsis thaliana chromosome II BAC T4E14 genomic sequence, complete sequence [Arabidopsis thaliana]
2853	GM_76_B2_D11_T7	g3097320	BLASTN	459	9e-14	78	Glycine max gene for Bd 30K, complete cds
2854	GM_76_B2_E05_T7	g3171875	BLASTN	396	7e-11	62	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.1...
2855	GM_76_B2_E06_MR	g3777526	BLASTN	369	1e-09	81	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
2856	GM_76_B2_E08_T7	g507910	BLASTN	371	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2857	GM_76_B2_E09_T7	g100484	BLASTX	329	4e-28	56	hypothetical protein - garden snapdragon
2858	GM_76_B2_E10_T7	g340798	BLASTN	337	3e-09	63	Figure 6. DNA sequence of three 3' apoB VNTR alleles.
2859	GM_76_B2_F02_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2860	GM_76_B2_F02_T7	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2861	GM_76_B2_F07_MR	g4063760	BLASTX	168	2e-10	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2862	GM_76_B2_F09_MR	g2262105	BLASTX	191	3e-13	78	(AC002343) unknown protein [Arabidopsis thaliana]
2863	GM_76_B2_F09_T7	g2065531	BLASTX	447	2e-41	67	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
2864	GM_76_B2_F10_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2865	GM_76_B2_F10_T7	g507910	BLASTN	407	9e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2866	GM_76_B2_G01_MR	g507910	BLASTN	371	4e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
2867	GM_76_B2_G01_T7	g507910	BLASTN	371	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2868	GM_76_B2_G03_MR	g507910	BLASTN	563	8e-19	83	Glycine max BSR-101 satellite SB92 genomic sequence.
2869	GM_76_B2_G04_T7	g3785980	BLASTX	181	2e-15	38	(AC005560) hypothetical protein [Arabidopsis thaliana]
2870	GM_76_B2_G06_MR	g14237	BLASTN	412	1e-12	62	Yeast mitochondrial gene fragment of tRNA synthesis locus (D273-10B)
2871	GM_76_B2_G09_MR	g3643603	BLASTX	260	2e-20	49	(AC005395) unknown protein [Arabidopsis thaliana]
2872	GM_76_B2_H01_T7	g2894496	BLASTN	366	2e-09	60	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-103, complete sequence [Plasmodium falciparum]
2873	GM_76_B2_H05_MR	g4063760	BLASTX	201	6e-14	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2874	GM_76_B2_H08_MR	g3550435	BLASTN	445	4e-13	62	Hordeum vulgare Hotr1 gene
2875	GM_76_B2_H08_T7	g507910	BLASTN	662	3e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
2876	GM_76_B2_H11_MR	g130582	BLASTX	204	3e-14	39	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
2877	GM_77_A1_A03_T7	g507910	BLASTN	607	8e-21	81	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2878	GM_77_A1_A05_MR	g2497540	BLASTX	361	2e-32	64	PYRUVATE KINASE, CHLOROPLAST ISOZYME G
2879	GM_77_A1_A06_T7	g2522228	BLASTX	327	9e-29	52	(AB007466) reverse transcriptase-like protein [Vicia faba]
2880	GM_77_A1_B02_T7	g2979597	BLASTN	382	3e-10	60	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
2881	GM_77_A1_B03_T7	g99730	BLASTX	196	4e-30	53	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
2882	GM_77_A1_B04_T7	g1769898	BLASTX	289	5e-24	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2883	GM_77_A1_B07_MR	g2995405	BLASTX	330	5e-28	48	(Y12432) polyprotein [Ananas comosus]
2884	GM_77_A1_B11_T7	g2961378	BLASTX	177	6e-23	53	(AL022141) putative protein [Arabidopsis thaliana]
2885	GM_77_A1_C07_MR	g1666236	BLASTX	159	2e-10	29	(U76261) unknown [Hordeum vulgare]
2886	GM_77_A1_C09_MR	g4038056	BLASTX	351	3e-30	53	(AC005897) putative transposon [Arabidopsis thaliana]
2887	GM_77_A1_C10_T7	g18559	BLASTN	403	3e-11	71	G.max gene for catalase
2888	GM_77_A1_D01_MR	g2129618	BLASTX	127	2e-12	52	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2889	GM_77_A1_D03_MR	g3599418	BLASTN	1007	1e-38	83	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
2890	GM_77_A1_D05_MR	g421954	BLASTX	239	4e-31	48	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
2891	GM_77_A1_D05_T7	g3319351	BLASTX	277	5e-22	40	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
2892	GM_77_A1_D07_MR	g2829887	BLASTX	351	2e-30	50	(AC002396) Hypothetical protein [Arabidopsis thaliana]
2893	GM_77_A1_D07_T7	g2760319	BLASTX	85	2e-10	76	(AC002130) F1N21.3 [Arabidopsis thaliana]
2894	GM_77_A1_D09_MR	g4063756	BLASTN	361	3e-09	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
2895	GM_77_A1_E02_MR	g2969943	BLASTN	377	5e-10	64	Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS
2896	GM_77_A1_E06_T7	g4063760	BLASTX	231	4e-17	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2897	GM_77_A1_E09_MR	g3319345	BLASTX	151	9e-09	29	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
2898	GM_77_A1_E10_T7	g4092471	BLASTN	536	4e-17	70	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
2899	GM_77_A1_F01_T7	g507910	BLASTN	404	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2900	GM_77_A1_F06_MR	g2764526	BLASTN	450	3e-13	62	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
2901	GM_77_A1_F10_MR	g1142701	BLASTN	235	1e-09	78	Glycine max satellite STR120-A.3.
2902	GM_77_A1_F11_MR	g507910	BLASTN	420	2e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2903	GM_77_A1_F12_T7	g3097320	BLASTN	438	9e-13	69	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2904	GM_77_A1_G02_MR	g170029	BLASTN	418	7e-12	82	Glycine max cv. Dare nodulin 26 gene fragment.
2905	GM_77_A1_G03_T7	g4049647	BLASTN	270	3e-09	64	Melanoplus sanguinipes entomopoxvirus, complete genome
2906	GM_77_A1_G04_T7	g3985949	BLASTN	412	1e-11	69	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]
2907	GM_77_A1_G05_T7	g1666236	BLASTX	234	6e-19	32	(U76261) unknown [Hordeum vulgare]
2908	GM_77_A1_G06_MR	g3142328	BLASTN	1110	2e-43	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2909	GM_77_A1_G08_MR	g3869075	BLASTN	405	3e-11	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]
2910	GM_77_A1_G09_MR	g3097320	BLASTN	422	4e-12	71	Glycine max gene for Bd 30K, complete cds
2911	GM_77_A1_G10_MR	g3063691	BLASTX	273	3e-22	56	(AL022537) putative protein [Arabidopsis thaliana]
2912	GM_77_A1_G11_MR	g3513745	BLASTX	169	2e-10	27	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
2913	GM_77_A1_H02_MR	g226407	BLASTX	250	4e-19	43	retrotransposon del1-46 [Lilium henryi]
2914	GM_77_A1_H04_T7	g13583	BLASTN	353	4e-09	64	Yeast mitochondrial ori(o) repeat unit of petite mutant 5 (petite strain s-10/7/2)
2915	GM_77_A1_H05_MR	g3142328	BLASTN	1232	6e-49	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2916	GM_77_A1_H06_MR	g3599418	BLASTN	377	5e-10	66	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
2917	GM_77_A1_H07_MR	g4063760	BLASTX	153	7e-09	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2918	GM_77_A1_H08_MR	g18559	BLASTN	337	8e-11	76	G.max gene for catalase
2919	GM_77_A1_H09_T7	g3881505	BLASTX	231	5e-18	43	(Z47357) similar to the mouse hypothetical protein D15Kz1 (PIR accession number A30222); cDNA EST EMBL:C08599 comes from this gene; cDNA EST EMBL:C07385 comes from this gene; cDNA EST EMBL:C08733 comes from this gene; cDNA E...
2920	GM_77_A1_H10_MR	g507910	BLASTN	352	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2921	GM_77_A1_H10_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
2922	GM_77_A1_H11_MR	g4038030	BLASTX	429	6e-39	73	(AC005936) putative protein kinase, 5' partial [Arabidopsis thaliana]
2923	GM_77_A2_A02_MR	g454847	BLASTN	435	1e-12	74	Glycine max ribosomal protein S11 gene, complete cds
2924	GM_77_A2_A03_T7	g975634	BLASTN	345	5e-09	65	Dictyostelium discoidium DDCOF1 gene for cofilin, complete cds (exon1-2)
2925	GM_77_A2_A09_MR	g3645899	BLASTX	339	2e-33	61	(U68408) 5' end not determined experimentally [Zea mays]
2926	GM_77_A2_B04_T7	g507910	BLASTN	455	6e-14	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2927	GM_77_A2_B09_T7	g3097320	BLASTN	693	2e-24	75	Glycine max gene for Bd 30K, complete cds
2928	GM_77_A2_C01_T7	g2522227	BLASTX	216	5e-17	38	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
2929	GM_77_A2_C05_MR	g2579860	BLASTN	342	3e-09	60	Homo sapiens genomic DNA, 21q region, clone: S39BG29

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2930	GM_77_A2_D01_MR	g1262440	BLASTX	230	1e-34	79	(U26457) lipoxygenase [Glycine max]
2931	GM_77_A2_D02_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
2932	GM_77_A2_D05_MR	g3777527	BLASTX	269	5e-21	91	(AF053008) gag-pol polyprotein [Glycine max]
2933	GM_77_A2_D07_MR	g2809249	BLASTX	170	5e-11	33	(AC002560) F21B7.18 [Arabidopsis thaliana]
2934	GM_77_A2_D10_MR	g4038056	BLASTX	316	2e-26	42	(AC005897) putative transposon [Arabidopsis thaliana]
2935	GM_77_A2_E01_MR	g3930515	BLASTX	116	3e-10	36	(AF059674) putative gag protein [Nicotiana tabacum]
2936	GM_77_A2_E02_T7	g507910	BLASTN	524	5e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
2937	GM_77_A2_E05_MR	g3281868	BLASTX	148	2e-10	81	(AL031004) putative protein [Arabidopsis thaliana]
2938	GM_77_A2_E08_MR	g320565	BLASTX	151	9e-14	48	transposon TA1-1 KAS-1 - Arabidopsis thaliana (fragment)
2939	GM_77_A2_F08_MR	g905361	BLASTX	160	6e-10	31	(U22103) gag-protease polyprotein [Glycine max]
2940	GM_77_A2_G02_MR	g507910	BLASTN	380	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2941	GM_77_A2_G02_T7	g507910	BLASTN	506	3e-16	79	Glycine max BSR-101 satellite SB92 genomic sequence.
2942	GM_77_A2_G03_T7	g454847	BLASTN	497	2e-15	66	Glycine max ribosomal protein S11 gene, complete cds
2943	GM_77_A2_G04_T7	g2129618	BLASTX	174	3e-11	30	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
2944	GM_77_A2_G05_MR	g18559	BLASTN	837	6e-31	74	G.max gene for catalase
2945	GM_77_A2_G05_T7	g3171875	BLASTN	353	7e-09	60	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.1...
2946	GM_77_A2_G06_MR	g1666236	BLASTX	197	1e-14	32	(U76261) unknown [Hordeum vulgare]
2947	GM_77_A2_G09_MR	g342954	BLASTN	362	4e-10	62	paramecium species 4.51b mt dna dimer: replication init. region, clone-1.
2948	GM_77_A2_G10_MR	g3738114	BLASTN	468	4e-14	62	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
2949	GM_77_A2_H01_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
2950	GM_77_A2_H03_T7	g3097320	BLASTN	1064	4e-41	79	Glycine max gene for Bd 30K, complete cds
2951	GM_77_A2_H05_MR	g3513747	BLASTX	183	7e-12	32	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
2952	GM_77_A2_H06_MR	g507910	BLASTN	436	4e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
2953	GM_77_A2_H06_T7	g3777527	BLASTX	238	8e-18	70	(AF053008) gag-pol polyprotein [Glycine max]
2954	GM_77_A2_H09_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2955	GM_77_A2_H09_T7	g507910	BLASTN	469	1e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
2956	GM_77_B1_A05_MR	g507910	BLASTN	367	6e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
2957	GM_77_B1_A05_T7	g507910	BLASTN	348	4e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
2958	GM_77_B1_A11_T7	g3377855	BLASTX	181	4e-26	73	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2959	GM_77_B1_B07_MR	g905361	BLASTX	235	5e-18	35	(U22103) gag-protease polyprotein [Glycine max]
2960	GM_77_B1_B10_T7	g4063760	BLASTX	374	2e-34	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
2961	GM_77_B1_C03_MR	g2995405	BLASTX	186	3e-22	51	(Y12432) polyprotein [Ananas comosus]
2962	GM_77_B1_C08_MR	g1055224	BLASTX	140	6e-09	39	(U20977) cellular nucleic acid binding protein [Xenopus laevis]
2963	GM_77_B1_C10_MR	g2996647	BLASTN	356	5e-09	61	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
2964	GM_77_B1_D01_T7	g170606	BLASTN	885	8e-34	68	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
2965	GM_77_B1_D03_T7	g18559	BLASTN	1460	3e-59	87	G.max gene for catalase
2966	GM_77_B1_D11_MR	g1666236	BLASTX	163	7e-11	30	(U76261) unknown [Hordeum vulgare]
2967	GM_77_B1_E02_T7	g1666236	BLASTX	172	7e-12	31	(U76261) unknown [Hordeum vulgare]
2968	GM_77_B1_E03_MR	g1666236	BLASTX	167	2e-14	35	(U76261) unknown [Hordeum vulgare]
2969	GM_77_B1_E11_MR	g3738114	BLASTN	361	3e-09	60	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
2970	GM_77_B1_F01_MR	g2580584	BLASTX	224	1e-17	47	(AF000976) 7-O-methyltransferase [Medicago sativa]
2971	GM_77_B1_F02_T7	g1769898	BLASTX	189	2e-18	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2972	GM_77_B1_F03_T7	g3779021	BLASTX	98	6e-09	36	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]
2973	GM_77_B1_F05_MR	g3777527	BLASTX	516	6e-69	95	(AF053008) gag-pol polyprotein [Glycine max]
2974	GM_77_B1_F09_MR	g461735	BLASTX	146	1e-18	96	MITOCHONDRIAL CHAPERONIN HSP60-1 PRECURSOR gi 478785 pir S29315 chaperonin 60 - cucurbit gi 12544 gnl PID e1188585 (X70867) chaperonin 60 [Cucurbita sp.]
2975	GM_77_B1_F09_T7	g3738337	BLASTX	101	5e-09	33	(AC005170) putative reverse transcriptase [Arabidopsis thaliana]
2976	GM_77_B1_F12_T7	g3777527	BLASTX	385	2e-33	87	(AF053008) gag-pol polyprotein [Glycine max]
2977	GM_77_B1_G04_MR	g3560029	BLASTN	434	9e-13	65	Schistosoma intercalatum ribosomal intergenic spacer DNA (2169 bp)
2978	GM_77_B1_G11_T7	g507910	BLASTN	364	8e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2979	GM_77_B1_G12_MR	g3777527	BLASTX	718	6e-69	91	(AF053008) gag-pol polyprotein [Glycine max]
2980	GM_77_B1_G12_T7	g2996647	BLASTN	379	4e-10	61	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
2981	GM_77_B1_H01_T7	g18559	BLASTN	710	4e-25	73	G.max gene for catalase
2982	GM_77_B1_H09_T7	g2522226	BLASTN	599	3e-20	67	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
2983	GM_77_B2_A03_T7	g2511590	BLASTX	268	2e-22	86	(Y13692) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana] gi 3421111 (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis thaliana]
2984	GM_77_B2_A07_MR	g2522227	BLASTX	175	2e-12	52	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
2985	GM_77_B2_A10_T7	g3142328	BLASTN	598	2e-43	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
2986	GM_77_B2_B05_T7	g3176806	BLASTN	347	1e-09	61	Homo sapiens allele 17 fragile site locus (FRA10B) minisatellite, 5' sequence
2987	GM_77_B2_B09_T7	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2988	GM_77_B2_B10_MR	g100484	BLASTX	212	2e-15	49	hypothetical protein - garden snapdragon
2989	GM_77_B2_B11_T7	g3142328	BLASTN	628	2e-21	69	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
2990	GM_77_B2_C03_T7	g349379	BLASTX	186	1e-13	56	(L22847) HAHB-1 [Helianthus annuus]
2991	GM_77_B2_C04_T7	g161752	BLASTX	153	1e-08	28	(L03710) cnjB [Tetrahymena thermophila] gi 737494 prf 1922371A cnjB gene [Tetrahymena thermophila]
2992	GM_77_B2_D01_T7	g507910	BLASTN	356	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
2993	GM_77_B2_D05_T7	g507910	BLASTN	584	9e-20	80	Glycine max BSR-101 satellite SB92 genomic sequence.
2994	GM_77_B2_D10_T7	g1769897	BLASTX	442	2e-48	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
2995	GM_77_B2_E06_T7	g3097320	BLASTN	360	3e-09	64	Glycine max gene for Bd 30K, complete cds
2996	GM_77_B2_E12_MR	g507910	BLASTN	428	1e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2997	GM_77_B2_E12_T7	g507910	BLASTN	411	6e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
2998	GM_77_B2_F01_T7	g3810596	BLASTX	271	1e-21	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
2999	GM_77_B2_F02_T7	g3947433	BLASTN	354	6e-09	60	Homo sapiens BAC clone RG060P12 from 7q21, complete sequence [Homo sapiens]
3000	GM_77_B2_F06_MR	g2316016	BLASTX	159	2e-09	47	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
3001	GM_77_B2_F11_T7	g2522230	BLASTX	289	1e-24	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
3002	GM_77_B2_F12_MR	g1813979	BLASTX	145	2e-09	70	(Y10860) hypothetical protein [Musa acuminata]
3003	GM_77_B2_G09_T7	g507910	BLASTN	378	2e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3004	GM_77_B2_G12_T7	g1524103	BLASTN	392	1e-10	63	Human DNA sequence from cosmid U223G7, between markers DXS6791 and DXS8038 on chromosome X
3005	GM_77_B2_H02_T7	g3080423	BLASTX	384	1e-33	53	(AL022604) putative protein [Arabidopsis thaliana]
3006	GM_77_B2_H08_T7	g2367675	BLASTX	202	3e-14	33	(AF017040) Pol [Dictyostelium discoideum]
3007	GM_77_B2_H12_T7	g2764526	BLASTN	566	1e-18	62	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
3008	GM_78_A1_A02_MR	g2367675	BLASTX	171	7e-11	35	(AF017040) Pol [Dictyostelium discoideum]
3009	GM_78_A1_A02_T7	g507910	BLASTN	384	9e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3010	GM_78_A1_A03_MR	g2443320	BLASTX	173	8e-12	46	(D85597) polyprotein [Oryza australiensis]
3011	GM_78_A1_A05_MR	g2997694	BLASTX	199	3e-15	42	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
3012	GM_78_A1_A08_MR	g507910	BLASTN	346	5e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
3013	GM_78_A1_A09_T7	g1514643	BLASTX	134	2e-10	50	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
3014	GM_78_A1_B01_MR	g100484	BLASTX	338	5e-29	62	hypothetical protein - garden snapdragon
3015	GM_78_A1_B02_T7	g226407	BLASTX	538	8e-50	62	retrotransposon del1-46 [Lilium henryi]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
3016	GM_78_A1_B09_T7	g3930515	BLASTX	126	1e-10	45	(AF059674) putative gag protein [Nicotiana tabacum]
3017	GM_78_A1_C02_MR	g3142328	BLASTN	1166	7e-46	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3018	GM_78_A1_C06_MR	g170602	BLASTN	453	2e-14	64	Broad bean (V.faba) BamHI repetitive element, 900 bp family.
3019	GM_78_A1_E01_T7	g507910	BLASTN	358	1e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3020	GM_78_A1_E02_T7	g1666236	BLASTX	170	1e-11	29	(U76261) unknown [Hordeum vulgare]
3021	GM_78_A1_F01_MR	g1769899	BLASTX	203	1e-15	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3022	GM_78_A1_G07_MR	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3023	GM_78_A1_H01_MR	g1431738	BLASTN	466	3e-14	90	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
3024	GM_78_A1_H12_MR	g2997694	BLASTX	166	1e-11	34	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
3025	GM_78_A2_A02_MR	g1076763	BLASTX	157	1e-11	38	AWJL218 protein - wheat gi 551212 (X81369) AWJL218 gene product [Triticum aestivum]
3026	GM_78_A2_A02_T7	g3033389	BLASTX	180	7e-12	32	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
3027	GM_78_A2_A03_MR	g507910	BLASTN	595	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3028	GM_78_A2_A06_MR	g1142703	BLASTN	261	5e-13	75	Glycine max satellite STR120-B.1.
3029	GM_78_A2_A06_T7	g2995405	BLASTX	253	1e-19	52	(Y12432) polyprotein [Ananas comosus]
3030	GM_78_A2_A08_MR	g3097320	BLASTN	690	3e-24	75	Glycine max gene for Bd 30K, complete cds
3031	GM_78_A2_A09_MR	g4063760	BLASTX	353	3e-30	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3032	GM_78_A2_A10_MR	g1666236	BLASTX	189	9e-14	30	(U76261) unknown [Hordeum vulgare]
3033	GM_78_A2_A10_T7	g905361	BLASTX	546	6e-52	86	(U22103) gag-protease polyprotein [Glycine max]
3034	GM_78_A2_B02_MR	g18559	BLASTN	981	2e-37	77	G.max gene for catalase
3035	GM_78_A2_B05_MR	g3452140	BLASTX	143	3e-09	36	(AJ004901) resistance protein [Glycine max]
3036	GM_78_A2_B05_T7	g742339	BLASTX	137	2e-20	58	S receptor kinase [Brassica oleracea]
3037	GM_78_A2_B07_T7	g3820757	BLASTN	344	1e-08	61	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
3038	GM_78_A2_B08_MR	g4115922	BLASTX	155	4e-09	40	(AF118222) contains similarity to ubiquitin carboxyl-terminal hydrolase family 2 (Pfam:PF00443, score=48.3, E=3.5e-13, N=2) and (Pfam:PF00442, Score=40.0 E=5.2e-08, N=1) [Arabidopsis thaliana]
3039	GM_78_A2_B10_MR	g3097320	BLASTN	454	2e-13	69	Glycine max gene for Bd 30K, complete cds
3040	GM_78_A2_B11_T7	g1171642	BLASTX	182	1e-14	80	PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK gi 481206 pir S38326 protein kinase - Arabidopsis thaliana gi 166809 (L07248) protein kinase [Arabidopsis thaliana]
3041	GM_78_A2_B12_MR	g340697	BLASTN	401	2e-11	79	Soybean chloroplast 16S/23S ribosomal intergenic spacer DNA.
3042	GM_78_A2_C01_MR	g507910	BLASTN	389	6e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
3043	GM_78_A2_C03_MR	g2129618	BLASTX	183	3e-12	37	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3044	GM_78_A2_C08_MR	g2129618	BLASTX	157	2e-09	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3045	GM_78_A2_D02_MR	g4090200	BLASTX	173	3e-12	74	(AJ012310) WUSCHEL protein [Arabidopsis thaliana]
3046	GM_78_A2_D03_T7	g3540186	BLASTX	113	3e-13	72	(AC004122) Hypothetical protein [Arabidopsis thaliana]
3047	GM_78_A2_D06_MR	g507910	BLASTN	541	8e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3048	GM_78_A2_D11_T7	g2264320	BLASTN	356	5e-09	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
3049	GM_78_A2_E06_T7	g18559	BLASTN	349	9e-09	72	G.max gene for catalase
3050	GM_78_A2_E07_MR	g3142328	BLASTN	1996	7e-84	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3051	GM_78_A2_E07_T7	g2129618	BLASTX	182	4e-12	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3052	GM_78_A2_E10_MR	g1142702	BLASTN	265	1e-12	73	Glycine max satellite STR120-A.4.
3053	GM_78_A2_F02_T7	g507910	BLASTN	668	1e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
3054	GM_78_A2_F03_T7	g3777527	BLASTX	239	3e-20	44	(AF053008) gag-pol polyprotein [Glycine max]
3055	GM_78_A2_F09_MR	g4038056	BLASTX	339	6e-29	51	(AC005897) putative transposon [Arabidopsis thaliana]
3056	GM_78_A2_F10_MR	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
3057	GM_78_A2_F10_T7	g507910	BLASTN	458	4e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
3058	GM_78_A2_G01_MR	g4039114	BLASTN	654	1e-22	67	Glycine max alcohol-dehydrogenase (Adh-2) gene, partial cds
3059	GM_78_A2_G02_MR	g4063760	BLASTX	430	2e-38	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3060	GM_78_A2_G08_MR	g3377834	BLASTX	210	3e-15	36	(AF075598) No definition line found [Arabidopsis thaliana]
3061	GM_78_A2_H05_MR	g871468	BLASTN	357	3e-09	89	H.annuus mitochondrion genes trnH and trnE
3062	GM_78_A2_H08_T7	g2129618	BLASTX	225	1e-16	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3063	GM_78_A2_H09_T7	g133750	BLASTX	196	3e-28	81	CHLOROPLAST 30S RIBOSOMAL PROTEIN S12 gi 320170 pir A26574 ribosomal protein S12 - soybean chloroplast gi 11572 (X05013) rps12 [Glycine max]
3064	GM_78_A2_H11_MR	g4063770	BLASTX	169	8e-11	44	(AB004906) transposase [Ipomoea purpurea]
3065	GM_78_A2_H12_T7	g4063760	BLASTX	172	6e-11	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3066	GM_78_B1_A07_T7	g507910	BLASTN	342	7e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3067	GM_78_B1_B09_T7	g2522228	BLASTX	395	2e-38	73	(AB007466) reverse transcriptase-like protein [Vicia faba]
3068	GM_78_B1_C05_MR	g3319345	BLASTX	170	8e-11	36	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
3069	GM_78_B1_C05_T7	g3645899	BLASTX	351	4e-30	54	(U68408) 5' end not determined experimentally [Zea mays]
3070	GM_78_B1_C08_T7	g2462058	BLASTX	349	4e-31	49	(Y13389) reverse transcriptase [Antirrhinum majus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
3071	GM_78_B1_C09_MR	g557882	BLASTX	153	4e-14	40	(U13923) putative serine/threonine protein kinase; similar to product encoded by Lycopersicon pimpinellifolium Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family [Solanum pimpinellifolium] gi 1809263 (U59317) serine/threonine protein kinase Fen [Lycopersicon pimpinellifolium] gi 1096880 prf 2112354B Fen gene [Lycopersicon esculentum] gi 1098334 prf 2115395A Fen gene [Lycopersicon esculentum]
3072	GM_78_B1_D02_T7	g2827715	BLASTX	300	1e-24	77	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
3073	GM_78_B1_D04_T7	g2052381	BLASTX	197	2e-30	81	(U66344) calreticulin [Arabidopsis thaliana]
3074	GM_78_B1_D06_MR	g1142699	BLASTN	300	4e-15	71	Glycine max satellite STR120-A.1.
3075	GM_78_B1_D10_T7	g2522230	BLASTX	240	1e-19	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
3076	GM_78_B1_E09_MR	g4063760	BLASTX	211	5e-15	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3077	GM_78_B1_E10_T7	g3355308	BLASTX	179	6e-12	40	(AJ009695) wall-associated kinase 4 [Arabidopsis thaliana]
3078	GM_78_B1_F05_MR	g3599418	BLASTN	464	5e-14	69	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
3079	GM_78_B1_F07_T7	g3319362	BLASTX	321	6e-27	42	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
3080	GM_78_B1_G04_T7	g2522228	BLASTX	236	2e-26	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
3081	GM_78_B1_G05_MR	g3142328	BLASTN	1636	2e-67	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3082	GM_78_B1_H01_MR	g1931654	BLASTX	123	1e-09	50	(U95973) BRCA1-associated RING domain protein isolog [Arabidopsis thaliana]
3083	GM_78_B1_H02_MR	g417154	BLASTX	171	4e-11	80	HEAT SHOCK PROTEIN 82 gi 100685 pir S25541 heat shock protein 82 - rice (strain Taichung Native One) gi 20256 (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]
3084	GM_78_B1_H07_MR	g3777527	BLASTX	420	4e-37	50	(AF053008) gag-pol polyprotein [Glycine max]
3085	GM_78_B1_H08_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3086	GM_78_B1_H08_T7	g507910	BLASTN	355	2e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3087	GM_78_B1_H09_T7	g4038056	BLASTX	263	5e-23	48	(AC005897) putative transposon [Arabidopsis thaliana]
3088	GM_78_B1_H11_MR	g905361	BLASTX	240	1e-18	33	(U22103) gag-protease polyprotein [Glycine max]
3089	GM_78_B1_H11_T7	g4063760	BLASTX	179	1e-11	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3090	GM_78_B1_H12_T7	g507910	BLASTN	360	1e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3091	GM_78_B2_A03_T7	g18559	BLASTN	1112	2e-43	79	G.max gene for catalase
3092	GM_78_B2_A04_MR	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3093	GM_78_B2_A09_MR	g4092471	BLASTN	528	8e-17	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
3094	GM_78_B2_A10_MR	g3777527	BLASTX	352	7e-30	75	(AF053008) gag-pol polyprotein [Glycine max]
3095	GM_78_B2_A12_T7	g421955	BLASTX	435	3e-40	50	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
3096	GM_78_B2_B02_MR	g1326016	BLASTX	190	7e-13	40	TY3-2 orfB
3097	GM_78_B2_B09_T7	g507910	BLASTN	446	1e-13	78	Glycine max BSR-101 satellite SB92 genomic sequence.
3098	GM_78_B2_C02_MR	g3097320	BLASTN	568	1e-18	80	Glycine max gene for Bd 30K, complete cds
3099	GM_78_B2_D10_MR	g132819	BLASTX	153	1e-20	72	50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR (CL24) gi 71307 pir R5PM24 ribosomal protein L24 precursor, chloroplast - garden pea gi 20873 (X14020) CL24 ribosomal preprotein (AA -39 to 155) [Pisum sativum]
3100	GM_78_B2_D11_T7	g3282159	BLASTN	470	3e-14	60	Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence [Homo sapiens]
3101	GM_78_B2_E07_MR	g3142328	BLASTN	528	6e-17	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3102	GM_78_B2_F05_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3103	GM_78_B2_F05_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3104	GM_78_B2_F10_MR	g905361	BLASTX	418	4e-38	92	(U22103) gag-protease polyprotein [Glycine max]
3105	GM_78_B2_F11_MR	g3142328	BLASTN	628	2e-21	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3106	GM_78_B2_F11_T7	g1142701	BLASTN	256	1e-19	74	Glycine max satellite STR120-A.3.
3107	GM_78_B2_G03_T7	g1769898	BLASTX	334	2e-30	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3108	GM_78_B2_G04_MR	g2462058	BLASTX	251	1e-20	57	(Y13389) reverse transcriptase [Antirrhinum majus]
3109	GM_78_B2_G07_MR	g18559	BLASTN	355	5e-09	69	G.max gene for catalase
3110	GM_78_B2_G07_T7	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3111	GM_78_B2_G10_T7	g2801677	BLASTN	947	1e-36	73	Glycine max telomere-associated sequence STAS6
3112	GM_78_B2_G11_MR	g507910	BLASTN	385	9e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3113	GM_78_B2_H02_T7	g3776574	BLASTX	231	8e-18	72	(AC005388) Similar to T11J7.13 gi 2880051 putative protein kinase from Arabidopsis thaliana BAC gb AC002340. [Arabidopsis thaliana]
3114	GM_78_B2_H03_T7	g99922	BLASTX	903	9e-90	78	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
3115	GM_78_B2_H04_MR	g507910	BLASTN	377	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3116	GM_78_B2_H06_T7	g2315153	BLASTX	229	7e-31	72	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
3117	GM_78_B2_H08_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3118	GM_78_B2_H08_T7	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
3119	GM_78_B2_H09_T7	g3171875	BLASTN	397	7e-11	65	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.1...
3120	GM_79_A2_A02_MR	g12212	BLASTN	1277	4e-52	93	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
3121	GM_79_A2_A02_T7	g1346258	BLASTX	301	5e-26	80	POTENTIAL HEME-BINDING PROTEIN PRECURSOR (ORF 229) gi 984314 (U26948) unknown [Glycine max]
3122	GM_79_A2_A04_MR	g2708524	BLASTX	211	2e-16	37	(AF038649) similar to resistance gene; region between conserved kinase-2 and P-Loop domains [Pinus radiata]
3123	GM_79_A2_A04_T7	g4063760	BLASTX	501	5e-46	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3124	GM_79_A2_A07_MR	g507910	BLASTN	562	9e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
3125	GM_79_A2_A08_MR	g4063760	BLASTX	238	6e-18	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3126	GM_79_A2_B02_MR	g2852684	BLASTX	244	7e-19	48	(AF017751) resistance protein candidate [Lactuca sativa]
3127	GM_79_A2_B04_T7	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
3128	GM_79_A2_B05_T7	g3142328	BLASTN	1627	6e-67	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3129	GM_79_A2_B06_MR	g2769655	BLASTN	554	5e-18	63	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
3130	GM_79_A2_B08_MR	g4092470	BLASTN	561	3e-18	62	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
3131	GM_79_A2_B10_T7	g3142328	BLASTN	528	6e-17	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3132	GM_79_A2_C03_MR	g2244802	BLASTX	410	4e-36	53	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
3133	GM_79_A2_C06_T7	g4063760	BLASTX	250	3e-19	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3134	GM_79_A2_C09_T7	g1524103	BLASTN	328	3e-09	61	Human DNA sequence from cosmid U223G7, between markers DXS6791 and DXS8038 on chromosome X
3135	GM_79_A2_C10_T7	g4063770	BLASTX	362	2e-31	49	(AB004906) transposase [Ipomoea purpurea]
3136	GM_79_A2_C12_MR	g4063760	BLASTX	241	3e-18	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3137	GM_79_A2_D03_MR	g2522227	BLASTX	146	4e-09	39	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
3138	GM_79_A2_D05_T7	g462013	BLASTX	100	7e-09	80	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) gi 542022 pir S39558 HSP90 homolog - Madagascar periwinkle gi 348696 (L14594) heat shock protein 90 [Catharanthus roseus]
3139	GM_79_A2_D10_T7	g507910	BLASTN	582	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
3140	GM_79_A2_E03_T7	g4063760	BLASTX	400	3e-35	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3141	GM_79_A2_E07_MR	g2864621	BLASTX	121	1e-10	42	hypothetical protein [Arabidopsis thaliana]
3142	GM_79_A2_E08_T7	g2407790	BLASTX	192	2e-13	39	(AF019910) grr1 [Glycine max]
3143	GM_79_A2_E10_MR	g2828773	BLASTN	352	7e-09	63	Homo sapiens chromosome 17, clone hRPC.18_F_17, complete sequence [Homo sapiens]
3144	GM_79_A2_F09_MR	g2129618	BLASTX	192	4e-13	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3145	GM_79_A2_F09_T7	g3319362	BLASTX	268	3e-22	52	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
3146	GM_79_A2_F10_T7	g1769898	BLASTX	135	7e-12	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3147	GM_79_A2_F11_MR	g507910	BLASTN	529	3e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
3148	GM_79_A2_G07_MR	g2289010	BLASTX	171	3e-12	82	(AC002335) FKBP type peptidyl-prolyl cis-trans isomerase isolog [Arabidopsis thaliana]
3149	GM_79_A2_G11_MR	g3779026	BLASTX	352	5e-30	51	(AC005171) putative retrotransposon [Arabidopsis thaliana]
3150	GM_79_A2_H01_MR	g18559	BLASTN	296	5e-09	76	G.max gene for catalase
3151	GM_79_A2_H03_MR	g905361	BLASTX	749	2e-73	92	(U22103) gag-protease polyprotein [Glycine max]
3152	GM_79_B2_A03_T7	g2642431	BLASTX	157	4e-19	56	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
3153	GM_79_B2_A04_T7	g3777527	BLASTX	219	3e-35	54	(AF053008) gag-pol polyprotein [Glycine max]
3154	GM_79_B2_A06_T7	g3219627	BLASTN	347	2e-09	64	Sesarma windsor 16S rRNA gene, isolate PC1
3155	GM_79_B2_A08_MR	g342964	BLASTN	419	7e-13	63	paramecium species 5,311 mt dna dimer: replication init. region.
3156	GM_79_B2_A11_T7	g3142328	BLASTN	1868	6e-78	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3157	GM_79_B2_B03_T7	g2618603	BLASTN	716	3e-25	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]
3158	GM_79_B2_B10_T7	g3281850	BLASTX	276	1e-22	94	(AL031004) monogalactosyldiacylglycerol synthase - like protein [Arabidopsis thaliana]
3159	GM_79_B2_B11_T7	g18559	BLASTN	417	7e-12	65	G.max gene for catalase
3160	GM_79_B2_C02_MR	g4063760	BLASTX	224	2e-16	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3161	GM_79_B2_C09_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3162	GM_79_B2_C09_T7	g507910	BLASTN	454	7e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3163	GM_79_B2_C11_T7	g3152618	BLASTX	236	2e-18	77	(AC004482) putative pectinesterase [Arabidopsis thaliana] gi 3242724 (AC003040) putative pectinesterase [Arabidopsis thaliana]
3164	GM_79_B2_D01_T7	g18559	BLASTN	518	2e-16	68	G.max gene for catalase
3165	GM_79_B2_D02_MR	g507910	BLASTN	374	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3166	GM_79_B2_D02_T7	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3167	GM_79_B2_D03_MR	g3142328	BLASTN	1178	2e-46	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
3168	GM_79_B2_E02_MR	g99730	BLASTX	287	5e-24	48	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
3169	GM_79_B2_E03_T7	g3645899	BLASTX	239	9e-21	45	(U68408) 5' end not determined experimentally [Zea mays]
3170	GM_79_B2_E06_T7	g4063760	BLASTX	295	5e-24	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3171	GM_79_B2_E09_T7	g4063760	BLASTX	163	6e-10	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3172	GM_79_B2_E11_MR	g3176806	BLASTN	361	4e-10	62	Homo sapiens allele 17 fragile site locus (FRA10B) minisatellite, 5' sequence
3173	GM_79_B2_E11_T7	g2104945	BLASTN	394	8e-13	70	Glycine max copia-like retrotransposon Tgmr, complete sequence
3174	GM_79_B2_F06_MR	g3097320	BLASTN	1167	8e-46	83	Glycine max gene for Bd 30K, complete cds
3175	GM_79_B2_F11_T7	g22490	BLASTX	187	6e-14	49	(X01380) ORF1 [Zea mays]
3176	GM_79_B2_G04_MR	g4063756	BLASTN	399	6e-11	68	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3177	GM_79_B2_G04_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3178	GM_79_B2_G05_MR	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
3179	GM_79_B2_G06_MR	g2435510	BLASTN	451	2e-13	71	Arabidopsis thaliana BAC TM017A05
3180	GM_79_B2_G06_T7	g2244839	BLASTX	215	9e-16	37	(Z97337) hypothetical protein [Arabidopsis thaliana]
3181	GM_79_B2_G08_MR	g226407	BLASTX	158	3e-09	28	retrotransposon del1-46 [Lilium henryi]
3182	GM_79_B2_G12_MR	g2511590	BLASTX	286	2e-24	88	(Y13692) multicatalytic endopeptidase complex, proteasome component, beta subunit [Arabidopsis thaliana] gi 3421111 (AF043534) 20S proteasome beta subunit PBD1 [Arabidopsis thaliana]
3183	GM_79_B2_H01_MR	g18559	BLASTN	487	5e-15	75	G.max gene for catalase
3184	GM_79_B2_H03_T7	g507910	BLASTN	437	4e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
3185	GM_79_B2_H04_MR	g4063760	BLASTX	233	5e-19	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3186	GM_79_B2_H08_MR	g2522230	BLASTX	287	2e-24	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
3187	GM_79_B2_H08_T7	g1666236	BLASTX	213	1e-16	28	(U76261) unknown [Hordeum vulgare]
3188	GM_79_B2_H11_MR	g3097320	BLASTN	485	6e-15	71	Glycine max gene for Bd 30K, complete cds
3189	GM_80_A1_A02_T7	g4063760	BLASTX	194	3e-13	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3190	GM_80_A1_A04_T7	g507910	BLASTN	370	4e-10	77	Glycine max BSR-101 satellite SB92 genomic sequence.
3191	GM_80_A1_A10_T7	g3746069	BLASTX	127	4e-12	32	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
3192	GM_80_A1_A11_MR	g729092	BLASTX	491	4e-46	78	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK) gi 477484 pir A49082 calcium-dependent protein kinase isoform AK1 - Arabidopsis thaliana gi 304105 (L14771) calcium-dependent protein kinase [Arabidopsis thaliana]
3193	GM_80_A1_B04_T7	g3860246	BLASTX	170	9e-12	52	(AC005824) putative reverse-transcriptase protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
3194	GM_80_A1_B05_T7	g2995405	BLASTX	223	2e-16	45	(Y12432) polyprotein [Ananas comosus]
3195	GM_80_A1_B06_MR	g3513747	BLASTX	190	1e-12	46	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
3196	GM_80_A1_B07_MR	g18559	BLASTN	767	9e-28	78	G.max gene for catalase
3197	GM_80_A1_B07_T7	g507910	BLASTN	418	3e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
3198	GM_80_A1_B10_MR	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3199	GM_80_A1_B10_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3200	GM_80_A1_B11_MR	g729092	BLASTX	523	2e-49	79	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK) gi 477484 pir A49082 calcium-dependent protein kinase isoform AK1 - Arabidopsis thaliana gi 304105 (L14771) calcium-dependent protein kinase [Arabidopsis thaliana]
3201	GM_80_A1_C12_T7	g507910	BLASTN	466	2e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.
3202	GM_80_A1_D01_T7	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3203	GM_80_A1_D02_MR	g99922	BLASTX	387	4e-35	73	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
3204	GM_80_A1_D03_T7	g3142328	BLASTN	1044	2e-40	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3205	GM_80_A1_D04_MR	g3097320	BLASTN	471	3e-14	70	Glycine max gene for Bd 30K, complete cds
3206	GM_80_A1_D04_T7	g100484	BLASTX	169	7e-11	56	hypothetical protein - garden snapdragon
3207	GM_80_A1_D05_T7	g3859610	BLASTN	450	3e-13	68	Arabidopsis thaliana BAC T9E19
3208	GM_80_A1_D07_T7	g18559	BLASTN	363	2e-09	72	G.max gene for catalase
3209	GM_80_A1_D09_T7	g4156188	BLASTN	358	4e-09	59	Homo sapiens clone DJ0784G16, complete sequence [Homo sapiens]
3210	GM_80_A1_E02_MR	g2098816	BLASTN	351	8e-09	72	Arabidopsis thaliana BAC F19G10, complete sequence
3211	GM_80_A1_E10_MR	g3777527	BLASTX	243	3e-38	76	(AF053008) gag-pol polyprotein [Glycine max]
3212	GM_80_A1_F01_MR	g2194136	BLASTX	111	5e-11	30	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
3213	GM_80_A1_F03_MR	g2995405	BLASTX	292	7e-24	46	(Y12432) polyprotein [Ananas comosus]
3214	GM_80_A1_F06_MR	g113515	BLASTX	88	4e-09	53	FLORAL HOMEOTIC PROTEIN AGL5 gi 81613 pir E39534 floral homeotic protein AGL5 - Arabidopsis thaliana gi 166596 (M55553) transcription factor [Arabidopsis thaliana]
3215	GM_80_A1_G02_MR	g507910	BLASTN	401	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3216	GM_80_A1_G06_MR	g4063760	BLASTX	175	3e-11	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3217	GM_80_A1_G07_T7	g3810596	BLASTX	192	4e-13	41	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3218	GM_80_A1_H01_MR	g507910	BLASTN	375	2e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3219	GM_80_A1_H01_T7	g3777527	BLASTX	726	8e-70	95	(AF053008) gag-pol polyprotein [Glycine max]

3220	GM_80_A1_H02_MR	g4115363	BLASTX	210	4e-15	41	(AC005957) putative disease resistance protein [Arabidopsis thaliana]
3221	GM_80_A1_H02_T7	g4115373	BLASTX	193	3e-13	46	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]
3222	GM_80_A1_H03_MR	g3097320	BLASTN	1031	1e-39	79	Glycine max gene for Bd 30K, complete cds
3223	GM_80_A1_H03_T7	g3142328	BLASTN	1208	8e-48	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3224	GM_80_A1_H05_MR	g1769898	BLASTX	164	1e-16	34	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3225	GM_80_A1_H06_MR	g507910	BLASTN	541	8e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
3226	GM_80_A1_H08_MR	g3790154	BLASTN	360	3e-09	62	Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs ...
3227	GM_80_A2_A07_T7	g3097320	BLASTN	404	3e-11	71	Glycine max gene for Bd 30K, complete cds
3228	GM_80_A2_A10_MR	g4063760	BLASTX	284	7e-23	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3229	GM_80_A2_B01_MR	g2529677	BLASTX	100	1e-08	52	(AC002535) kinesin-like protein, heavy chain [Arabidopsis thaliana]
3230	GM_80_A2_B02_T7	g2586081	BLASTX	186	8e-13	45	(U72725) receptor kinase-like protein [Oryza longistaminata]
3231	GM_80_A2_B03_MR	g4006831	BLASTX	308	2e-25	34	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
3232	GM_80_A2_C04_MR	g2997694	BLASTX	279	1e-23	39	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
3233	GM_80_A2_C07_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3234	GM_80_A2_C07_T7	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3235	GM_80_A2_D06_MR	g3142328	BLASTN	2141	1e-90	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3236	GM_80_A2_E01_T7	g3142328	BLASTN	1024	2e-39	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3237	GM_80_A2_E02_MR	g4164556	BLASTN	381	3e-10	60	Rhipicephalus sanguineus mitochondrial DNA, complete genome
3238	GM_80_A2_E03_MR	g3914199	BLASTX	168	5e-12	76	OLEOSIN 1 >gi 460803 (X78118) oleosin [Prunus dulcis]
3239	GM_80_A2_E08_MR	g4063760	BLASTX	211	5e-15	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3240	GM_80_A2_E10_MR	g14227	BLASTN	405	4e-12	65	Yeast cytochrome c oxidase transcription initiation region subunit 1 (COX1) from mitochondrial DNA
3241	GM_80_A2_E10_T7	g1431738	BLASTN	681	5e-24	83	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
3242	GM_80_A2_F02_MR	g2129618	BLASTX	220	4e-16	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3243	GM_80_A2_F05_MR	g2832245	BLASTX	162	3e-11	28	(AF031569) hypothetical protein [Zea mays]
3244	GM_80_A2_F06_MR	g4063760	BLASTX	256	7e-20	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3245	GM_80_A2_F07_MR	g3097320	BLASTN	1069	2e-41	76	Glycine max gene for Bd 30K, complete cds
3246	GM_80_A2_F09_MR	g320565	BLASTX	205	8e-16	46	transposon TA1-1 KAS-1 - Arabidopsis thaliana (fragment)
3247	GM_80_A2_F11_MR	g3928086	BLASTX	281	6e-24	52	(AC005770) unknown protein [Arabidopsis thaliana]

3248	GM_80_A2_G01_T7	g13773	BLASTN	474	2e-15	67	Torulopsis glabrata mitochondrial genes for tRNAs -Tyr, -Asn, -Ala, -Ile -Trp (from Var1-LrRNA intergenic region) >gi 343959 gb M11906 YSLMTIG09 Yeast (T.glabrata) mitochondrial DNA between var1 and L rRNA genes.
3249	GM_80_A2_G03_T7	g2522228	BLASTX	344	6e-37	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
3250	GM_80_A2_G04_T7	g3033375	BLASTX	530	3e-50	74	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]
3251	GM_80_A2_G08_MR	g507910	BLASTN	481	4e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
3252	GM_80_A2_G08_T7	g507910	BLASTN	431	7e-13	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3253	GM_80_A2_H01_MR	g3645899	BLASTX	282	1e-22	43	(U68408) 5' end not determined experimentally [Zea mays]
3254	GM_80_A2_H03_T7	g507910	BLASTN	343	7e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3255	GM_80_A2_H04_MR	g505129	BLASTN	348	9e-09	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
3256	GM_80_A2_H08_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3257	GM_80_A2_H08_T7	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
3258	GM_80_A2_H10_T7	g2764526	BLASTN	358	4e-09	65	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
3259	GM_80_A2_H11_MR	g100484	BLASTX	406	2e-36	54	hypothetical protein - garden snapdragon
3260	GM_80_B1_A02_T7	g4038056	BLASTX	89	9e-12	65	(AC005897) putative transposon [Arabidopsis thaliana]
3261	GM_80_B1_A04_MR	g1709814	BLASTX	171	5e-11	56	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A1 >gi 2147916 pir S73205 photosystem I p700 chlorophyll A apoprotein A1 - Porphyra purpurea chloroplast >gi 1276750 (U38804) Photosystem I p700 chlorophyll A apoprotein A1 [Porphyra purpurea]
3262	GM_80_B1_A10_MR	g2246449	BLASTN	497	2e-15	66	Lycopersicon esculentum copia-like retrotransposon ToRTL1, 3-hydroxy-3-methylglutaryl CoA reductase 2 (HMG2) gene, complete cds.
3263	GM_80_B1_B07_T7	g905361	BLASTX	120	5e-11	47	(U22103) gag-protease polyprotein [Glycine max]
3264	GM_80_B1_C10_MR	g2995405	BLASTX	229	4e-17	49	(Y12432) polyprotein [Ananas comosus]
3265	GM_80_B1_D01_MR	g3449330	BLASTN	595	8e-20	65	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence [Arabidopsis thaliana]
3266	GM_80_B1_D02_T7	g18559	BLASTN	788	1e-28	74	G.max gene for catalase
3267	GM_80_B1_D03_T7	g3319351	BLASTX	292	1e-23	48	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
3268	GM_80_B1_D05_MR	g131276	BLASTX	550	2e-52	90	PHOTOSYSTEM II P680 CHLOROPHYLL A APOPROTEIN (CP-47 PROTEIN) >gi 72704 pir QJNT6A photosystem II chlorophyll a-binding protein psbB - common tobacco chloroplast >gi 11856 (Z00044) PSII 47kD protein [Nicotiana tabacum] >gi 225224 prf 1211235BF photosystem II P680 apoprotein [Nicotiana tabacum]

3269	GM_80_B1_D05_T7	g114532	BLASTX	433	5e-40	92	ATP SYNTHASE ALPHA CHAIN gi 67824 pir PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast gi 11769 (V00162) alpha subunit of ATPase [Nicotiana tabacum] gi 11811 (Z00044) ATPase alpha subunit [Nicotiana tabacum] gi 225270 prf 1211235E ATPase alpha [Nicotiana tabacum]
3270	GM_80_B1_D07_T7	g3097320	BLASTN	876	1e-32	77	Glycine max gene for Bd 30K, complete cds
3271	GM_80_B1_D11_T7	g13596	BLASTN	353	8e-10	62	Yeast mit DNA for promoter upstream of tRNA-Leu gene 3 *Source:
3272	GM_80_B1_D12_T7	g629693	BLASTX	158	4e-10	34	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
3273	GM_80_B1_E02_T7	g1813979	BLASTX	254	4e-21	67	(Y10860) hypothetical protein [Musa acuminata]
3274	GM_80_B1_E03_MR	g3142328	BLASTN	1139	1e-44	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3275	GM_80_B1_E05_T7	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3276	GM_80_B1_E08_MR	g99730	BLASTX	221	3e-20	55	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
3277	GM_80_B1_E08_T7	g18559	BLASTN	946	7e-36	76	G.max gene for catalase
3278	GM_80_B1_E11_MR	g3845097	BLASTN	376	6e-10	64	Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence
3279	GM_80_B1_E12_T7	g3645899	BLASTX	207	1e-14	46	(U68408) 5' end not determined experimentally [Zea mays]
3280	GM_80_B1_F04_T7	g4115365	BLASTX	318	2e-26	45	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
3281	GM_80_B1_G02_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3282	GM_80_B1_G04_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3283	GM_80_B1_G04_T7	g507910	BLASTN	350	3e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
3284	GM_80_B1_G05_MR	g3097320	BLASTN	1195	4e-47	78	Glycine max gene for Bd 30K, complete cds
3285	GM_80_B1_G05_T7	g2651310	BLASTX	282	3e-23	38	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]
3286	GM_80_B1_G06_T7	g18768	BLASTN	515	6e-17	68	Soybean Tgm6 transposable element 3' end
3287	GM_80_B1_G12_T7	g3171159	BLASTN	509	6e-16	62	Homo sapiens chromosome 21q22.3 PAC 21L13, complete sequence [Homo sapiens]
3288	GM_80_B1_H01_T7	g1171583	BLASTN	529	7e-17	63	P.falciparum complete gene map of plastid-like DNA (IR-A)
3289	GM_80_B1_H04_MR	g4115365	BLASTX	177	2e-11	38	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
3290	GM_80_B1_H04_T7	g507910	BLASTN	372	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3291	GM_80_B1_H05_T7	g18559	BLASTN	875	1e-32	75	G.max gene for catalase
3292	GM_80_B1_H07_MR	g3142328	BLASTN	1025	2e-39	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3293	GM_80_B1_H09_T7	g18559	BLASTN	1358	1e-54	81	G.max gene for catalase
3294	GM_80_B1_H10_MR	g2443320	BLASTX	162	7e-15	36	(D85597) polyprotein [Oryza australiensis]

3295	GM_80_B2_A01_T7	g2464864	BLASTX	239	2e-18	37	(Z99707) selenium-binding protein homolog [Arabidopsis thaliana]
3296	GM_80_B2_A02_MR	g4063760	BLASTX	164	5e-10	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3297	GM_80_B2_A02_T7	g507910	BLASTN	369	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3298	GM_80_B2_A03_T7	g507910	BLASTN	347	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3299	GM_80_B2_A04_MR	g3777526	BLASTN	463	6e-14	82	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
3300	GM_80_B2_A05_MR	g2827514	BLASTX	356	3e-31	74	(AL021633) predicted protein [Arabidopsis thaliana]
3301	GM_80_B2_A08_MR	g507910	BLASTN	538	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3302	GM_80_B2_A11_T7	g4038056	BLASTX	303	5e-25	48	(AC005897) putative transposon [Arabidopsis thaliana]
3303	GM_80_B2_A12_T7	g462137	BLASTX	180	1e-24	75	GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE, CYTOSOLIC
3304	GM_80_B2_B03_MR	g2618698	BLASTX	118	2e-11	77	(AC002510) unknown protein [Arabidopsis thaliana]
3305	GM_80_B2_B06_T7	g4063760	BLASTX	453	8e-49	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3306	GM_80_B2_B07_MR	g2522228	BLASTX	377	4e-46	66	(AB007466) reverse transcriptase-like protein [Vicia faba]
3307	GM_80_B2_B09_T7	g3777527	BLASTX	649	1e-61	90	(AF053008) gag-pol polyprotein [Glycine max]
3308	GM_80_B2_B11_T7	g4106061	BLASTX	164	3e-11	45	(AF053318) CCR4-associated factor 1 [Homo sapiens]
3309	GM_80_B2_B12_MR	g507910	BLASTN	405	1e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
3310	GM_80_B2_C01_T7	g3241935	BLASTN	459	1e-13	64	Arabidopsis thaliana chromosome IV from 19 cM, complete sequence [Arabidopsis thaliana]
3311	GM_80_B2_C04_MR	g3738114	BLASTN	496	2e-15	57	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
3312	GM_80_B2_C05_MR	g507910	BLASTN	645	1e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
3313	GM_80_B2_C09_T7	g3097320	BLASTN	1142	1e-44	83	Glycine max gene for Bd 30K, complete cds
3314	GM_80_B2_C10_T7	g3779030	BLASTX	258	2e-21	39	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
3315	GM_80_B2_D01_T7	g421955	BLASTX	180	1e-12	40	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
3316	GM_80_B2_D04_T7	g226407	BLASTX	307	4e-25	43	retrotransposon del1-46 [Lilium henryi]
3317	GM_80_B2_D05_MR	g1142702	BLASTN	423	1e-12	73	Glycine max satellite STR120-A.4.
3318	GM_80_B2_D10_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3319	GM_80_B2_E01_MR	g1750376	BLASTX	170	1e-10	72	(U80808) ubiquitin activating enzyme [Arabidopsis thaliana] gi 3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]
3320	GM_80_B2_E02_MR	g18559	BLASTN	488	4e-15	68	G.max gene for catalase
3321	GM_80_B2_E08_MR	g1666236	BLASTX	220	2e-17	32	(U76261) unknown [Hordeum vulgare]
3322	GM_80_B2_E12_MR	g3548803	BLASTX	327	5e-28	82	(AC005313) putative DNA-binding protein [Arabidopsis thaliana]
3323	GM_80_B2_F02_T7	g3845197	BLASTN	525	1e-16	65	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence

3324	GM_80_B2_F07_T7	g3142328	BLASTN	754	4e-27	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3325	GM_80_B2_G02_MR	g3599418	BLASTN	543	1e-17	92	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
3326	GM_80_B2_G02_T7	g2522230	BLASTX	180	3e-13	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
3327	GM_80_B2_G09_T7	g18559	BLASTN	1366	6e-55	76	G.max gene for catalase
3328	GM_80_B2_H03_T7	g4038056	BLASTX	247	5e-19	44	(AC005897) putative transposon [Arabidopsis thaliana]
3329	GM_80_B2_H04_T7	g130582	BLASTX	154	9e-18	48	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
3330	GM_80_B2_H05_MR	g4063760	BLASTX	288	3e-23	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3331	GM_80_B2_H05_T7	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3332	GM_80_B2_H07_T7	g3033389	BLASTX	188	1e-12	36	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
3333	GM_80_B2_H08_MR	g3273115	BLASTN	401	4e-11	63	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-15, complete sequence [Plasmodium falciparum]
3334	GM_81_A1_A03_MR	g3550435	BLASTN	565	2e-18	61	Hordeum vulgare Hotr1 gene
3335	GM_81_A1_A03_T7	g2642431	BLASTX	253	2e-19	49	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
3336	GM_81_A1_A04_MR	g3337361	BLASTX	213	1e-15	45	(AC004481) ankyrin-like protein [Arabidopsis thaliana]
3337	GM_81_A1_B01_MR	g2104945	BLASTN	362	2e-09	72	Glycine max copia-like retrotransposon Tgmr, complete sequence
3338	GM_81_A1_B05_MR	g1146165	BLASTX	155	7e-10	72	(L47479) urophorphyrin III methylase [Arabidopsis thaliana]
3339	GM_81_A1_B07_T7	g3810596	BLASTX	288	2e-23	49	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3340	GM_81_A1_B11_MR	g2443320	BLASTX	189	1e-12	35	(D85597) polyprotein [Oryza australiensis]
3341	GM_81_A1_B12_T7	g1769898	BLASTX	216	5e-16	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3342	GM_81_A1_C01_MR	g4063760	BLASTX	368	8e-32	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3343	GM_81_A1_C01_T7	g507910	BLASTN	440	3e-13	78	Glycine max BSR-101 satellite SB92 genomic sequence.
3344	GM_81_A1_C04_MR	g507910	BLASTN	600	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3345	GM_81_A1_C04_T7	g4063756	BLASTN	404	3e-11	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3346	GM_81_A1_C06_MR	g2995405	BLASTX	383	1e-33	51	(Y12432) polyprotein [Ananas comosus]
3347	GM_81_A1_C07_MR	g18559	BLASTN	951	4e-36	77	G.max gene for catalase
3348	GM_81_A1_C09_MR	g3777527	BLASTX	568	6e-53	94	(AF053008) gag-pol polyprotein [Glycine max]
3349	GM_81_A1_D04_MR	g3810596	BLASTX	246	6e-19	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3350	GM_81_A1_D05_MR	g2213608	BLASTX	173	5e-11	40	(AC000103) F21J9.2 [Arabidopsis thaliana]
3351	GM_81_A1_D09_MR	g1236334	BLASTX	144	2e-09	77	(U34283) T3/T7-like RNA polymerase [Oryza sativa]
3352	GM_81_A1_D10_MR	g18559	BLASTN	789	9e-29	74	G.max gene for catalase

3353	GM_81_A1_E02_MR	g840618	BLASTN	347	7e-09	64	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
3354	GM_81_A1_E07_T7	g4063760	BLASTX	461	1e-41	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3355	GM_81_A1_E11_T7	g905361	BLASTX	252	7e-20	88	(U22103) gag-protease polyprotein [Glycine max]
3356	GM_81_A1_F03_T7	g100484	BLASTX	353	1e-30	61	hypothetical protein - garden snapdragon
3357	GM_81_A1_F04_T7	g507910	BLASTN	348	4e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
3358	GM_81_A1_F05_T7	g133917	BLASTX	245	4e-20	84	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 gi 70856 pir R3NT2 ribosomal protein S2 - common tobacco chloroplast gi 11814 (Z00044) ribosomal protein S2 [Nicotiana tabacum] gi 225274 prf 1211235J ribosomal protein S2 [Nicotiana tabacum]
3359	GM_81_A1_F07_T7	g905361	BLASTX	522	1e-54	89	(U22103) gag-protease polyprotein [Glycine max]
3360	GM_81_A1_F08_T7	g505129	BLASTN	375	5e-10	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
3361	GM_81_A1_F09_T7	g3142328	BLASTN	397	6e-11	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3362	GM_81_A1_F12_T7	g1769898	BLASTX	237	3e-18	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3363	GM_81_A1_G03_MR	g3319372	BLASTX	175	3e-11	33	(AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]
3364	GM_81_A1_G05_T7	g3287696	BLASTX	488	3e-45	72	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]
3365	GM_81_A1_G07_MR	g3142328	BLASTN	1804	5e-75	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3366	GM_81_A1_G10_T7	g18559	BLASTN	522	1e-16	73	G.max gene for catalase
3367	GM_81_A1_H02_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3368	GM_81_A1_H03_MR	g421948	BLASTX	220	1e-16	35	UDP rhamnose--anthocyanidin-3-glucoside rhamnosyltransferase - garden petunia
3369	GM_81_A1_H04_MR	g4063760	BLASTX	589	2e-55	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3370	GM_81_A1_H05_T7	g507910	BLASTN	365	7e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3371	GM_81_A1_H08_MR	g13558	BLASTN	553	3e-18	67	Yeast mitochondrial DNA with the gene for tRNA-Glu >gi 13599 emb X04566 MISCTRNE Yeast mitochondrial gene for transfer RNA-Glu >gi 343972 gb K03309 YSTMTTGE Saccharomyces cerevisiae mitochondrial tRNA-Glu gene.
3372	GM_81_A1_H12_T7	g3695062	BLASTN	426	2e-12	74	Lotus japonicus rac GTPase activating protein 3 mRNA, partial cds
3373	GM_81_A2_A03_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
3374	GM_81_A2_A03_T7	g507910	BLASTN	350	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
3375	GM_81_A2_A06_T7	g170080	BLASTN	523	1e-16	93	Soybean seed lectin gene transposable element tgm1.
3376	GM_81_A2_A08_MR	g507910	BLASTN	347	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3377	GM_81_A2_A08_T7	g507910	BLASTN	393	4e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.

3378	GM_81_A2_A09_T7	g3335375	BLASTX	206	6e-15	74	(AC003028) putative amidase [Arabidopsis thaliana]
3379	GM_81_A2_A11_MR	g531389	BLASTX	217	1e-15	43	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
3380	GM_81_A2_A12_MR	g2995405	BLASTX	394	7e-35	66	(Y12432) polyprotein [Ananas comosus]
3381	GM_81_A2_B01_T7	g18559	BLASTN	944	9e-36	73	G.max gene for catalase
3382	GM_81_A2_B02_MR	g2522228	BLASTX	390	2e-35	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
3383	GM_81_A2_B02_T7	g3097320	BLASTN	466	5e-14	71	Glycine max gene for Bd 30K, complete cds
3384	GM_81_A2_B05_T7	g1666236	BLASTX	206	1e-15	31	(U76261) unknown [Hordeum vulgare]
3385	GM_81_A2_B08_MR	g3645899	BLASTX	270	2e-21	43	(U68408) 5' end not determined experimentally [Zea mays]
3386	GM_81_A2_B09_T7	g3142328	BLASTN	1183	1e-46	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3387	GM_81_A2_B11_T7	g2462936	BLASTX	308	9e-27	48	(Y12321) open reading frame 2 [Brassica oleracea]
3388	GM_81_A2_B12_MR	g4063760	BLASTX	572	1e-53	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3389	GM_81_A2_C04_T7	g2827713	BLASTX	149	5e-09	82	(AL021684) pyridoxal-phosphate-dependent aminotransferase - like protein [Arabidopsis thaliana]
3390	GM_81_A2_C05_MR	g507910	BLASTN	548	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3391	GM_81_A2_C05_T7	g507910	BLASTN	583	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
3392	GM_81_A2_C06_T7	g905361	BLASTX	176	1e-11	29	(U22103) gag-protease polyprotein [Glycine max]
3393	GM_81_A2_C07_T7	g507910	BLASTN	693	1e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
3394	GM_81_A2_C10_T7	g4063760	BLASTX	265	7e-21	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3395	GM_81_A2_D01_MR	g18767	BLASTN	365	4e-18	78	Soybean Tgm6 transposable element 5' end
3396	GM_81_A2_D03_MR	g507910	BLASTN	666	2e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
3397	GM_81_A2_D04_MR	g18559	BLASTN	1021	3e-39	76	G.max gene for catalase
3398	GM_81_A2_D10_T7	g4063760	BLASTX	566	6e-53	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3399	GM_81_A2_E03_MR	g3169065	BLASTX	191	4e-14	40	(AL023704) translocation elongation factor [Schizosaccharomyces pombe]
3400	GM_81_A2_E03_T7	g13100	BLASTN	406	2e-11	62	M. javanica mitochondrion ATPase 6, and putative tRNA-f-Met and tRNA-His genes
3401	GM_81_A2_E05_T7	g3695395	BLASTX	251	9e-20	39	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
3402	GM_81_A2_F06_T7	g3645899	BLASTX	203	2e-16	41	(U68408) 5' end not determined experimentally [Zea mays]
3403	GM_81_A2_F10_T7	g2660669	BLASTX	617	7e-58	90	(AC002342) human Mi-2 autoantigen-like protein [Arabidopsis thaliana]
3404	GM_81_A2_F12_MR	g4063760	BLASTX	203	3e-14	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3405	GM_81_A2_G03_MR	g2956679	BLASTN	351	8e-09	62	Human DNA sequence from clone 343C1 on chromosome 22, complete sequence [Homo sapiens]
3406	GM_81_A2_G04_MR	g2443320	BLASTX	313	6e-26	45	(D85597) polyprotein [Oryza australiensis]
3407	GM_81_A2_G06_MR	g3142379	BLASTX	213	2e-28	80	(AF053008) envelope-like [Glycine max]
3408	GM_81_A2_G09_MR	g3426334	BLASTN	364	2e-09	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds

3409	GM_81_A2_H01_T7	g507910	BLASTN	560	1e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
3410	GM_81_A2_H03_MR	g2443320	BLASTX	277	5e-22	41	(D85597) polyprotein [Oryza australiensis]
3411	GM_81_A2_H03_T7	g4063756	BLASTN	469	4e-14	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3412	GM_81_A2_H04_MR	g505129	BLASTN	360	3e-09	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
3413	GM_81_A2_H05_MR	g3097320	BLASTN	434	1e-12	73	Glycine max gene for Bd 30K, complete cds
3414	GM_81_A2_H09_MR	g4063760	BLASTX	303	7e-25	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3415	GM_81_A2_H09_T7	g170608	BLASTN	352	2e-09	66	Broad bean (V.faba) BamHI repetitive element, clone 1.
3416	GM_81_A2_H10_MR	g3738114	BLASTN	360	3e-09	60	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
3417	GM_81_B1_A08_MR	g2522227	BLASTX	221	2e-17	56	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
3418	GM_81_B1_A08_T7	g3777527	BLASTX	283	8e-42	87	(AF053008) gag-pol polyprotein [Glycine max]
3419	GM_81_B1_A10_T7	g2121303	BLASTN	573	7e-19	64	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
3420	GM_81_B1_B05_MR	g14293	BLASTN	370	1e-10	65	Yeast R0.54 mutant mitochondrial DNA lacking ori1 sequence recombination junction with tRNA-Pro and 15S rRNA genes
3421	GM_81_B1_B06_MR	g3786414	BLASTN	381	4e-10	59	Caenorhabditis elegans cosmid H28G03
3422	GM_81_B1_B07_MR	g13533	BLASTN	416	7e-12	62	Yeast mitochondrial tRNA genes (several, map positions 3.5 to 8.6) encoding tRNAs for Lys, Arg, Gly, Asp, Ser, Arg, and Ala.
3423	GM_81_B1_B07_T7	g3953479	BLASTX	198	1e-13	46	(AC002328) F22O2.24 [Arabidopsis thaliana]
3424	GM_81_B1_B12_T7	g3810596	BLASTX	229	4e-17	53	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3425	GM_81_B1_C01_MR	g2262177	BLASTX	339	1e-29	71	(AC002329) hypothetical protein similar to T18A10.3 [Arabidopsis thaliana]
3426	GM_81_B1_C02_MR	g4063760	BLASTX	278	3e-22	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3427	GM_81_B1_C03_MR	g3810596	BLASTX	190	5e-13	38	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3428	GM_81_B1_C08_MR	g2121303	BLASTN	387	2e-10	61	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
3429	GM_81_B1_C09_T7	g226407	BLASTX	186	4e-13	54	retrotransposon del1-46 [Lilium henryi]
3430	GM_81_B1_D02_MR	g2832611	BLASTN	426	3e-12	68	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)
3431	GM_81_B1_D02_T7	g629626	BLASTX	212	1e-16	81	Rab protein - alfalfa gi 488700 (X79278) Rab gene product [Medicago sativa]
3432	GM_81_B1_D06_T7	g3176798	BLASTN	365	3e-10	64	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite, 5' sequence
3433	GM_81_B1_D08_MR	g3777527	BLASTX	701	4e-67	97	(AF053008) gag-pol polyprotein [Glycine max]
3434	GM_81_B1_E02_T7	g2443320	BLASTX	216	1e-22	41	(D85597) polyprotein [Oryza australiensis]

3435	GM_81_B1_E06_MR	g4150930	BLASTN	437	1e-12	63	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
3436	GM_81_B1_E07_T7	g1514643	BLASTX	241	4e-18	57	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
3437	GM_81_B1_E09_T7	g2618600	BLASTN	324	7e-09	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDC12, complete sequence [Arabidopsis thaliana]
3438	GM_81_B1_F05_MR	g2961349	BLASTX	279	2e-22	52	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
3439	GM_81_B1_G02_MR	g3097320	BLASTN	353	6e-09	72	Glycine max gene for Bd 30K, complete cds
3440	GM_81_B1_G04_T7	g2969943	BLASTN	444	5e-13	62	Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS
3441	GM_81_B1_G06_MR	g3687828	BLASTN	391	1e-10	62	Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence [Homo sapiens]
3442	GM_81_B1_G07_MR	g2129709	BLASTX	275	8e-22	40	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
3443	GM_81_B1_G08_T7	g2995405	BLASTX	249	3e-19	44	(Y12432) polyprotein [Ananas comosus]
3444	GM_81_B1_H01_MR	g18768	BLASTN	421	1e-12	64	Soybean Tgm6 transposable element 3' end
3445	GM_81_B1_H11_MR	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3446	GM_81_B2_A03_MR	g2129709	BLASTX	259	4e-20	38	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
3447	GM_81_B2_A03_T7	g3930515	BLASTX	115	8e-11	45	(AF059674) putative gag protein [Nicotiana tabacum]
3448	GM_81_B2_A08_MR	g1351834	BLASTX	298	1e-25	62	PROBABLE ATP-DEPENDENT TRANSPORTER YCF16 gi 1016162 (U30821) ABC transporter subunit [Cyanophora paradoxa]
3449	GM_81_B2_A10_MR	g507910	BLASTN	668	1e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
3450	GM_81_B2_B11_MR	g507910	BLASTN	341	8e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3451	GM_81_B2_D06_MR	g2649054	BLASTX	296	2e-27	60	(AE000998) long-chain-fatty-acid--CoA ligase (fadD-6) [Archaeoglobus fulgidus]
3452	GM_81_B2_D09_MR	g2462745	BLASTX	242	8e-19	50	(AC002292) Hypothetical protein [Arabidopsis thaliana]
3453	GM_81_B2_E03_MR	g2979574	BLASTN	468	4e-14	66	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence [Homo sapiens]
3454	GM_81_B2_F02_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3455	GM_81_B2_F04_MR	g2522227	BLASTX	222	1e-17	56	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
3456	GM_81_B2_F06_MR	g2586082	BLASTX	140	9e-17	47	(U72725) retrofit [Oryza longistaminata]
3457	GM_81_B2_F08_MR	g3777527	BLASTX	493	5e-46	79	(AF053008) gag-pol polyprotein [Glycine max]
3458	GM_81_B2_G03_MR	g2809249	BLASTX	209	3e-15	33	(AC002560) F21B7.18 [Arabidopsis thaliana]
3459	GM_81_B2_H06_MR	g1480927	BLASTN	353	5e-09	84	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
3460	GM_82_A1_A04_MR	g2995405	BLASTX	304	3e-25	48	(Y12432) polyprotein [Ananas comosus]
3461	GM_82_A1_A05_T7	g4063756	BLASTN	472	3e-14	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]

3462	GM_82_A1_A06_MR	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3463	GM_82_A1_A10_MR	g1045530	BLASTN	356	3e-09	62	Magnaporthe grisea host-species specificity (Pwl1) gene, complete cds.
3464	GM_82_A1_A11_T7	g2245073	BLASTN	444	5e-13	65	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8
3465	GM_82_A1_A12_T7	g2462935	BLASTX	152	8e-09	30	(Y12321) open reading frame 1 [Brassica oleracea]
3466	GM_82_A1_B04_MR	g3264565	BLASTN	425	4e-12	65	Homo sapiens chromosome 17, clone hRPC.1037_O_7, complete sequence [Homo sapiens]
3467	GM_82_A1_B08_T7	g3097320	BLASTN	675	2e-23	72	Glycine max gene for Bd 30K, complete cds
3468	GM_82_A1_C03_T7	g4063760	BLASTX	186	1e-22	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3469	GM_82_A1_C05_T7	g3142328	BLASTN	1037	5e-40	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3470	GM_82_A1_C06_T7	g2995405	BLASTX	366	8e-32	54	(Y12432) polyprotein [Ananas comosus]
3471	GM_82_A1_D04_MR	g507910	BLASTN	513	1e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
3472	GM_82_A1_D12_MR	g1769898	BLASTX	142	1e-10	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3473	GM_82_A1_E01_MR	g3645899	BLASTX	195	2e-13	50	(U68408) 5' end not determined experimentally [Zea mays]
3474	GM_82_A1_E03_T7	g2764526	BLASTN	408	2e-11	63	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
3475	GM_82_A1_E05_MR	g1084334	BLASTX	217	2e-16	81	calcium-dependent protein kinase (EC 2.7.1.-) 1 - Arabidopsis thaliana gi 604880 gnl PID d1005364 (D21805) calcium-dependent protein kinase [Arabidopsis thaliana]
3476	GM_82_A1_E05_T7	g3548803	BLASTX	267	2e-21	71	(AC005313) putative DNA-binding protein [Arabidopsis thaliana]
3477	GM_82_A1_E06_MR	g3645899	BLASTX	291	1e-23	56	(U68408) 5' end not determined experimentally [Zea mays]
3478	GM_82_A1_E06_T7	g1666236	BLASTX	147	4e-09	28	(U76261) unknown [Hordeum vulgare]
3479	GM_82_A1_E07_MR	g1143016	BLASTN	349	6e-09	62	Spiroplasma citri Spiroplasma virus SpV1-derived ORF3 gene, partial cds.
3480	GM_82_A1_E10_T7	g4063760	BLASTX	220	5e-16	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3481	GM_82_A1_F02_T7	g3059060	BLASTN	402	4e-11	62	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
3482	GM_82_A1_F03_T7	g3142328	BLASTN	1151	3e-45	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3483	GM_82_A1_F04_MR	g3097320	BLASTN	367	1e-09	71	Glycine max gene for Bd 30K, complete cds
3484	GM_82_A1_F05_T7	g2522228	BLASTX	403	4e-41	64	(AB007466) reverse transcriptase-like protein [Vicia faba]
3485	GM_82_A1_F06_MR	g4063760	BLASTX	444	6e-40	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3486	GM_82_A1_F06_T7	g1769897	BLASTX	99	2e-10	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3487	GM_82_A1_F08_T7	g3645899	BLASTX	203	3e-14	42	(U68408) 5' end not determined experimentally [Zea mays]
3488	GM_82_A1_F11_MR	g507910	BLASTN	505	3e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.

3489	GM_82_A1_F12_T7	g100484	BLASTX	208	5e-15	44	hypothetical protein - garden snapdragon
3490	GM_82_A1_G05_T7	g2129618	BLASTX	202	3e-14	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3491	GM_82_A1_G06_MR	g507910	BLASTN	388	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3492	GM_82_A1_G10_MR	g3859610	BLASTN	518	2e-16	65	Arabidopsis thaliana BAC T9E19
3493	GM_82_A1_H02_MR	g1165321	BLASTN	771	6e-28	82	Glycine max extensin (SbHRGP3) gene, complete cds
3494	GM_82_A1_H03_MR	g3097320	BLASTN	665	4e-23	69	Glycine max gene for Bd 30K, complete cds
3495	GM_82_A1_H04_T7	g2995405	BLASTX	220	4e-19	46	(Y12432) polyprotein [Ananas comosus]
3496	GM_82_A1_H08_MR	g2522228	BLASTX	209	3e-19	48	(AB007466) reverse transcriptase-like protein [Vicia faba]
3497	GM_82_A1_H09_MR	g1167523	BLASTX	329	1e-27	54	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
3498	GM_82_A2_A02_MR	g3979928	BLASTN	429	2e-12	62	Caenorhabditis elegans cosmid Y18D10A, complete sequence [Caenorhabditis elegans]
3499	GM_82_A2_A03_T7	g576752	BLASTN	346	6e-09	62	Myrmecia pilosula HI91-035 mitochondrion cytochrome b gene, partial cds.
3500	GM_82_A2_A06_T7	g3777527	BLASTX	705	1e-67	95	(AF053008) gag-pol polyprotein [Glycine max]
3501	GM_82_A2_A08_MR	g507910	BLASTN	398	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3502	GM_82_A2_A12_MR	g507910	BLASTN	523	5e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
3503	GM_82_A2_B02_T7	g507910	BLASTN	344	6e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
3504	GM_82_A2_B05_MR	g1480526	BLASTN	342	3e-09	62	Rhagoletis meigeni cytochrome oxidase subunit II (COII) gene, mitochondrial gene encoding mitochondrial protein, partial cds
3505	GM_82_A2_B09_MR	g18559	BLASTN	359	3e-09	71	G.max gene for catalase
3506	GM_82_A2_B10_MR	g2598589	BLASTX	225	1e-22	41	(Y15367) MtN19 [Medicago truncatula]
3507	GM_82_A2_B11_MR	g905361	BLASTX	676	1e-65	93	(U22103) gag-protease polyprotein [Glycine max]
3508	GM_82_A2_C02_T7	g507910	BLASTN	589	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3509	GM_82_A2_C06_T7	g507910	BLASTN	621	2e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3510	GM_82_A2_C08_MR	g180902	BLASTN	370	1e-10	60	Human variable number tandem repeat (VNTR) region, allele 14R2 3' to collagen type II (COL2A1) gene.
3511	GM_82_A2_C09_MR	g3142328	BLASTN	915	2e-34	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3512	GM_82_A2_C10_T7	g4038057	BLASTX	163	4e-10	44	(AC005897) hypothetical protein [Arabidopsis thaliana]
3513	GM_82_A2_D03_MR	g1168471	BLASTX	145	2e-09	86	PROTEIN KINASE APK1B gi 2160295 gnl PID d1001485 (D10152) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]
3514	GM_82_A2_D05_MR	g2769655	BLASTN	378	5e-10	63	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
3515	GM_82_A2_D07_T7	g2459440	BLASTX	126	4e-09	40	(AC002332) putative receptor kinase [Arabidopsis thaliana]
3516	GM_82_A2_D08_MR	g507910	BLASTN	527	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.

3517	GM_82_A2_D10_MR	g2392895	BLASTX	307	3e-25	50	(AF017056) brassinosteroid insensitive 1 [Arabidopsis thaliana]
3518	GM_82_A2_D11_T7	g2129618	BLASTX	188	9e-13	47	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3519	GM_82_A2_D12_MR	g4056421	BLASTX	410	1e-37	78	(AC005322) Similar to gb Z30094 basic transcripion factor 2, 44 kD subunit from Homo sapiens. EST gb W43325 comes from this gene. [Arabidopsis thaliana]
3520	GM_82_A2_E02_MR	g4063760	BLASTX	489	1e-44	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3521	GM_82_A2_E02_T7	g1769897	BLASTX	173	2e-11	30	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3522	GM_82_A2_E04_MR	g130582	BLASTX	101	1e-08	36	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
3523	GM_82_A2_E04_T7	g2865424	BLASTX	393	3e-34	52	(AF039371) polyprotein [Arabidopsis thaliana]
3524	GM_82_A2_E05_T7	g3892061	BLASTX	147	1e-08	25	(AC002330) putative reverse transcriptase [Arabidopsis thaliana]
3525	GM_82_A2_E11_MR	g99730	BLASTX	270	4e-22	50	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
3526	GM_82_A2_F05_MR	g1669680	BLASTN	459	1e-13	63	Human DNA sequence from PAC 293E14 contains ESTs, STS
3527	GM_82_A2_F05_T7	g13596	BLASTN	335	6e-09	58	Yeast mit DNA for promoter upstream of tRNA-Leu gene 3 *Source:
3528	GM_82_A2_F07_MR	g507910	BLASTN	525	4e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
3529	GM_82_A2_F11_MR	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
3530	GM_82_A2_F11_T7	g3777527	BLASTX	208	2e-16	47	(AF053008) gag-pol polyprotein [Glycine max]
3531	GM_82_A2_G03_T7	g3201682	BLASTX	157	9e-14	67	(AF060942) extra-large G-protein [Arabidopsis thaliana]
3532	GM_82_A2_G12_MR	g3287270	BLASTX	134	3e-11	44	(Y09533) involved in starch metabalism [Solanum tuberosum]
3533	GM_82_A2_G12_T7	g170029	BLASTN	405	3e-11	81	Glycine max cv. Dare nodulin 26 gene fragment.
3534	GM_82_A2_H01_MR	g1326016	BLASTX	298	2e-24	45	TY3-2 orfB
3535	GM_82_A2_H04_MR	g987979	BLASTX	166	1e-11	67	(X91248) high mobility group-like protein [Zinnia elegans]
3536	GM_82_A2_H05_MR	g2462134	BLASTX	183	1e-12	36	(Y13368) reverse transcriptase [Beta vulgaris]
3537	GM_82_A2_H06_MR	g3928116	BLASTN	430	2e-12	63	, complete sequence [Homo sapiens]
3538	GM_82_A2_H11_MR	g2522226	BLASTN	537	2e-17	63	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
3539	GM_82_B1_A09_T7	g4063760	BLASTX	321	8e-27	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3540	GM_82_B1_A10_MR	g2335061	BLASTN	457	1e-13	70	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence [Homo sapiens]
3541	GM_82_B1_A12_MR	g2443320	BLASTX	461	1e-41	44	(D85597) polyprotein [Oryza australiensis]
3542	GM_82_B1_B01_MR	g2522230	BLASTX	171	3e-12	41	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
3543	GM_82_B1_B03_T7	g4038056	BLASTX	304	4e-25	53	(AC005897) putative transposon [Arabidopsis thaliana]
3544	GM_82_B1_B07_MR	g3097320	BLASTN	1034	8e-40	79	Glycine max gene for Bd 30K, complete cds

3545	GM_82_B1_C02_MR	g2995405	BLASTX	288	1e-38	46	(Y12432) polyprotein [Ananas comosus]
3546	GM_82_B1_C02_T7	g4063760	BLASTX	517	1e-47	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3547	GM_82_B1_C07_T7	g18559	BLASTN	496	2e-15	86	G.max gene for catalase
3548	GM_82_B1_C10_T7	g3142328	BLASTN	708	4e-25	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3549	GM_82_B1_D01_MR	g2995405	BLASTX	423	5e-38	66	(Y12432) polyprotein [Ananas comosus]
3550	GM_82_B1_D05_MR	g2760839	BLASTX	225	6e-17	45	(AC003105) putative receptor kinase [Arabidopsis thaliana]
3551	GM_82_B1_D05_T7	g2969888	BLASTN	476	1e-14	68	Daucus carota mRNA for sucrose-H+ symporter, SUT1b.
3552	GM_82_B1_D10_MR	g226407	BLASTX	295	2e-26	48	retrotransposon del1-46 [Lilium henryi]
3553	GM_82_B1_D12_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3554	GM_82_B1_E03_T7	g2618601	BLASTN	403	4e-11	74	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHJ24, complete sequence [Arabidopsis thaliana]
3555	GM_82_B1_E06_T7	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3556	GM_82_B1_E07_T7	g99922	BLASTX	332	3e-29	72	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
3557	GM_82_B1_E08_MR	g4115379	BLASTX	195	1e-29	47	(AC005967) putative carbonyl reductase [Arabidopsis thaliana]
3558	GM_82_B1_E12_MR	g905361	BLASTX	174	2e-11	29	(U22103) gag-protease polyprotein [Glycine max]
3559	GM_82_B1_F02_T7	g4063756	BLASTN	349	1e-08	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3560	GM_82_B1_F04_MR	g2522227	BLASTX	222	1e-17	56	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
3561	GM_82_B1_F04_T7	g3142328	BLASTN	819	4e-30	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3562	GM_82_B1_F07_T7	g3777527	BLASTX	642	8e-61	95	(AF053008) gag-pol polyprotein [Glycine max]
3563	GM_82_B1_F09_MR	g3080401	BLASTX	261	9e-22	65	(AL022603) putative protein [Arabidopsis thaliana]
3564	GM_82_B1_F10_MR	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
3565	GM_82_B1_F11_MR	g905361	BLASTX	789	4e-87	89	(U22103) gag-protease polyprotein [Glycine max]
3566	GM_82_B1_G01_MR	g2852684	BLASTX	324	2e-27	40	(AF017751) resistance protein candidate [Lactuca sativa]
3567	GM_82_B1_G03_T7	g1877279	BLASTX	176	3e-14	50	(Z92770) fadE2 [Mycobacterium tuberculosis]
3568	GM_82_B1_G04_MR	g18559	BLASTN	409	2e-11	65	G.max gene for catalase
3569	GM_82_B1_G04_T7	g1707020	BLASTX	321	2e-27	67	(U78721) hypothetical protein [Arabidopsis thaliana]
3570	GM_82_B1_G05_T7	g2129618	BLASTX	191	5e-13	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3571	GM_82_B1_G06_MR	g3777527	BLASTX	396	1e-34	41	(AF053008) gag-pol polyprotein [Glycine max]
3572	GM_82_B1_G09_MR	g507910	BLASTN	387	7e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
3573	GM_82_B1_G09_T7	g507910	BLASTN	384	9e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3574	GM_82_B1_G10_T7	g99922	BLASTX	516	9e-49	81	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]

3575	GM_82_B1_G12_MR	g3142328	BLASTN	1423	1e-57	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3576	GM_82_B1_H02_MR	g3142328	BLASTN	1416	3e-57	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3577	GM_82_B1_H03_MR	g2632254	BLASTX	131	5e-15	70	(Y12465) serine/threonine kinase [Sorghum bicolor]
3578	GM_82_B1_H03_T7	g2522227	BLASTX	169	1e-11	45	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
3579	GM_82_B1_H05_MR	g2462936	BLASTX	298	1e-25	35	(Y12321) open reading frame 2 [Brassica oleracea]
3580	GM_82_B1_H05_T7	g3319362	BLASTX	188	9e-13	44	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
3581	GM_82_B2_A01_T7	g507910	BLASTN	533	2e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3582	GM_82_B2_A04_MR	g507910	BLASTN	561	1e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
3583	GM_82_B2_A05_T7	g3142328	BLASTN	907	4e-34	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3584	GM_82_B2_A06_MR	g421955	BLASTX	170	2e-11	44	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
3585	GM_82_B2_A10_MR	g4063756	BLASTN	483	9e-15	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3586	GM_82_B2_A10_T7	g507910	BLASTN	693	1e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
3587	GM_82_B2_B01_MR	g2129709	BLASTX	173	6e-11	42	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
3588	GM_82_B2_B02_T7	g1431738	BLASTN	353	5e-09	77	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
3589	GM_82_B2_B03_MR	g2689221	BLASTX	255	2e-20	39	(Y10098) 7-ethoxycoumarin O-deethylase [Helianthus tuberosus]
3590	GM_82_B2_B04_MR	g729460	BLASTX	86	1e-11	72	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE II (BETA-KETOACYL-ACP SYNTHASE II) (KAS II) >gi 2121046 pir I41060 3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41) II - Escherichia coli >gi 572680 (Z34979) beta ketoacyl-acyl carrier protein synthase [Escherichia coli] >gi 664870 (U20767) beta-ketoacyl-acyl carrier protein synthase II [Escherichia coli] >gi 1787337 (AE000210) 3-oxoacyl-[acyl-carrier-protein] synthase II [Escherichia coli]
3591	GM_82_B2_B07_MR	g130398	BLASTX	220	5e-16	40	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 297) gi 85089 pir B24872 retrovirus-related pol polyprotein homolog - fruit fly (Drosophila melanogaster) transposon 297

3592	GM_82_B2_C01_MR	g13581	BLASTN	482	1e-15	65	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTCG10 Saccharomyces cerevisiae mitochondrion DNA segment.
3593	GM_82_B2_C01_T7	g3097320	BLASTN	481	1e-14	67	Glycine max gene for Bd 30K, complete cds
3594	GM_82_B2_C03_MR	g3777527	BLASTX	235	2e-17	38	(AF053008) gag-pol polyprotein [Glycine max]
3595	GM_82_B2_D09_MR	g2244839	BLASTX	265	4e-21	35	(Z97337) hypothetical protein [Arabidopsis thaliana]
3596	GM_82_B2_D11_MR	g3777527	BLASTX	624	6e-59	87	(AF053008) gag-pol polyprotein [Glycine max]
3597	GM_82_B2_E01_T7	g2522227	BLASTX	158	2e-10	54	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
3598	GM_82_B2_E03_MR	g2623299	BLASTX	319	2e-27	54	(AC002409) hypothetical protein [Arabidopsis thaliana]
3599	GM_82_B2_E05_T7	g3449329	BLASTN	448	3e-13	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]
3600	GM_82_B2_G03_MR	g3777527	BLASTX	512	6e-47	88	(AF053008) gag-pol polyprotein [Glycine max]
3601	GM_82_B2_G03_T7	g3450889	BLASTX	228	9e-31	67	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
3602	GM_82_B2_G04_T7	g99922	BLASTX	287	2e-31	63	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
3603	GM_82_B2_G05_T7	g3645899	BLASTX	220	2e-19	54	(U68408) 5' end not determined experimentally [Zea mays]
3604	GM_82_B2_G07_MR	g3142328	BLASTN	853	1e-31	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3605	GM_82_B2_G08_T7	g2522228	BLASTX	242	5e-24	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
3606	GM_82_B2_G09_MR	g3250687	BLASTX	306	2e-26	44	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
3607	GM_82_B2_G11_MR	g505129	BLASTN	373	7e-10	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
3608	GM_82_B2_H02_T7	g308769	BLASTN	350	9e-10	60	Budworm mitochondrial partial transfer RNA-Met (tRNA-Met) gene, and partial 12S ribosomal RNA (12S rRNA) gene.
3609	GM_82_B2_H10_T7	g3334666	BLASTN	939	2e-36	89	G.max mRNA for putative cytochrome P450, clone CP7
3610	GM_82_B2_H11_MR	g3845197	BLASTN	367	1e-09	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
3611	GM_82_B2_H12_MR	g3426334	BLASTN	458	1e-13	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
3612	GM_83_A1_A03_MR	g3287269	BLASTN	484	7e-15	67	S.tuberosum mRNA for protein involved in starch metabolism
3613	GM_83_A1_A05_MR	g3779030	BLASTX	161	3e-11	38	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
3614	GM_83_A1_A05_T7	g2708743	BLASTX	100	3e-09	31	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
3615	GM_83_A1_A06_T7	g2443320	BLASTX	299	2e-24	49	(D85597) polyprotein [Oryza australiensis]
3616	GM_83_A1_A11_MR	g1769898	BLASTX	141	7e-18	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3617	GM_83_A1_A11_T7	g99922	BLASTX	371	2e-33	58	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
3618	GM_83_A1_B01_T7	g3930515	BLASTX	117	4e-12	47	(AF059674) putative gag protein [Nicotiana tabacum]

3619	GM_83_A1_B04_T7	g3777527	BLASTX	191	9e-13	43	(AF053008) gag-pol polyprotein [Glycine max]
3620	GM_83_A1_B11_MR	g2586082	BLASTX	268	5e-21	44	(U72725) retrofit [Oryza longistaminata]
3621	GM_83_A1_C01_T7	g3650039	BLASTX	158	9e-10	44	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
3622	GM_83_A1_C05_MR	g1346261	BLASTX	315	5e-27	60	GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR) gi 1015319 gnl PID d1011751 (D67088) glutamyl-tRNA reductase [Cucumis sativus]
3623	GM_83_A1_C05_T7	g4115938	BLASTX	115	6e-10	71	(AF118223) contains similarity several bacterial glutathione-regulated potassium efflux system proteins [Arabidopsis thaliana]
3624	GM_83_A1_D02_MR	g3097320	BLASTN	382	3e-10	72	Glycine max gene for Bd 30K, complete cds
3625	GM_83_A1_D04_MR	g4063760	BLASTX	321	3e-38	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3626	GM_83_A1_D05_MR	g1346261	BLASTX	424	5e-39	71	GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR) gi 1015319 gnl PID d1011751 (D67088) glutamyl-tRNA reductase [Cucumis sativus]
3627	GM_83_A1_D05_T7	g4115930	BLASTN	346	6e-16	76	Arabidopsis thaliana BAC T4B21
3628	GM_83_A1_D12_MR	g507910	BLASTN	529	3e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
3629	GM_83_A1_E09_T7	g2462134	BLASTX	344	2e-30	50	(Y13368) reverse transcriptase [Beta vulgaris]
3630	GM_83_A1_E11_MR	g18559	BLASTN	728	6e-26	77	G.max gene for catalase
3631	GM_83_A1_E12_MR	g100484	BLASTX	350	2e-30	61	hypothetical protein - garden snapdragon
3632	GM_83_A1_F02_MR	g1142702	BLASTN	975	2e-37	93	Glycine max satellite STR120-A.4.
3633	GM_83_A1_F05_MR	g2842478	BLASTX	218	3e-16	48	(AL021749) receptor protein kinase like protein [Arabidopsis thaliana]
3634	GM_83_A1_F05_T7	g2924653	BLASTN	361	3e-09	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]
3635	GM_83_A1_F07_MR	g3810596	BLASTX	189	7e-13	37	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3636	GM_83_A1_F09_MR	g4063756	BLASTN	377	5e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3637	GM_83_A1_G05_MR	g4063760	BLASTX	401	4e-39	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3638	GM_83_A1_G05_T7	g507910	BLASTN	402	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3639	GM_83_A1_G07_MR	g1769898	BLASTX	105	2e-12	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3640	GM_83_A1_H07_T7	g3097320	BLASTN	687	4e-24	83	Glycine max gene for Bd 30K, complete cds
3641	GM_83_A1_H09_T7	g18559	BLASTN	636	8e-22	80	G.max gene for catalase
3642	GM_83_A1_H10_MR	g3142328	BLASTN	601	2e-36	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3643	GM_83_A2_A04_T7	g3036785	BLASTN	379	4e-10	66	Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains histone genes H2A/l,H2B.1A,H4,H2A.1b,H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG island
3644	GM_83_A2_A05_T7	g1680686	BLASTX	402	3e-36	67	(U51330) rust resistance kinase Lr10 [Triticum aestivum]

3645	GM_83_A2_A08_T7	g3928116	BLASTN	351	8e-09	59	, complete sequence [Homo sapiens]
3646	GM_83_A2_B07_T7	g3142328	BLASTN	699	1e-24	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3647	GM_83_A2_C02_MR	g4063756	BLASTN	663	7e-23	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3648	GM_83_A2_C05_MR	g1769898	BLASTX	504	2e-47	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3649	GM_83_A2_C11_MR	g1480927	BLASTN	644	2e-22	83	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
3650	GM_83_A2_C12_MR	g2827621	BLASTX	171	9e-18	43	(AL021636) putative protein [Arabidopsis thaliana]
3651	GM_83_A2_D05_MR	g3687234	BLASTX	192	5e-13	53	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
3652	GM_83_A2_D08_MR	g505129	BLASTN	390	1e-10	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
3653	GM_83_A2_D12_MR	g4063760	BLASTX	248	5e-19	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3654	GM_83_A2_E04_T7	g18559	BLASTN	352	6e-09	74	G.max gene for catalase
3655	GM_83_A2_E10_T7	g1742955	BLASTX	233	1e-17	65	(Z71446) CLC-b chloride channel protein [Arabidopsis thaliana]
3656	GM_83_A2_F04_T7	g3142328	BLASTN	1006	1e-38	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3657	GM_83_A2_F10_T7	g3319362	BLASTX	231	3e-17	43	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
3658	GM_83_A2_G02_MR	g3452140	BLASTX	179	4e-13	43	(AJ004901) resistance protein [Glycine max]
3659	GM_83_A2_G05_T7	g3777527	BLASTX	550	5e-51	90	(AF053008) gag-pol polyprotein [Glycine max]
3660	GM_83_A2_G10_MR	g3777527	BLASTX	759	2e-73	93	(AF053008) gag-pol polyprotein [Glycine max]
3661	GM_83_A2_H05_T7	g3777527	BLASTX	492	8e-45	93	(AF053008) gag-pol polyprotein [Glycine max]
3662	GM_83_B1_A08_T7	g18559	BLASTN	796	5e-29	76	G.max gene for catalase
3663	GM_83_B1_B03_MR	g3097320	BLASTN	1076	1e-41	80	Glycine max gene for Bd 30K, complete cds
3664	GM_83_B1_B04_T7	g3777527	BLASTX	515	3e-47	94	(AF053008) gag-pol polyprotein [Glycine max]
3665	GM_83_B1_B06_MR	g507910	BLASTN	612	5e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
3666	GM_83_B1_B11_MR	g669002	BLASTN	1655	4e-69	97	Glycine max calnexin mRNA, complete cds.
3667	GM_83_B1_B12_T7	g3176806	BLASTN	478	2e-15	65	Homo sapiens allele 17 fragile site locus (FRA10B) minisatellite, 5' sequence
3668	GM_83_B1_C11_MR	g507910	BLASTN	348	4e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
3669	GM_83_B1_C11_T7	g507910	BLASTN	352	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
3670	GM_83_B1_D08_T7	g1710587	BLASTX	172	8e-23	87	60S ACIDIC RIBOSOMAL PROTEIN P0 gi 1196897 (L46848) acidic ribosomal protein P0 [Glycine max]
3671	GM_83_B1_D09_MR	g3097320	BLASTN	791	9e-29	75	Glycine max gene for Bd 30K, complete cds
3672	GM_83_B1_D12_T7	g1769899	BLASTX	265	4e-22	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3673	GM_83_B1_F06_MR	g3695395	BLASTX	158	1e-09	35	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]

3674	GM_83_B1_F07_MR	g20886	BLASTN	446	3e-13	64	Pea S2 organ specific gene
3675	GM_83_B1_G02_MR	g2129618	BLASTX	181	6e-12	32	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3676	GM_83_B1_G04_T7	g2656024	BLASTN	378	5e-10	71	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6
3677	GM_83_B1_G11_T7	g18559	BLASTN	865	3e-32	78	G.max gene for catalase
3678	GM_83_B1_H03_MR	g3097320	BLASTN	1103	6e-43	82	Glycine max gene for Bd 30K, complete cds
3679	GM_83_B1_H08_T7	g2815075	BLASTN	393	1e-10	62	Caenorhabditis elegans cosmid Y38H8A, complete sequence [Caenorhabditis elegans]
3680	GM_83_B1_H12_MR	g3283026	BLASTX	211	2e-15	39	putative transposase [Arabidopsis thaliana]
3681	GM_83_B2_A01_MR	g4063756	BLASTN	389	1e-10	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3682	GM_83_B2_A02_MR	g4063760	BLASTX	174	4e-11	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3683	GM_83_B2_A06_MR	g226407	BLASTX	268	5e-21	38	retrotransposon del1-46 [Lilium henryi]
3684	GM_83_B2_A06_T7	g1769899	BLASTX	256	3e-21	67	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3685	GM_83_B2_A08_MR	g507910	BLASTN	478	5e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3686	GM_83_B2_A08_T7	g507910	BLASTN	600	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3687	GM_83_B2_A11_T7	g3142328	BLASTN	903	6e-34	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3688	GM_83_B2_B01_MR	g507910	BLASTN	427	1e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
3689	GM_83_B2_B03_T7	g3426334	BLASTN	574	6e-19	63	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
3690	GM_83_B2_B07_T7	g3033389	BLASTX	161	7e-10	36	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
3691	GM_83_B2_B08_T7	g3097320	BLASTN	353	6e-09	73	Glycine max gene for Bd 30K, complete cds
3692	GM_83_B2_B09_MR	g2462936	BLASTX	181	3e-26	51	(Y12321) open reading frame 2 [Brassica oleracea]
3693	GM_83_B2_B09_T7	g3335357	BLASTX	212	8e-24	70	(AC003028) putative diphenol oxidase [Arabidopsis thaliana]
3694	GM_83_B2_C01_T7	g3461840	BLASTX	228	1e-16	40	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
3695	GM_83_B2_C05_T7	g3810596	BLASTX	238	5e-18	34	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3696	GM_83_B2_C11_T7	g99726	BLASTX	102	7e-12	42	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976) orf 3 [Arabidopsis thaliana]
3697	GM_83_B2_D08_MR	g2160155	BLASTN	340	2e-18	67	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
3698	GM_83_B2_D12_T7	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3699	GM_83_B2_E04_MR	g4006831	BLASTX	206	2e-14	35	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
3700	GM_83_B2_E04_T7	g2995405	BLASTX	228	5e-17	35	(Y12432) polyprotein [Ananas comosus]
3701	GM_83_B2_E06_MR	g1480927	BLASTN	1007	4e-39	84	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
3702	GM_83_B2_E12_T7	g18559	BLASTN	860	6e-32	76	G.max gene for catalase
3703	GM_83_B2_F06_MR	g3645899	BLASTX	342	4e-29	49	(U68408) 5' end not determined experimentally [Zea mays]

3704	GM_83_B2_G01_T7	g2341032	BLASTX	207	5e-15	61	(AC000104) EST gb ATTS0956 comes from this gene. [Arabidopsis thaliana]
3705	GM_83_B2_G03_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3706	GM_83_B2_G04_MR	g507910	BLASTN	621	2e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3707	GM_83_B2_G12_T7	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
3708	GM_83_B2_H03_MR	g18559	BLASTN	819	4e-30	71	G.max gene for catalase
3709	GM_83_B2_H07_T7	g3395436	BLASTX	218	2e-17	49	(AC004683) unknown protein [Arabidopsis thaliana]
3710	GM_83_B2_H09_T7	g3097320	BLASTN	472	2e-14	75	Glycine max gene for Bd 30K, complete cds
3711	GM_83_B2_H12_T7	g3928116	BLASTN	400	5e-11	67	, complete sequence [Homo sapiens]
3712	GM_84_A1_A02_T7	g3777527	BLASTX	693	3e-66	92	(AF053008) gag-pol polyprotein [Glycine max]
3713	GM_84_A1_A03_T7	g2997694	BLASTX	254	5e-21	38	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
3714	GM_84_A1_A08_MR	g3142328	BLASTN	972	4e-37	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3715	GM_84_A1_A09_MR	g2995405	BLASTX	401	1e-35	62	(Y12432) polyprotein [Ananas comosus]
3716	GM_84_A1_A10_T7	g3513725	BLASTN	437	1e-12	77	Arabidopsis thaliana BAC F8M12
3717	GM_84_A1_A11_T7	g3810596	BLASTX	118	4e-10	53	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3718	GM_84_A1_C04_T7	g345511	BLASTX	325	2e-27	44	retrovirus-related copia polyprotein - fruit fly (Drosophila simulans) (fragments)
3719	GM_84_A1_D03_T7	g3810596	BLASTX	202	5e-19	57	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3720	GM_84_A1_D10_MR	g130582	BLASTX	357	1e-30	44	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
3721	GM_84_A1_D10_T7	g1707019	BLASTX	290	7e-25	58	(U78721) hypothetical protein [Arabidopsis thaliana]
3722	GM_84_A1_E01_T7	g18559	BLASTN	1127	4e-44	76	G.max gene for catalase
3723	GM_84_A1_E07_T7	g4063760	BLASTX	214	2e-15	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3724	GM_84_A1_E08_MR	g3859610	BLASTN	537	3e-17	65	Arabidopsis thaliana BAC T9E19
3725	GM_84_A1_E10_T7	g508826	BLASTN	259	4e-11	70	Drosophila melanogaster Oregon-R mitochondrial A+T region.
3726	GM_84_A1_E11_T7	g3204134	BLASTX	201	3e-14	70	(AJ006771) beta-galactosidase [Cicer arietinum]
3727	GM_84_A1_F01_MR	g1666236	BLASTX	202	3e-15	32	(U76261) unknown [Hordeum vulgare]
3728	GM_84_A1_F01_T7	g3777527	BLASTX	257	8e-20	41	(AF053008) gag-pol polyprotein [Glycine max]
3729	GM_84_A1_F05_MR	g1184075	BLASTX	304	5e-25	43	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
3730	GM_84_A1_F06_T7	g905361	BLASTX	704	1e-68	95	(U22103) gag-protease polyprotein [Glycine max]
3731	GM_84_A1_F07_T7	g2522228	BLASTX	155	9e-10	34	(AB007466) reverse transcriptase-like protein [Vicia faba]
3732	GM_84_A1_F08_MR	g3193314	BLASTX	248	1e-19	61	(AF069299) contains similarity to Arabidopsis scarecrow (GB:U62798) [Arabidopsis thaliana]

3733	GM_84_A1_F08_T7	g2522230	BLASTX	218	3e-17	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
3734	GM_84_A1_F10_MR	g905361	BLASTX	383	4e-34	94	(U22103) gag-protease polyprotein [Glycine max]
3735	GM_84_A1_G03_T7	g4063760	BLASTX	533	2e-49	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3736	GM_84_A1_G07_T7	g3142328	BLASTN	998	3e-38	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3737	GM_84_A1_G09_MR	g1633043	BLASTN	603	2e-20	76	Lupinus angustifolius conglutin gamma gene, complete cds
3738	GM_84_A1_G10_MR	g3142328	BLASTN	794	5e-29	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3739	GM_84_A1_H01_T7	g18559	BLASTN	382	3e-10	70	G.max gene for catalase
3740	GM_84_A1_H08_T7	g18559	BLASTN	399	5e-11	78	G.max gene for catalase
3741	GM_84_A1_H09_MR	g507910	BLASTN	361	1e-09	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3742	GM_84_A1_H09_T7	g3142328	BLASTN	1114	2e-43	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3743	GM_84_A1_H12_T7	g3142328	BLASTN	991	6e-38	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3744	GM_84_A2_A01_T7	g226407	BLASTX	196	2e-13	37	retrotransposon del1-46 [Lilium henryi]
3745	GM_84_A2_A04_MR	g3097320	BLASTN	430	2e-12	72	Glycine max gene for Bd 30K, complete cds
3746	GM_84_A2_A05_MR	g3243214	BLASTN	384	3e-10	67	Arabidopsis thaliana BAC T19B17 from chromsome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]
3747	GM_84_A2_A05_T7	g507910	BLASTN	545	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
3748	GM_84_A2_A10_MR	g1272349	BLASTX	188	3e-13	53	(U51740) secreted glycoprotein 3 [Ipomoea trifida]
3749	GM_84_A2_A11_T7	g99729	BLASTX	127	5e-12	47	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
3750	GM_84_A2_B02_MR	g3645899	BLASTX	206	6e-19	52	(U68408) 5' end not determined experimentally [Zea mays]
3751	GM_84_A2_B06_MR	g2827663	BLASTX	163	3e-10	30	(AL021637) membrane-associated salt-inducible-like protein [Arabidopsis thaliana]
3752	GM_84_A2_B06_T7	g2244839	BLASTX	169	4e-24	52	(Z97337) hypothetical protein [Arabidopsis thaliana]
3753	GM_84_A2_C01_T7	g2129618	BLASTX	200	5e-14	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3754	GM_84_A2_C07_T7	g3599418	BLASTN	353	6e-09	63	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
3755	GM_84_A2_C12_T7	g1778843	BLASTN	429	2e-12	66	Dictyostelium discoideum LimA (limA) mRNA, partial cds
3756	GM_84_A2_D01_MR	g18559	BLASTN	1077	8e-42	75	G.max gene for catalase
3757	GM_84_A2_D08_MR	g2462134	BLASTX	106	1e-12	42	(Y13368) reverse transcriptase [Beta vulgaris]
3758	GM_84_A2_E01_MR	g4063760	BLASTX	420	4e-43	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3759	GM_84_A2_E01_T7	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3760	GM_84_A2_E02_T7	g3777527	BLASTX	815	2e-79	97	(AF053008) gag-pol polyprotein [Glycine max]

3761	GM_84_A2_E03_MR	g1236920	BLASTN	508	4e-16	64	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
3762	GM_84_A2_E05_MR	g1272349	BLASTX	181	2e-12	55	(U51740) secreted glycoprotein 3 [Ipomoea trifida]
3763	GM_84_A2_E07_T7	g3777527	BLASTX	257	9e-20	52	(AF053008) gag-pol polyprotein [Glycine max]
3764	GM_84_A2_F03_MR	g2760839	BLASTX	195	1e-13	35	(AC003105) putative receptor kinase [Arabidopsis thaliana]
3765	GM_84_A2_F04_T7	g122106	BLASTX	289	9e-25	93	HISTONE H4 gi 70771 pir HSZM4 histone H4 - maize gi 81642 pir S06904 histone H4 - Arabidopsis thaliana gi 2119028 pir S60475 histone H4 - garden pea gi 21795 (X00043) histone H4 [Triticum aestivum] gi 166740 (M17132) histone H4 [Arabidopsis thaliana] gi 166742 (M17133) histone H4 [Arabidopsis thaliana] gi 168499 (M36659) histone H4 (H4C13) [Zea mays] gi 168501 (M13370) histone H4 [Zea mays] gi 168503 (M13377) histone H4 [Zea mays] gi 498898 (U10042) histone H4 homolog [Pisum sativum] gi 1806285 gnl PID e263432 (Z79638) histone H4 homologue [Sesbania rostrata] gi 225838 prf 1314298A histone H4 [Arabidopsis thaliana]
3766	GM_84_A2_F07_T7	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3767	GM_84_A2_F09_MR	g3097320	BLASTN	438	9e-13	70	Glycine max gene for Bd 30K, complete cds
3768	GM_84_A2_F09_T7	g3451069	BLASTX	192	4e-13	63	(AL031326) hypothetical protein [Arabidopsis thaliana]
3769	GM_84_A2_F11_T7	g3777527	BLASTX	184	9e-15	40	(AF053008) gag-pol polyprotein [Glycine max]
3770	GM_84_A2_G03_MR	g2129618	BLASTX	227	7e-17	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3771	GM_84_A2_G08_MR	g3845108	BLASTN	386	2e-10	63	Plasmodium falciparum chromosome 2, section 13 of 73 of the complete sequence
3772	GM_84_A2_H02_T7	g2618603	BLASTN	545	1e-17	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]
3773	GM_84_A2_H06_MR	g3142328	BLASTN	978	2e-37	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3774	GM_84_A2_H09_MR	g507910	BLASTN	355	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3775	GM_84_A2_H09_T7	g3777527	BLASTX	573	2e-53	92	(AF053008) gag-pol polyprotein [Glycine max]
3776	GM_84_A2_H10_MR	g3142328	BLASTN	380	3e-10	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3777	GM_84_B1_A01_MR	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3778	GM_84_B1_A01_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3779	GM_84_B1_A06_MR	g3097320	BLASTN	604	3e-20	76	Glycine max gene for Bd 30K, complete cds
3780	GM_84_B1_A08_MR	g3335331	BLASTN	303	4e-09	84	Arabidopsis thaliana chromosome 1 BAC T8F5 sequence, complete sequence [Arabidopsis thaliana]
3781	GM_84_B1_A08_T7	g3894193	BLASTX	219	7e-17	37	(AC005662) putative strictosidine synthase [Arabidopsis thaliana]

3782	GM_84_B1_A09_T7	g343760	BLASTN	250	3e-11	73	Yeast mitochondrial oxi3 gene, 3' end, ATPase subunit 3 (aap1) and ATPase subunit 6 (oli2) gene, complete cds.
3783	GM_84_B1_A10_MR	g1142701	BLASTN	1132	8e-45	82	Glycine max satellite STR120-A.3.
3784	GM_84_B1_A11_T7	g18559	BLASTN	401	4e-11	66	G.max gene for catalase
3785	GM_84_B1_B01_MR	g2443320	BLASTX	389	6e-34	49	(D85597) polyprotein [Oryza australiensis]
3786	GM_84_B1_B01_T7	g3097320	BLASTN	944	1e-35	73	Glycine max gene for Bd 30K, complete cds
3787	GM_84_B1_B03_T7	g3097320	BLASTN	492	3e-15	70	Glycine max gene for Bd 30K, complete cds
3788	GM_84_B1_B06_MR	g3426334	BLASTN	485	6e-15	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
3789	GM_84_B1_B08_MR	g3068582	BLASTN	357	4e-09	61	Dictyostelium discoideum plasmid Ddp5, complete genome
3790	GM_84_B1_B08_T7	g99801	BLASTX	230	1e-17	61	chaperonine 60K alpha chain - rape plastid (fragment)
3791	GM_84_B1_B10_T7	g3777527	BLASTX	244	2e-18	42	(AF053008) gag-pol polyprotein [Glycine max]
3792	GM_84_B1_C01_MR	g18559	BLASTN	553	5e-18	73	G.max gene for catalase
3793	GM_84_B1_C04_MR	g629693	BLASTX	178	2e-12	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
3794	GM_84_B1_C07_MR	g18695	BLASTN	421	4e-12	85	Soybean nodulin 22 gene
3795	GM_84_B1_C10_T7	g3142328	BLASTN	648	2e-22	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3796	GM_84_B1_D01_MR	g1871180	BLASTX	226	4e-18	76	(U90439) unknown protein [Arabidopsis thaliana]
3797	GM_84_B1_D02_MR	g3645899	BLASTX	398	4e-35	50	(U68408) 5' end not determined experimentally [Zea mays]
3798	GM_84_B1_D03_T7	g18768	BLASTN	517	5e-17	73	Soybean Tgm6 transposable element 3' end
3799	GM_84_B1_D05_MR	g1770192	BLASTX	138	2e-29	70	(X98357) NADP-malate dehydrogenase [Chlamydomonas reinhardtii]
3800	GM_84_B1_D07_T7	g18559	BLASTN	1026	2e-39	73	G.max gene for catalase
3801	GM_84_B1_D10_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
3802	GM_84_B1_D10_T7	g507910	BLASTN	376	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
3803	GM_84_B1_D11_MR	g2995405	BLASTX	284	5e-23	45	(Y12432) polyprotein [Ananas comosus]
3804	GM_84_B1_E02_MR	g3413707	BLASTX	344	7e-34	73	(AC004747) hypothetical protein [Arabidopsis thaliana]
3805	GM_84_B1_E05_T7	g2832245	BLASTX	138	1e-08	32	(AF031569) hypothetical protein [Zea mays]
3806	GM_84_B1_E06_T7	g3142328	BLASTN	923	7e-35	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3807	GM_84_B1_E07_MR	g2780194	BLASTX	166	5e-11	44	(AJ003197) adenine nucleotide translocator [Lupinus albus]
3808	GM_84_B1_E07_T7	g2827662	BLASTX	247	3e-19	48	(AL021637) Phosphoribosylanthranilate transferase [Arabidopsis thaliana]
3809	GM_84_B1_E11_MR	g2264306	BLASTN	349	1e-08	60	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBK5, complete sequence [Arabidopsis thaliana]
3810	GM_84_B1_E11_T7	g2586082	BLASTX	202	5e-14	43	(U72725) retrofit [Oryza longistaminata]
3811	GM_84_B1_E12_T7	g3152594	BLASTX	189	3e-13	42	(AC002986) Contains repeats similar to RECA protein gb L26100 from Acinetobacter calcoaceticus. [Arabidopsis thaliana]
3812	GM_84_B1_F01_MR	g905361	BLASTX	424	9e-39	95	(U22103) gag-protease polyprotein [Glycine max]

3813	GM_84_B1_F02_MR	g1769898	BLASTX	303	2e-25	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3814	GM_84_B1_F02_T7	g2522227	BLASTX	180	5e-13	60	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
3815	GM_84_B1_F05_T7	g13617	BLASTN	403	3e-11	61	S.douglasii gene for cytochrome b
3816	GM_84_B1_F08_MR	g507910	BLASTN	443	2e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3817	GM_84_B1_F08_T7	g507910	BLASTN	367	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
3818	GM_84_B1_F09_T7	g2245044	BLASTX	121	2e-13	34	(Z97342) similarity to reverse transcriptase - Arabidopsis thaliana retrotransposon 2 (fragment) [Arabidopsis thaliana]
3819	GM_84_B1_G01_MR	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3820	GM_84_B1_G01_T7	g507910	BLASTN	404	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3821	GM_84_B1_G02_MR	g99922	BLASTX	577	3e-55	71	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
3822	GM_84_B1_G02_T7	g2995405	BLASTX	198	9e-21	41	(Y12432) polyprotein [Ananas comosus]
3823	GM_84_B1_G03_MR	g1431738	BLASTN	713	2e-25	76	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
3824	GM_84_B1_G04_MR	g507910	BLASTN	384	9e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3825	GM_84_B1_G07_MR	g3142328	BLASTN	1066	2e-41	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3826	GM_84_B1_G08_MR	g18559	BLASTN	349	9e-09	71	G.max gene for catalase
3827	GM_84_B1_G10_MR	g2443320	BLASTX	366	2e-31	55	(D85597) polyprotein [Oryza australiensis]
3828	GM_84_B1_H01_MR	g99755	BLASTX	339	2e-29	46	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
3829	GM_84_B1_H06_MR	g12628	BLASTN	417	5e-12	62	Aedes albopictus mit-gene for large ribosomal subunit RNA (LSU)
3830	GM_84_B1_H09_MR	g170080	BLASTN	355	4e-09	63	Soybean seed lectin gene transposable element tgm1.
3831	GM_84_B1_H10_T7	g3522933	BLASTX	169	1e-11	78	(AC004411) putative anion exchange protein 3 [Arabidopsis thaliana]
3832	GM_84_B1_H12_MR	g2462134	BLASTX	243	4e-19	35	(Y13368) reverse transcriptase [Beta vulgaris]
3833	GM_84_B2_A01_MR	g3645899	BLASTX	215	8e-25	51	(U68408) 5' end not determined experimentally [Zea mays]
3834	GM_84_B2_A03_MR	g18559	BLASTN	472	2e-14	67	G.max gene for catalase
3835	GM_84_B2_A03_T7	g3845197	BLASTN	424	4e-12	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
3836	GM_84_B2_A05_MR	g3142328	BLASTN	660	7e-23	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3837	GM_84_B2_B01_T7	g2995405	BLASTX	289	3e-30	71	(Y12432) polyprotein [Ananas comosus]
3838	GM_84_B2_B03_T7	g3688808	BLASTX	148	9e-09	52	(AF084104) AcsA [Bacillus firmus]
3839	GM_84_B2_B04_T7	g2443320	BLASTX	362	4e-31	49	(D85597) polyprotein [Oryza australiensis]
3840	GM_84_B2_B05_MR	g3264544	BLASTN	420	6e-12	62	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]

3841	GM_84_B2_B06_MR	g1666236	BLASTX	207	7e-16	36	(U76261) unknown [Hordeum vulgare]
3842	GM_84_B2_B07_MR	g4063760	BLASTX	388	6e-34	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3843	GM_84_B2_B08_MR	g18695	BLASTN	545	7e-18	70	Soybean nodulin 22 gene
3844	GM_84_B2_B08_T7	g2245109	BLASTX	162	7e-16	88	(Z97343) carboxyl-terminal proteinase homolog [Arabidopsis thaliana]
3845	GM_84_B2_B12_MR	g2995405	BLASTX	415	4e-37	57	(Y12432) polyprotein [Ananas comosus]
3846	GM_84_B2_C06_T7	g467491	BLASTN	397	1e-11	69	Chlorella vulgaris genomic DNA, telomeric repeat
3847	GM_84_B2_C08_T7	g18559	BLASTN	1017	4e-39	76	G.max gene for catalase
3848	GM_84_B2_C09_MR	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
3849	GM_84_B2_C09_T7	g905361	BLASTX	669	5e-65	94	(U22103) gag-protease polyprotein [Glycine max]
3850	GM_84_B2_C11_T7	g3319362	BLASTX	167	1e-19	52	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
3851	GM_84_B2_C12_MR	g100484	BLASTX	227	5e-17	48	hypothetical protein - garden snapdragon
3852	GM_84_B2_D02_T7	g99726	BLASTX	115	1e-16	50	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976) orf 3 [Arabidopsis thaliana]
3853	GM_84_B2_D08_MR	g905361	BLASTX	353	8e-31	96	(U22103) gag-protease polyprotein [Glycine max]
3854	GM_84_B2_D12_T7	g1666236	BLASTX	199	7e-15	33	(U76261) unknown [Hordeum vulgare]
3855	GM_84_B2_E01_T7	g507910	BLASTN	362	9e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3856	GM_84_B2_E02_MR	g3650039	BLASTX	241	1e-18	38	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
3857	GM_84_B2_E03_MR	g1769898	BLASTX	394	2e-35	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3858	GM_84_B2_E03_T7	g3777527	BLASTX	353	5e-30	50	(AF053008) gag-pol polyprotein [Glycine max]
3859	GM_84_B2_E05_T7	g3142328	BLASTN	970	5e-37	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3860	GM_84_B2_E09_T7	g2764526	BLASTN	673	2e-23	66	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
3861	GM_84_B2_E10_MR	g4063760	BLASTX	406	8e-36	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3862	GM_84_B2_E11_T7	g2129618	BLASTX	176	2e-11	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3863	GM_84_B2_E12_MR	g18559	BLASTN	952	4e-36	75	G.max gene for catalase
3864	GM_84_B2_F12_MR	g3142328	BLASTN	782	2e-28	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3865	GM_84_B2_G01_MR	g4063760	BLASTX	296	4e-24	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3866	GM_84_B2_G04_MR	g507910	BLASTN	433	6e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3867	GM_84_B2_G04_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3868	GM_84_B2_G08_MR	g1236920	BLASTN	405	2e-11	66	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.

3869	GM_84_B2_G10_MR	g1769899	BLASTX	214	2e-19	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3870	GM_84_B2_G11_T7	g3142330	BLASTX	523	2e-49	86	(U96295) envelope-like [Glycine max]
3871	GM_84_B2_H12_T7	g170029	BLASTN	380	4e-10	79	Glycine max cv. Dare nodulin 26 gene fragment.
3872	GM_85_A1_A05_MR	g3142330	BLASTX	580	1e-55	83	(U96295) envelope-like [Glycine max]
3873	GM_85_A1_A09_T7	g2995405	BLASTX	265	5e-21	46	(Y12432) polyprotein [Ananas comosus]
3874	GM_85_A1_A12_MR	g4063760	BLASTX	194	3e-13	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3875	GM_85_A1_B03_MR	g4063760	BLASTX	300	1e-24	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3876	GM_85_A1_B04_MR	g1039432	BLASTN	432	1e-12	65	Glycine max cellulase gene, partial cds.
3877	GM_85_A1_B04_T7	g2182286	BLASTN	353	7e-09	61	Sequence of BAC F20P5 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
3878	GM_85_A1_B05_MR	g2522228	BLASTX	215	7e-34	63	(AB007466) reverse transcriptase-like protein [Vicia faba]
3879	GM_85_A1_B06_MR	g505129	BLASTN	384	2e-10	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
3880	GM_85_A1_B07_MR	g2335067	BLASTN	317	2e-09	63	Human BAC clone GS200K05 from 7q21-q22, complete sequence [Homo sapiens]
3881	GM_85_A1_B08_MR	g3660471	BLASTX	167	1e-10	84	(AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]
3882	GM_85_A1_B09_T7	g1236920	BLASTN	368	1e-09	62	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
3883	GM_85_A1_B11_T7	g531389	BLASTX	145	4e-09	41	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
3884	GM_85_A1_B12_T7	g1616609	BLASTX	248	2e-20	55	(Y08641) PR10-1 protein [Medicago truncatula]
3885	GM_85_A1_C01_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3886	GM_85_A1_C01_T7	g507910	BLASTN	403	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3887	GM_85_A1_C03_MR	g4063760	BLASTX	165	4e-19	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3888	GM_85_A1_C03_T7	g1480927	BLASTN	473	2e-14	73	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
3889	GM_85_A1_C05_MR	g2244855	BLASTX	194	8e-18	58	(Z97337) hypothetical protein [Arabidopsis thaliana]
3890	GM_85_A1_C06_MR	g4063760	BLASTX	425	7e-38	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3891	GM_85_A1_C06_T7	g507910	BLASTN	565	6e-19	79	Glycine max BSR-101 satellite SB92 genomic sequence.
3892	GM_85_A1_C11_MR	g3176659	BLASTX	209	4e-15	62	(AC004393) Strong similarity to receptor kinase gb M80238 from A. thaliana. [Arabidopsis thaliana]
3893	GM_85_A1_D01_MR	g18559	BLASTN	621	8e-31	77	G.max gene for catalase
3894	GM_85_A1_D03_MR	g3650035	BLASTX	165	3e-10	36	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
3895	GM_85_A1_D04_MR	g100484	BLASTX	211	6e-31	54	hypothetical protein - garden snapdragon
3896	GM_85_A1_D04_T7	g99922	BLASTX	435	3e-40	63	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
3897	GM_85_A1_D08_T7	g1468969	BLASTX	104	3e-09	52	(D30666) brain acyl-CoA synthtase II [Rattus norvegicus]

3898	GM_85_A1_D12_MR	g507910	BLASTN	594	3e-20	84	Glycine max BSR-101 satellite SB92 genomic sequence.
3899	GM_85_A1_E01_T7	g4063760	BLASTX	260	1e-21	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3900	GM_85_A1_E02_T7	g18693	BLASTN	455	1e-14	66	Soybean mRNA for Nodulin-21.
3901	GM_85_A1_E04_MR	g3241926	BLASTN	577	5e-19	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSG15, complete sequence [Arabidopsis thaliana]
3902	GM_85_A1_E05_T7	g3513451	BLASTX	135	3e-09	58	(U78090) potassium channel regulator 1 [Rattus norvegicus]
3903	GM_85_A1_E07_MR	g4063760	BLASTX	516	1e-47	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3904	GM_85_A1_E09_MR	g2462744	BLASTX	134	1e-09	36	(AC002292) Hypothetical protein [Arabidopsis thaliana]
3905	GM_85_A1_E12_MR	g18559	BLASTN	1037	5e-40	76	G.max gene for catalase
3906	GM_85_A1_F01_MR	g1142703	BLASTN	295	7e-17	77	Glycine max satellite STR120-B.1.
3907	GM_85_A1_F03_MR	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3908	GM_85_A1_F04_MR	g99922	BLASTX	236	4e-19	65	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
3909	GM_85_A1_G04_MR	g2129472	BLASTX	123	3e-13	72	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) precursor - Scotch pine gi 1100225 (L32561) glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
3910	GM_85_A1_G04_T7	g3810596	BLASTX	359	5e-31	49	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3911	GM_85_A1_G10_T7	g2443320	BLASTX	154	6e-09	32	(D85597) polyprotein [Oryza australiensis]
3912	GM_85_A1_H01_T7	g4092471	BLASTN	540	2e-17	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
3913	GM_85_A1_H05_MR	g3599418	BLASTN	366	1e-09	74	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
3914	GM_85_A1_H07_T7	g3097320	BLASTN	451	2e-13	70	Glycine max gene for Bd 30K, complete cds
3915	GM_85_A1_H08_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3916	GM_85_A1_H10_T7	g1778105	BLASTX	269	1e-22	81	(U64893) expansin [Pinus taeda]
3917	GM_85_A2_A04_MR	g3097320	BLASTN	379	4e-10	71	Glycine max gene for Bd 30K, complete cds
3918	GM_85_A2_A05_MR	g1142701	BLASTN	1301	2e-52	85	Glycine max satellite STR120-A.3.
3919	GM_85_A2_A06_MR	g3746069	BLASTX	118	4e-10	38	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
3920	GM_85_A2_A07_MR	g3097320	BLASTN	1075	1e-41	79	Glycine max gene for Bd 30K, complete cds
3921	GM_85_A2_A10_T7	g1167523	BLASTX	270	3e-21	41	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
3922	GM_85_A2_B03_T7	g1666236	BLASTX	104	1e-12	46	(U76261) unknown [Hordeum vulgare]
3923	GM_85_A2_B04_MR	g507910	BLASTN	398	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3924	GM_85_A2_B04_T7	g4063760	BLASTX	269	3e-21	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3925	GM_85_A2_B05_MR	g2708743	BLASTX	183	5e-12	30	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
3926	GM_85_A2_B05_T7	g3021268	BLASTX	191	9e-24	45	(AL022347) putative protein [Arabidopsis thaliana]
3927	GM_85_A2_B06_T7	g2443320	BLASTX	193	4e-13	36	(D85597) polyprotein [Oryza australiensis]
3928	GM_85_A2_C07_T7	g3510505	BLASTX	161	3e-15	45	(AF030881) pol polyprotein [Fugu rubripes]
3929	GM_85_A2_C08_MR	g1666236	BLASTX	109	7e-14	33	(U76261) unknown [Hordeum vulgare]

3930	GM_85_A2_C09_MR	g2842482	BLASTX	188	4e-14	57	(AL021749) protein phosphatase 2C-like protein [Arabidopsis thaliana]
3931	GM_85_A2_C10_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3932	GM_85_A2_C10_T7	g4063760	BLASTX	237	8e-18	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3933	GM_85_A2_C12_MR	g2842482	BLASTX	195	9e-15	58	(AL021749) protein phosphatase 2C-like protein [Arabidopsis thaliana]
3934	GM_85_A2_D02_T7	g2190263	BLASTX	101	1e-11	58	(D86387) A-type cyclin [Catharanthus roseus]
3935	GM_85_A2_D03_T7	g507910	BLASTN	401	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
3936	GM_85_A2_D05_MR	g3047060	BLASTN	371	2e-10	67	Arabidopsis thaliana BAC F7N22
3937	GM_85_A2_D05_T7	g3810596	BLASTX	151	9e-09	36	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3938	GM_85_A2_D07_MR	g3378649	BLASTN	352	4e-09	74	M.sativa mRNA translated from abscisic activated gene
3939	GM_85_A2_D07_T7	g857393	BLASTX	111	2e-11	48	(D50868) mitotic cyclin a1-type [Glycine max]
3940	GM_85_A2_D09_T7	g2443320	BLASTX	204	3e-14	51	(D85597) polyprotein [Oryza australiensis]
3941	GM_85_A2_D10_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
3942	GM_85_A2_D12_MR	g170606	BLASTN	743	4e-27	66	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
3943	GM_85_A2_E01_MR	g2462936	BLASTX	361	2e-32	49	(Y12321) open reading frame 2 [Brassica oleracea]
3944	GM_85_A2_E02_MR	g4063760	BLASTX	256	7e-20	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3945	GM_85_A2_E02_T7	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
3946	GM_85_A2_E08_MR	g4063760	BLASTX	494	3e-45	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3947	GM_85_A2_E08_T7	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
3948	GM_85_A2_E09_MR	g2429543	BLASTX	163	6e-10	37	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]
3949	GM_85_A2_E11_MR	g2443320	BLASTX	296	5e-24	49	(D85597) polyprotein [Oryza australiensis]
3950	GM_85_A2_E12_MR	g3777526	BLASTN	508	6e-16	87	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
3951	GM_85_A2_F02_MR	g2129618	BLASTX	170	8e-11	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3952	GM_85_A2_F03_T7	g4033838	BLASTX	286	4e-28	70	(Y18550) sigma-like factor [Arabidopsis thaliana]
3953	GM_85_A2_F05_MR	g2129618	BLASTX	182	4e-12	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3954	GM_85_A2_F05_T7	g18559	BLASTN	840	5e-31	75	G.max gene for catalase
3955	GM_85_A2_F08_MR	g2924781	BLASTX	146	7e-16	45	(AC002334) putative cellulose synthase [Arabidopsis thaliana]
3956	GM_85_A2_F09_MR	g3845084	BLASTN	362	3e-09	65	Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence
3957	GM_85_A2_G03_MR	g3142328	BLASTN	805	2e-29	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3958	GM_85_A2_G07_MR	g507910	BLASTN	344	6e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.

3959	GM_85_A2_H02_MR	g3763850	BLASTN	640	6e-22	66	Glycine max GmENOD93 gene for early nodulin, complete cds
3960	GM_85_A2_H03_MR	g3142328	BLASTN	1243	2e-49	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3961	GM_85_A2_H08_MR	g18559	BLASTN	814	7e-30	72	G.max gene for catalase
3962	GM_85_A2_H09_MR	g18559	BLASTN	823	3e-30	75	G.max gene for catalase
3963	GM_85_B1_A04_MR	g2464905	BLASTX	197	5e-15	53	(Z99708) minor allergen [Arabidopsis thaliana]
3964	GM_85_B1_A08_T7	g100484	BLASTX	365	6e-32	53	hypothetical protein - garden snapdragon
3965	GM_85_B1_B02_T7	g507910	BLASTN	376	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
3966	GM_85_B1_C01_T7	g2129618	BLASTX	154	4e-09	37	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3967	GM_85_B1_C02_T7	g3142328	BLASTN	619	5e-21	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3968	GM_85_B1_C07_MR	g3645899	BLASTX	389	4e-34	56	(U68408) 5' end not determined experimentally [Zea mays]
3969	GM_85_B1_E01_T7	g2522228	BLASTX	193	3e-16	50	(AB007466) reverse transcriptase-like protein [Vicia faba]
3970	GM_85_B1_E05_T7	g3777526	BLASTN	448	3e-13	91	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
3971	GM_85_B1_E06_MR	g1769898	BLASTX	153	1e-16	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
3972	GM_85_B1_F09_T7	g4063756	BLASTN	482	1e-14	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3973	GM_85_B1_G03_T7	g3080532	BLASTX	111	2e-11	64	(AL022600) hypothetical protein [Schizosaccharomyces pombe]
3974	GM_85_B1_G05_MR	g4038056	BLASTX	321	5e-27	48	(AC005897) putative transposon [Arabidopsis thaliana]
3975	GM_85_B1_G06_MR	g3386614	BLASTX	146	1e-09	77	(AC004665) putative transcription factor SF3 [Arabidopsis thaliana]
3976	GM_85_B1_G10_MR	g4006831	BLASTX	191	6e-13	40	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
3977	GM_85_B1_G11_MR	g3319366	BLASTX	104	2e-09	41	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
3978	GM_85_B1_H12_T7	g2190544	BLASTX	148	4e-09	84	(AC001229) Similar to Saccharomyces hypothetical protein P9642.2 (gb U40828). [Arabidopsis thaliana]
3979	GM_85_B2_A04_MR	g18559	BLASTN	675	5e-36	79	G.max gene for catalase
3980	GM_85_B2_A07_MR	g1171583	BLASTN	354	6e-09	61	P.falciparum complete gene map of plastid-like DNA (IR-A)
3981	GM_85_B2_A12_MR	g2462756	BLASTX	184	2e-12	67	(AC002292) putative receptor kinase [Arabidopsis thaliana]
3982	GM_85_B2_A12_T7	g3777527	BLASTX	699	6e-67	90	(AF053008) gag-pol polyprotein [Glycine max]
3983	GM_85_B2_B04_MR	g3810596	BLASTX	231	2e-17	34	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
3984	GM_85_B2_B05_T7	g3097320	BLASTN	1022	3e-39	78	Glycine max gene for Bd 30K, complete cds
3985	GM_85_B2_B07_T7	g3777527	BLASTX	647	2e-61	87	(AF053008) gag-pol polyprotein [Glycine max]
3986	GM_85_B2_B10_T7	g4063756	BLASTN	559	3e-18	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
3987	GM_85_B2_B11_MR	g2462756	BLASTX	183	2e-12	70	(AC002292) putative receptor kinase [Arabidopsis thaliana]
3988	GM_85_B2_B11_T7	g3777527	BLASTX	753	1e-72	96	(AF053008) gag-pol polyprotein [Glycine max]

3989	GM_85_B2_B12_T7	g3426033	BLASTN	730	6e-26	71	Arabidopsis thaliana chromosome II BAC F12C20 genomic sequence, complete sequence [Arabidopsis thaliana]
3990	GM_85_B2_C06_T7	g3810595	BLASTX	130	3e-16	33	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
3991	GM_85_B2_C12_MR	g4063760	BLASTX	495	2e-45	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3992	GM_85_B2_D01_T7	g3243214	BLASTN	463	7e-14	69	Arabidopsis thaliana BAC T19B17 from chromsome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]
3993	GM_85_B2_D02_T7	g4063760	BLASTX	514	2e-47	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
3994	GM_85_B2_D03_MR	g3142328	BLASTN	1062	4e-41	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
3995	GM_85_B2_D04_T7	g2129618	BLASTX	264	7e-21	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
3996	GM_85_B2_E02_T7	g507910	BLASTN	579	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
3997	GM_85_B2_E03_MR	g905361	BLASTX	153	3e-09	34	(U22103) gag-protease polyprotein [Glycine max]
3998	GM_85_B2_E06_MR	g3695395	BLASTX	250	1e-19	45	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
3999	GM_85_B2_F01_MR	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
4000	GM_85_B2_F01_T7	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4001	GM_85_B2_F05_MR	g3021696	BLASTN	387	2e-10	62	Homo sapiens genomic DNA for centromeric end of MHC class I region on chromosome 6, cosmid clone: TY2F10, complete sequence [Homo sapiens]
4002	GM_85_B2_F08_MR	g886130	BLASTX	304	2e-26	60	(U28148) putative pectinesterase [Medicago sativa]
4003	GM_85_B2_G02_MR	g2367431	BLASTX	395	6e-36	50	(AF000403) putative cytochrome P450 [Lotus japonicus]
4004	GM_85_B2_G05_T7	g2995405	BLASTX	311	6e-26	46	(Y12432) polyprotein [Ananas comosus]
4005	GM_85_B2_G07_MR	g1785729	BLASTN	366	2e-09	62	A.thaliana mitochondrial genome, part B
4006	GM_85_B2_G09_T7	g4063760	BLASTX	382	3e-33	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4007	GM_85_B2_G12_MR	g4079614	BLASTN	592	1e-19	67	Arabidopsis thaliana chromosome I BAC F21M11 genomic sequence, complete sequence [Arabidopsis thaliana]
4008	GM_85_B2_H01_MR	g18559	BLASTN	770	7e-28	72	G.max gene for catalase
4009	GM_85_B2_H03_MR	g1769899	BLASTX	164	2e-11	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4010	GM_85_B2_H04_MR	g3777527	BLASTX	192	7e-13	42	(AF053008) gag-pol polyprotein [Glycine max]
4011	GM_85_B2_H04_T7	g3097320	BLASTN	778	4e-44	82	Glycine max gene for Bd 30K, complete cds
4012	GM_85_B2_H05_MR	g4056485	BLASTX	196	8e-14	48	(AC005896) hypothetical protein [Arabidopsis thaliana]
4013	GM_85_B2_H08_T7	g3097320	BLASTN	453	2e-13	75	Glycine max gene for Bd 30K, complete cds
4014	GM_86_A2_A03_MR	g4063760	BLASTX	142	2e-19	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4015	GM_86_A2_A04_MR	g3142328	BLASTN	700	1e-24	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4016	GM_86_A2_A08_T7	g4063760	BLASTX	158	2e-09	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4017	GM_86_A2_A09_MR	g18559	BLASTN	983	2e-37	75	G.max gene for catalase
4018	GM_86_A2_B03_MR	g3859610	BLASTN	691	3e-24	66	Arabidopsis thaliana BAC T9E19

4019	GM_86_A2_B07_MR	g507910	BLASTN	536	1e-17	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4020	GM_86_A2_B08_MR	g3820757	BLASTN	383	2e-10	60	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
4021	GM_86_A2_C02_T7	g100484	BLASTX	149	7e-15	52	hypothetical protein - garden snapdragon
4022	GM_86_A2_C05_MR	g4063760	BLASTX	292	1e-23	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4023	GM_86_A2_C09_T7	g3377855	BLASTX	233	8e-19	77	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
4024	GM_86_A2_D03_MR	g3810596	BLASTX	183	3e-12	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4025	GM_86_A2_D03_T7	g2281094	BLASTX	167	9e-18	67	(AC002333) molybdenum cofactor biosynthesis protein E isolog [Arabidopsis thaliana]
4026	GM_86_A2_D07_MR	g4050011	BLASTN	427	3e-12	70	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
4027	GM_86_A2_D09_MR	g507910	BLASTN	574	3e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4028	GM_86_A2_D09_T7	g507910	BLASTN	527	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
4029	GM_86_A2_E03_MR	g4056466	BLASTX	155	6e-10	37	(AC005990) F5O8.39 [Arabidopsis thaliana]
4030	GM_86_A2_E08_MR	g507910	BLASTN	403	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
4031	GM_86_A2_E10_T7	g13520	BLASTN	248	5e-11	67	Two yeast mitochondrial genes for transfer RNA.
4032	GM_86_A2_F01_MR	g507910	BLASTN	550	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
4033	GM_86_A2_F01_T7	g4063756	BLASTN	410	2e-11	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
4034	GM_86_A2_F07_MR	g3256035	BLASTX	315	2e-27	54	(Y14274) putative serine/threonine protein kinase [Sorghum bicolor]
4035	GM_86_A2_F11_MR	g3097320	BLASTN	726	8e-26	80	Glycine max gene for Bd 30K, complete cds
4036	GM_86_A2_G01_MR	g2961377	BLASTX	188	1e-12	38	(AL022141) putative receptor protein kinase [Arabidopsis thaliana]
4037	GM_86_A2_G02_T7	g3355478	BLASTX	151	1e-09	37	(AC004218) hypothetical protein [Arabidopsis thaliana]
4038	GM_86_A2_G03_MR	g2995405	BLASTX	556	2e-52	69	(Y12432) polyprotein [Ananas comosus]
4039	GM_86_A2_G04_MR	g4158219	BLASTX	184	3e-13	53	(Y18623) amylogenin [Oryza sativa]
4040	GM_86_A2_G06_MR	g3097320	BLASTN	354	5e-09	72	Glycine max gene for Bd 30K, complete cds
4041	GM_86_A2_G09_MR	g2970554	BLASTN	384	3e-10	65	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
4042	GM_86_A2_H01_MR	g507910	BLASTN	504	4e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
4043	GM_86_A2_H04_MR	g4038056	BLASTX	127	6e-12	43	(AC005897) putative transposon [Arabidopsis thaliana]
4044	GM_86_A2_H06_MR	g3645899	BLASTX	271	2e-21	47	(U68408) 5' end not determined experimentally [Zea mays]
4045	GM_86_A2_H08_MR	g3097320	BLASTN	1128	5e-44	81	Glycine max gene for Bd 30K, complete cds
4046	GM_86_A2_H09_MR	g1769897	BLASTX	237	2e-34	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4047	GM_86_B1_A01_MR	g1518625	BLASTN	362	6e-10	62	Cerataphis freycinetiae cytochrome oxidase I and II gene, mitochondrial genes encoding mitochondrial proteins, partial cds and tRNA-Leu gene, complete sequence
4048	GM_86_B1_A01_T7	g1418331	BLASTX	154	7e-11	46	(X95909) receptor like protein kinase [Arabidopsis thaliana]

4049	GM_86_B1_A06_MR	g505129	BLASTN	360	3e-09	69	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
4050	GM_86_B1_A08_MR	g99922	BLASTX	241	7e-28	75	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
4051	GM_86_B1_A12_MR	g3695395	BLASTX	170	5e-11	43	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
4052	GM_86_B1_B01_MR	g507910	BLASTN	502	4e-16	79	Glycine max BSR-101 satellite SB92 genomic sequence.
4053	GM_86_B1_B04_T7	g507910	BLASTN	527	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
4054	GM_86_B1_B05_MR	g3142330	BLASTX	562	1e-53	93	(U96295) envelope-like [Glycine max]
4055	GM_86_B1_B07_MR	g507910	BLASTN	612	5e-21	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4056	GM_86_B1_C02_T7	g4140712	BLASTX	266	2e-22	63	(AF110183) putative integrase [Oryza sativa]
4057	GM_86_B1_C03_T7	g3777527	BLASTX	713	2e-68	98	(AF053008) gag-pol polyprotein [Glycine max]
4058	GM_86_B1_C05_MR	g226407	BLASTX	471	1e-42	53	retrotransposon del1-46 [Lilium henryi]
4059	GM_86_B1_C06_T7	g170606	BLASTN	425	2e-12	64	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
4060	GM_86_B1_D03_T7	g2443320	BLASTX	171	9e-11	35	(D85597) polyprotein [Oryza australiensis]
4061	GM_86_B1_D05_MR	g3142328	BLASTN	1054	8e-41	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4062	GM_86_B1_D07_MR	g3777527	BLASTX	679	8e-65	84	(AF053008) gag-pol polyprotein [Glycine max]
4063	GM_86_B1_D08_MR	g2522230	BLASTX	247	3e-20	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4064	GM_86_B1_D09_MR	g507910	BLASTN	529	3e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4065	GM_86_B1_D10_MR	g3097320	BLASTN	991	8e-38	79	Glycine max gene for Bd 30K, complete cds
4066	GM_86_B1_D12_MR	g2129618	BLASTX	189	8e-13	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4067	GM_86_B1_E02_MR	g3650039	BLASTX	257	2e-22	50	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
4068	GM_86_B1_E02_T7	g4038056	BLASTX	314	3e-26	54	(AC005897) putative transposon [Arabidopsis thaliana]
4069	GM_86_B1_E03_T7	g3184285	BLASTX	189	1e-15	64	(AC004136) hypothetical protein [Arabidopsis thaliana]
4070	GM_86_B1_F01_T7	g3142328	BLASTN	1783	4e-74	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4071	GM_86_B1_F06_T7	g18559	BLASTN	471	3e-14	67	G.max gene for catalase
4072	GM_86_B1_F07_MR	g226407	BLASTX	299	2e-35	49	retrotransposon del1-46 [Lilium henryi]
4073	GM_86_B1_G01_T7	g3777527	BLASTX	329	2e-27	53	(AF053008) gag-pol polyprotein [Glycine max]
4074	GM_86_B1_G03_MR	g2832245	BLASTX	150	5e-10	31	(AF031569) hypothetical protein [Zea mays]
4075	GM_86_B1_H02_MR	g507910	BLASTN	377	2e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4076	GM_86_B1_H02_T7	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
4077	GM_86_B1_H03_MR	g4063760	BLASTX	218	2e-20	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4078	GM_86_B1_H06_T7	g4063760	BLASTX	218	7e-16	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4079	GM_86_B1_H09_T7	g3142330	BLASTX	676	1e-65	97	(U96295) envelope-like [Glycine max]

4080	GM_86_B1_H11_MR	g2462058	BLASTX	205	1e-24	46	(Y13389) reverse transcriptase [Antirrhinum majus]
4081	GM_86_B2_A02_MR	g3142328	BLASTN	750	5e-27	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4082	GM_86_B2_A03_T7	g2914696	BLASTX	164	1e-10	64	(AC003974) putative purple acid phosphatase [Arabidopsis thaliana]
4083	GM_86_B2_A08_MR	g3097320	BLASTN	487	5e-15	68	Glycine max gene for Bd 30K, complete cds
4084	GM_86_B2_A10_T7	g3777527	BLASTX	312	1e-25	43	(AF053008) gag-pol polyprotein [Glycine max]
4085	GM_86_B2_B04_MR	g1651451	BLASTX	126	1e-18	75	(D90730) Asparagine-tRNA ligase [Escherichia coli]
4086	GM_86_B2_B05_T7	g3097320	BLASTN	483	8e-15	71	Glycine max gene for Bd 30K, complete cds
4087	GM_86_B2_B12_T7	g1142703	BLASTN	271	5e-14	76	Glycine max satellite STR120-B.1.
4088	GM_86_B2_C08_T7	g3193290	BLASTX	175	1e-11	45	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabido...
4089	GM_86_B2_C12_MR	g2832608	BLASTX	160	1e-10	40	(AL021637) leucine rich repeat-like protein (fragment) [Arabidopsis thaliana]
4090	GM_86_B2_D08_MR	g1071924	BLASTX	165	1e-14	50	Kunitz trypsin inhibitor precursor - soybean gi 510515 (X80039) Kunitz trypsin inhibitor [Glycine max]
4091	GM_86_B2_D10_T7	g2245004	BLASTX	225	5e-17	47	(Z97341) similarity to membrane transport protein [Arabidopsis thaliana]
4092	GM_86_B2_E04_MR	g13619	BLASTN	392	1e-11	63	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
4093	GM_86_B2_F03_MR	g226407	BLASTX	270	5e-29	45	retrotransposon del1-46 [Lilium henryi]
4094	GM_86_B2_F10_MR	g18559	BLASTN	896	1e-33	76	G.max gene for catalase
4095	GM_86_B2_G02_MR	g3142328	BLASTN	1237	4e-49	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4096	GM_86_B2_G02_T7	g136251	BLASTX	256	1e-20	73	TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR gi 99767 pir A31393 tryptophan synthase (EC 4.2.1.20) beta chain - Arabidopsis thaliana gi 166892 (M23872) tryptophan synthase beta subunit [Arabidopsis thaliana]
4097	GM_86_B2_G04_T7	g3695403	BLASTX	179	1e-12	72	(AF096373) contains similarity to the pfkB family of carbohydrate kinases (Pfam: PF00294, E=1.6e-75) [Arabidopsis thaliana]
4098	GM_86_B2_G10_MR	g2501460	BLASTX	202	4e-14	52	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) gi 1545952 gnl PID e244584 (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]
4099	GM_86_B2_H05_T7	g3777527	BLASTX	242	8e-22	73	(AF053008) gag-pol polyprotein [Glycine max]

4100	GM_86_B2_H08_MR	g3142328	BLASTN	1261	3e-50	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4101	GM_86_B2_H11_T7	g3746069	BLASTX	164	5e-10	48	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
4102	GM_87_A1_A01_MR	g1480927	BLASTN	713	2e-25	91	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
4103	GM_87_A1_A01_T7	g170029	BLASTN	413	1e-11	87	Glycine max cv. Dare nodulin 26 gene fragment.
4104	GM_87_A1_A04_MR	g505129	BLASTN	364	2e-09	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
4105	GM_87_A1_A04_T7	g2769655	BLASTN	469	4e-14	66	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
4106	GM_87_A1_A07_MR	g2708743	BLASTX	243	2e-18	32	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
4107	GM_87_A1_A09_MR	g2522228	BLASTX	424	5e-39	77	(AB007466) reverse transcriptase-like protein [Vicia faba]
4108	GM_87_A1_B02_MR	g3377855	BLASTX	302	4e-48	73	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
4109	GM_87_A1_B04_MR	g3056590	BLASTX	298	1e-24	59	(AC004255) T1F9.11 [Arabidopsis thaliana]
4110	GM_87_A1_B05_T7	g3777527	BLASTX	308	3e-25	47	(AF053008) gag-pol polyprotein [Glycine max]
4111	GM_87_A1_B07_MR	g2995405	BLASTX	127	9e-13	39	(Y12432) polyprotein [Ananas comosus]
4112	GM_87_A1_B09_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4113	GM_87_A1_C03_T7	g507910	BLASTN	556	2e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
4114	GM_87_A1_C08_MR	g100484	BLASTX	153	4e-09	42	hypothetical protein - garden snapdragon
4115	GM_87_A1_C10_MR	g3142328	BLASTN	651	2e-22	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4116	GM_87_A1_C10_T7	g3777527	BLASTX	596	2e-56	88	(AF053008) gag-pol polyprotein [Glycine max]
4117	GM_87_A1_C11_T7	g2522227	BLASTX	143	8e-09	47	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
4118	GM_87_A1_D04_T7	g3097320	BLASTN	930	4e-35	74	Glycine max gene for Bd 30K, complete cds
4119	GM_87_A1_D10_MR	g2642450	BLASTX	156	1e-09	63	(AC002391) putative metal ion transporter (Nramp) [Arabidopsis thaliana] gi 3169188 (AC004401) putative metal ion transporter (Nramp) [Arabidopsis thaliana]
4120	GM_87_A1_D11_T7	g4063760	BLASTX	356	1e-30	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4121	GM_87_A1_E07_MR	g2275207	BLASTX	302	4e-26	52	(AC002337) hypothetical protein [Arabidopsis thaliana]
4122	GM_87_A1_E08_MR	g4115565	BLASTX	273	5e-23	53	(AB013599) MYB homologue [Perilla frutescens]
4123	GM_87_A1_E11_T7	g4063760	BLASTX	374	2e-36	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4124	GM_87_A1_F04_MR	g3021268	BLASTX	431	2e-38	52	(AL022347) putative protein [Arabidopsis thaliana]
4125	GM_87_A1_F04_T7	g1707642	BLASTX	217	7e-17	32	(Y07748) TMK [Oryza sativa]

4126	GM_87_A1_H01_MR	g3947439	BLASTX	151	7e-09	26	(AC005034) gc-rich sequence dna-binding factor [Homo sapiens]
4127	GM_87_A1_H03_MR	g226407	BLASTX	158	3e-09	32	retrotransposon del1-46 [Lilium henryi]
4128	GM_87_A1_H04_MR	g1666236	BLASTX	199	6e-15	32	(U76261) unknown [Hordeum vulgare]
4129	GM_87_A1_H04_T7	g3033398	BLASTX	202	4e-20	88	(AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana]
4130	GM_87_A1_H05_MR	g3021268	BLASTX	373	3e-32	52	(AL022347) putative protein [Arabidopsis thaliana]
4131	GM_87_A1_H05_T7	g1707642	BLASTX	194	2e-13	30	(Y07748) TMK [Oryza sativa]
4132	GM_87_A1_H06_T7	g3777527	BLASTX	708	7e-68	95	(AF053008) gag-pol polyprotein [Glycine max]
4133	GM_87_A1_H10_MR	g1276977	BLASTX	154	3e-21	74	(U47143) nonsymbiotic hemoglobin [Glycine max]
4134	GM_87_A2_A01_T7	g2462058	BLASTX	160	4e-11	51	(Y13389) reverse transcriptase [Antirrhinum majus]
4135	GM_87_A2_A02_T7	g1769899	BLASTX	192	2e-14	67	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4136	GM_87_A2_A07_T7	g1769899	BLASTX	244	6e-20	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4137	GM_87_A2_A10_MR	g2443320	BLASTX	259	4e-20	43	(D85597) polyprotein [Oryza australiensis]
4138	GM_87_A2_A10_T7	g905361	BLASTX	199	4e-14	32	(U22103) gag-protease polyprotein [Glycine max]
4139	GM_87_A2_B03_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
4140	GM_87_A2_B04_T7	g3746069	BLASTX	189	1e-12	41	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
4141	GM_87_A2_B05_MR	g14353	BLASTN	354	6e-09	60	Euglena gracilis Z Chloroplast DNA
4142	GM_87_A2_B05_T7	g2689221	BLASTX	189	4e-23	46	(Y10098) 7-ethoxycoumarin O-deethylase [Helianthus tuberosus]
4143	GM_87_A2_B06_MR	g2995405	BLASTX	170	7e-11	55	(Y12432) polyprotein [Ananas comosus]
4144	GM_87_A2_B08_T7	g507910	BLASTN	595	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4145	GM_87_A2_B10_T7	g507910	BLASTN	361	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4146	GM_87_A2_B12_T7	g3142379	BLASTX	184	3e-21	86	(AF053008) envelope-like [Glycine max]
4147	GM_87_A2_C03_MR	g4115565	BLASTX	298	1e-25	54	(AB013599) MYB homologue [Perilla frutescens]
4148	GM_87_A2_C04_MR	g3859610	BLASTN	379	4e-10	69	Arabidopsis thaliana BAC T9E19
4149	GM_87_A2_C04_T7	g2462134	BLASTX	161	3e-10	29	(Y13368) reverse transcriptase [Beta vulgaris]
4150	GM_87_A2_C06_T7	g507910	BLASTN	377	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4151	GM_87_A2_C11_MR	g1769898	BLASTX	251	9e-20	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4152	GM_87_A2_D03_T7	g3142328	BLASTN	1952	8e-82	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4153	GM_87_A2_D04_MR	g507910	BLASTN	586	7e-20	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4154	GM_87_A2_D05_MR	g1040717	BLASTN	411	2e-12	64	D.polychroa microsatellite sequence (clone Dp ch1 F3)
4155	GM_87_A2_D06_T7	g3097320	BLASTN	1092	2e-42	78	Glycine max gene for Bd 30K, complete cds
4156	GM_87_A2_D08_MR	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
4157	GM_87_A2_D08_T7	g507910	BLASTN	356	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4158	GM_87_A2_E01_MR	g2462058	BLASTX	174	2e-12	50	(Y13389) reverse transcriptase [Antirrhinum majus]
4159	GM_87_A2_E04_MR	g507910	BLASTN	636	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
4160	GM_87_A2_E04_T7	g507910	BLASTN	377	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4161	GM_87_A2_E06_MR	g3426334	BLASTN	348	1e-08	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds

4162	GM_87_A2_E12_MR	g1345132	BLASTX	140	5e-09	37	(U47029) ERECTA [Arabidopsis thaliana] gi 1389566 gnl PID d1012536 (D83257) receptor protein kinase [Arabidopsis thaliana] gi 3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]
4163	GM_87_A2_F02_T7	g3777527	BLASTX	382	4e-33	77	(AF053008) gag-pol polyprotein [Glycine max]
4164	GM_87_A2_F07_MR	g3142328	BLASTN	722	1e-25	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4165	GM_87_A2_G01_MR	g4115365	BLASTX	275	8e-22	52	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
4166	GM_87_A2_G01_T7	g4063760	BLASTX	552	9e-54	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4167	GM_87_A2_G02_MR	g340797	BLASTN	360	3e-10	62	Figure 6. DNA sequence of three 3' apoB VNTR alleles.
4168	GM_87_A2_G03_T7	g2264320	BLASTN	591	1e-19	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
4169	GM_87_A2_H02_MR	g4063760	BLASTX	458	2e-41	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4170	GM_87_A2_H03_MR	g2443320	BLASTX	238	1e-27	46	(D85597) polyprotein [Oryza australiensis]
4171	GM_87_A2_H06_T7	g4063760	BLASTX	394	1e-34	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4172	GM_87_A2_H07_MR	g3777527	BLASTX	244	2e-18	61	(AF053008) gag-pol polyprotein [Glycine max]
4173	GM_87_A2_H08_MR	g2522230	BLASTX	250	1e-23	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4174	GM_87_A2_H10_T7	g3142328	BLASTN	910	3e-34	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4175	GM_87_A2_H11_T7	g3097320	BLASTN	691	3e-24	69	Glycine max gene for Bd 30K, complete cds
4176	GM_87_B1_A02_T7	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
4177	GM_87_B1_A03_MR	g170029	BLASTN	394	8e-11	80	Glycine max cv. Dare nodulin 26 gene fragment.
4178	GM_87_B1_A09_T7	g3810596	BLASTX	179	9e-12	53	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4179	GM_87_B1_B02_MR	g3777527	BLASTX	296	6e-24	91	(AF053008) gag-pol polyprotein [Glycine max]
4180	GM_87_B1_B02_T7	g3128143	BLASTN	456	1e-13	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]
4181	GM_87_B1_B08_MR	g4063760	BLASTX	233	2e-17	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4182	GM_87_B1_B12_T7	g2541876	BLASTX	198	3e-14	43	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
4183	GM_87_B1_C01_T7	g13373	BLASTN	400	6e-12	65	Terminal inverted repeat from Paramecium mitochondrion >gi 342968 gb J01432 PARMTDIN1 paramecium species 1 mitochondria dimer initiation region dna.
4184	GM_87_B1_C02_MR	g3953479	BLASTX	296	4e-24	42	(AC002328) F22O2.24 [Arabidopsis thaliana]
4185	GM_87_B1_C07_T7	g507910	BLASTN	642	2e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
4186	GM_87_B1_C11_T7	g1666236	BLASTX	215	9e-17	39	(U76261) unknown [Hordeum vulgare]
4187	GM_87_B1_D03_MR	g2213600	BLASTX	194	1e-13	33	(AC000348) T7N9.20 [Arabidopsis thaliana]
4188	GM_87_B1_D04_MR	g1769898	BLASTX	350	4e-40	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4189	GM_87_B1_D04_T7	g81704	BLASTX	130	2e-14	43	S-locus-specific glycoprotein precursor - kale

4190	GM_87_B1_D09_MR	g3810595	BLASTX	250	4e-19	43	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
4191	GM_87_B1_E05_T7	g3777527	BLASTX	749	3e-72	96	(AF053008) gag-pol polyprotein [Glycine max]
4192	GM_87_B1_E07_MR	g130398	BLASTX	193	3e-13	43	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 297) gi 85089 pir B24872 retrovirus-related pol polyprotein homolog - fruit fly (Drosophila melanogaster) transposon 297
4193	GM_87_B1_E07_T7	g2522228	BLASTX	236	1e-18	53	(AB007466) reverse transcriptase-like protein [Vicia faba]
4194	GM_87_B1_E08_MR	g2618696	BLASTX	119	2e-16	44	(AC002510) hypothetical protein [Arabidopsis thaliana]
4195	GM_87_B1_E09_T7	g3687234	BLASTX	191	5e-13	52	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
4196	GM_87_B1_F03_T7	g441205	BLASTN	449	3e-20	71	Soybean lox1gm4 gene encoding lipxygenase L-4
4197	GM_87_B1_G02_MR	g507910	BLASTN	499	6e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
4198	GM_87_B1_G05_MR	g507910	BLASTN	373	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4199	GM_87_B1_G06_MR	g3810596	BLASTX	202	3e-14	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4200	GM_87_B1_G11_T7	g2462134	BLASTX	354	1e-31	54	(Y13368) reverse transcriptase [Beta vulgaris]
4201	GM_87_B1_H01_MR	g3176800	BLASTN	220	4e-10	64	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite, 3' sequence
4202	GM_87_B1_H01_T7	g2914696	BLASTX	168	9e-14	45	(AC003974) putative purple acid phosphatase [Arabidopsis thaliana]
4203	GM_87_B1_H04_T7	g2443320	BLASTX	311	1e-25	51	(D85597) polyprotein [Oryza australiensis]
4204	GM_87_B1_H06_T7	g4063760	BLASTX	543	2e-50	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4205	GM_87_B1_H09_MR	g170606	BLASTN	841	1e-31	68	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
4206	GM_87_B1_H10_MR	g2864621	BLASTX	151	3e-09	30	hypothetical protein [Arabidopsis thaliana]
4207	GM_87_B1_H10_T7	g3645899	BLASTX	165	3e-10	50	(U68408) 5' end not determined experimentally [Zea mays]
4208	GM_87_B1_H11_MR	g170029	BLASTN	401	4e-11	81	Glycine max cv. Dare nodulin 26 gene fragment.
4209	GM_87_B1_H12_MR	g2497953	BLASTX	159	8e-10	53	MOLYBDOPTERIN BIOSYNTHESIS CNX1 PROTEIN (MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX1) gi 1263314 (L47323) molybdenum cofactor biosynthesis enzyme [Arabidopsis thaliana]
4210	GM_87_B2_A01_T7	g4115377	BLASTX	273	4e-22	42	(AC005967) unknown protein [Arabidopsis thaliana]
4211	GM_87_B2_A02_MR	g1155261	BLASTX	577	3e-55	92	(U40217) eukaryotic release factor 1 homolog [Arabidopsis thaliana]
4212	GM_87_B2_A06_T7	g2864621	BLASTX	152	2e-09	38	hypothetical protein [Arabidopsis thaliana]
4213	GM_87_B2_A07_MR	g4063760	BLASTX	240	3e-30	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4214	GM_87_B2_A11_T7	g3777527	BLASTX	711	3e-68	93	(AF053008) gag-pol polyprotein [Glycine max]
4215	GM_87_B2_B02_MR	g2583130	BLASTX	258	6e-20	41	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
4216	GM_87_B2_B03_T7	g1685003	BLASTX	274	1e-22	47	(U32643) immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]

4217	GM_87_B2_B05_MR	g1236920	BLASTN	367	1e-09	63	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
4218	GM_87_B2_B07_T7	g3142328	BLASTN	897	1e-33	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4219	GM_87_B2_C01_T7	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
4220	GM_87_B2_C04_MR	g2073447	BLASTN	362	3e-09	62	L.japonicus gln1, pge1 & krm genes
4221	GM_87_B2_C08_MR	g507910	BLASTN	504	4e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
4222	GM_87_B2_C08_T7	g507910	BLASTN	417	3e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
4223	GM_87_B2_C09_T7	g3142328	BLASTN	887	3e-33	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4224	GM_87_B2_D03_MR	g4092470	BLASTN	392	1e-10	62	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
4225	GM_87_B2_D05_MR	g1785740	BLASTX	126	8e-11	31	(Y08502) orf170 [Arabidopsis thaliana]
4226	GM_87_B2_D06_MR	g1335862	BLASTX	243	3e-18	90	(U42608) clathrin heavy chain [Glycine max]
4227	GM_87_B2_D08_T7	g2827662	BLASTX	209	4e-15	55	(AL021637) Phosphoribosylanthranilate transferase [Arabidopsis thaliana]
4228	GM_87_B2_D11_MR	g507910	BLASTN	487	2e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
4229	GM_87_B2_E01_T7	g100484	BLASTX	404	3e-36	55	hypothetical protein - garden snapdragon
4230	GM_87_B2_E03_T7	g3097320	BLASTN	484	7e-15	70	Glycine max gene for Bd 30K, complete cds
4231	GM_87_B2_E08_T7	g100484	BLASTX	362	1e-31	51	hypothetical protein - garden snapdragon
4232	GM_87_B2_E10_T7	g4063760	BLASTX	202	3e-15	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4233	GM_87_B2_E12_MR	g1234900	BLASTX	249	2e-20	90	(X92489) homeobox-leucine zipper protein [Glycine max]
4234	GM_87_B2_F02_T7	g18559	BLASTN	842	4e-31	72	G.max gene for catalase
4235	GM_87_B2_F05_MR	g507910	BLASTN	569	4e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4236	GM_87_B2_F05_T7	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4237	GM_87_B2_F08_T7	g629693	BLASTX	255	4e-21	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
4238	GM_87_B2_F11_T7	g4092470	BLASTN	419	7e-12	62	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
4239	GM_87_B2_G02_MR	g3810596	BLASTX	219	5e-16	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4240	GM_87_B2_G05_MR	g4063760	BLASTX	238	6e-18	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4241	GM_87_B2_H03_MR	g99755	BLASTX	332	1e-28	50	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
4242	GM_87_B2_H04_T7	g2982247	BLASTX	177	7e-13	48	(AF051206) probable thioredoxin H [Picea mariana]
4243	GM_87_B2_H11_T7	g3047060	BLASTN	393	1e-10	66	Arabidopsis thaliana BAC F7N22
4244	GM_88_A1_A04_MR	g2522228	BLASTX	306	2e-26	70	(AB007466) reverse transcriptase-like protein [Vicia faba]
4245	GM_88_A1_A05_T7	g3461813	BLASTX	106	6e-16	61	(AC004138) putative sucrose/H+ symporter [Arabidopsis thaliana]

4246	GM_88_A1_A07_T7	g3025708	BLASTN	305	1e-09	64	Plasmodium falciparum subclone R5 variant surface antigen (var7b) gene, upstream regulatory region and partial cds
4247	GM_88_A1_A09_MR	g4063760	BLASTX	175	3e-11	33	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4248	GM_88_A1_B03_MR	g4063760	BLASTX	461	8e-42	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4249	GM_88_A1_B04_T7	g4063760	BLASTX	480	9e-44	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4250	GM_88_A1_B05_MR	g2244950	BLASTN	493	3e-15	71	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 5
4251	GM_88_A1_B07_T7	g4115365	BLASTX	175	2e-17	58	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
4252	GM_88_A1_B09_MR	g3142328	BLASTN	831	1e-30	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4253	GM_88_A1_C03_T7	g4038056	BLASTX	316	2e-26	43	(AC005897) putative transposon [Arabidopsis thaliana]
4254	GM_88_A1_D02_MR	g905361	BLASTX	158	9e-10	40	(U22103) gag-protease polyprotein [Glycine max]
4255	GM_88_A1_D08_MR	g1142699	BLASTN	300	5e-17	77	Glycine max satellite STR120-A.1.
4256	GM_88_A1_D09_MR	g4150930	BLASTN	367	1e-09	60	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
4257	GM_88_A1_D11_MR	g4092470	BLASTN	374	7e-10	69	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
4258	GM_88_A1_E03_T7	g2769655	BLASTN	457	1e-13	63	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
4259	GM_88_A1_E06_MR	g1167523	BLASTX	180	1e-11	46	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
4260	GM_88_A1_E07_MR	g507910	BLASTN	395	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4261	GM_88_A1_E09_MR	g2673766	BLASTN	325	2e-11	65	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-110, complete sequence [Plasmodium falciparum]
4262	GM_88_A1_E10_MR	g1063404	BLASTN	375	1e-10	61	S.gregaria mitochondrial control region DNA
4263	GM_88_A1_E10_T7	g2961349	BLASTX	327	2e-27	54	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
4264	GM_88_A1_F02_T7	g507910	BLASTN	488	2e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
4265	GM_88_A1_F06_T7	g548774	BLASTX	256	3e-21	74	60S RIBOSOMAL PROTEIN L7A gi 542158 pir S38360 ribosomal protein L7a - rice gi 303855 gnl PID d1002646 (D12631) ribosomal protein L7A [Oryza sativa]
4266	GM_88_A1_G02_T7	g507910	BLASTN	426	1e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
4267	GM_88_A1_G03_T7	g439857	BLASTX	286	3e-23	91	(U04785) lipoxygenase [Glycine max]
4268	GM_88_A1_H03_MR	g4063760	BLASTX	204	3e-14	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4269	GM_88_A1_H03_T7	g905361	BLASTX	216	5e-16	36	(U22103) gag-protease polyprotein [Glycine max]
4270	GM_88_A1_H05_T7	g1167523	BLASTX	213	4e-15	40	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]

4271	GM_88_A1_H07_MR	g3820976	BLASTN	463	7e-14	64	Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complet...
4272	GM_88_A2_A02_T7	g505129	BLASTN	301	4e-12	71	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
4273	GM_88_A2_A04_T7	g1171591	BLASTN	417	8e-12	60	P.falciparum complete gene map of plastid-like DNA (IR-B)
4274	GM_88_A2_A05_MR	g4063760	BLASTX	205	2e-14	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4275	GM_88_A2_A07_T7	g3142328	BLASTN	466	4e-14	62	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4276	GM_88_A2_A08_T7	g2264320	BLASTN	463	5e-15	61	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
4277	GM_88_A2_A09_MR	g4063760	BLASTX	271	2e-21	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4278	GM_88_A2_A10_T7	g2129618	BLASTX	249	3e-19	46	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4279	GM_88_A2_A11_T7	g3142328	BLASTN	745	9e-27	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4280	GM_88_A2_B01_T7	g3645899	BLASTX	254	1e-32	51	(U68408) 5' end not determined experimentally [Zea mays]
4281	GM_88_A2_B02_MR	g18559	BLASTN	973	4e-37	75	G.max gene for catalase
4282	GM_88_A2_B10_MR	g3810596	BLASTX	223	2e-16	58	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4283	GM_88_A2_B12_MR	g1946279	BLASTX	331	3e-29	53	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
4284	GM_88_A2_C02_MR	g4063760	BLASTX	612	7e-58	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4285	GM_88_A2_C04_T7	g507910	BLASTN	453	7e-14	77	Glycine max BSR-101 satellite SB92 genomic sequence.
4286	GM_88_A2_C06_MR	g4063770	BLASTX	142	3e-09	35	(AB004906) transposase [Ipomoea purpurea]
4287	GM_88_A2_C07_T7	g3599418	BLASTN	419	6e-12	91	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
4288	GM_88_A2_C09_MR	g1142703	BLASTN	294	7e-17	76	Glycine max satellite STR120-B.1.
4289	GM_88_A2_E02_T7	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
4290	GM_88_A2_E05_MR	g1326016	BLASTX	296	4e-24	45	TY3-2 orfB
4291	GM_88_A2_E09_T7	g1899175	BLASTX	243	5e-19	79	(U90262) calcium-dependent calmodulin-independent protein kinase CDPK [Cucurbita pepo]
4292	GM_88_A2_E12_MR	g1946279	BLASTX	173	9e-21	42	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
4293	GM_88_A2_F02_MR	g18559	BLASTN	523	1e-16	69	G.max gene for catalase
4294	GM_88_A2_F03_T7	g2522228	BLASTX	128	9e-11	53	(AB007466) reverse transcriptase-like protein [Vicia faba]
4295	GM_88_A2_F05_MR	g2335061	BLASTN	397	7e-11	62	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence [Homo sapiens]

4296	GM_88_A2_F09_T7	g3142328	BLASTN	791	7e-29	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4297	GM_88_A2_G02_MR	g2522230	BLASTX	214	8e-17	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4298	GM_88_A2_G03_MR	g4063756	BLASTN	374	7e-10	73	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
4299	GM_88_A2_G04_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4300	GM_88_A2_G06_MR	g100484	BLASTX	164	3e-10	57	hypothetical protein - garden snapdragon
4301	GM_88_A2_G11_T7	g2769655	BLASTN	426	3e-12	62	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
4302	GM_88_A2_H08_T7	g1666236	BLASTX	214	1e-16	35	(U76261) unknown [Hordeum vulgare]
4303	GM_88_B1_A01_T7	g3142328	BLASTN	972	4e-37	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4304	GM_88_B1_A06_T7	g3777526	BLASTN	1530	3e-62	86	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
4305	GM_88_B1_A09_MR	g4038056	BLASTX	288	2e-23	45	(AC005897) putative transposon [Arabidopsis thaliana]
4306	GM_88_B1_B05_MR	g300517	BLASTN	452	2e-14	61	Apo(B) (HVE36)=Apolipoprotein B {3' region, AT rich minisatellite, VNTR} [human, caucasian, Genomic, 802 nt]
4307	GM_88_B1_B09_MR	g4063760	BLASTX	656	3e-68	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4308	GM_88_B1_B10_MR	g2586087	BLASTX	169	9e-11	35	(U72724) receptor kinase-like protein [Oryza sativa]
4309	GM_88_B1_C04_MR	g4063760	BLASTX	315	2e-51	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4310	GM_88_B1_C04_T7	g1666236	BLASTX	132	1e-11	27	(U76261) unknown [Hordeum vulgare]
4311	GM_88_B1_C06_MR	g1000971	BLASTN	434	1e-12	62	Hansenula wingei mitochondrial DNA, complete sequence
4312	GM_88_B1_C08_T7	g1769898	BLASTX	244	5e-19	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4313	GM_88_B1_C10_MR	g2289001	BLASTX	116	8e-16	67	(AC002335) small nuclear ribonucleoprotein isolog [Arabidopsis thaliana]
4314	GM_88_B1_C12_MR	g343746	BLASTN	357	2e-09	58	Yeast (S.cerevisiae) mitochondrial ATPase subunit gene, 3' spacer.
4315	GM_88_B1_D01_MR	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
4316	GM_88_B1_D05_T7	g1769896	BLASTN	435	1e-12	61	A.thaliana lectin receptor kinase gene
4317	GM_88_B1_D11_T7	g3645899	BLASTX	354	2e-30	47	(U68408) 5' end not determined experimentally [Zea mays]
4318	GM_88_B1_D12_T7	g3777527	BLASTX	365	3e-31	62	(AF053008) gag-pol polyprotein [Glycine max]
4319	GM_88_B1_E01_MR	g4063760	BLASTX	213	3e-15	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4320	GM_88_B1_E03_T7	g3777527	BLASTX	772	3e-77	86	(AF053008) gag-pol polyprotein [Glycine max]
4321	GM_88_B1_E04_MR	g2995405	BLASTX	434	3e-39	54	(Y12432) polyprotein [Ananas comosus]
4322	GM_88_B1_E05_MR	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4323	GM_88_B1_E05_T7	g507910	BLASTN	569	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.

4324	GM_88_B1_E07_MR	g543905	BLASTX	290	8e-25	86	BRASSINOSTEROID-REGULATED PROTEIN BRU1 gi 347459 (L22162) brassinosteroid-regulated protein [Glycine max]
4325	GM_88_B1_E09_MR	g1769898	BLASTX	185	1e-12	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4326	GM_88_B1_E12_T7	g4063760	BLASTX	616	3e-58	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4327	GM_88_B1_F01_T7	g2623296	BLASTX	191	5e-13	46	(AC002409) hypothetical protein [Arabidopsis thaliana]
4328	GM_88_B1_F02_T7	g3283026	BLASTX	212	2e-15	33	putative transposase [Arabidopsis thaliana]
4329	GM_88_B1_F05_MR	g3142328	BLASTN	476	1e-14	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4330	GM_88_B1_F09_MR	g726334	BLASTX	287	2e-50	87	(U22533) NADP-malate dehydrogenase [Flaveria trinervia]
4331	GM_88_B1_F09_T7	g3021268	BLASTX	339	1e-28	45	(AL022347) putative protein [Arabidopsis thaliana]
4332	GM_88_B1_F10_MR	g1769897	BLASTX	345	2e-30	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4333	GM_88_B1_G04_T7	g507910	BLASTN	348	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4334	GM_88_B1_G08_MR	g18695	BLASTN	506	4e-16	87	Soybean nodulin 22 gene
4335	GM_88_B1_G11_T7	g421955	BLASTX	333	2e-29	59	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
4336	GM_88_B1_H06_T7	g3273387	BLASTN	457	1e-13	62	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
4337	GM_88_B1_H10_MR	g3777527	BLASTX	119	2e-17	42	(AF053008) gag-pol polyprotein [Glycine max]
4338	GM_88_B1_H12_T7	g255576	BLASTN	338	7e-09	95	small auxin up RNA gene cluster: orf 6B [Glycine max=soybeans, cv. Wayne, Genomic, 665 nt]
4339	GM_89_A1_A03_MR	g507910	BLASTN	526	4e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
4340	GM_89_A1_A05_MR	g4063756	BLASTN	544	2e-17	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
4341	GM_89_A1_A08_T7	g4038056	BLASTX	267	3e-21	48	(AC005897) putative transposon [Arabidopsis thaliana]
4342	GM_89_A1_A10_T7	g3599418	BLASTN	795	5e-29	72	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
4343	GM_89_A1_B03_T7	g2462134	BLASTX	215	2e-24	46	(Y13368) reverse transcriptase [Beta vulgaris]
4344	GM_89_A1_B06_MR	g2708743	BLASTX	140	5e-09	35	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
4345	GM_89_A1_B07_MR	g3176788	BLASTN	364	3e-10	65	Homo sapiens allele 8 fragile site locus (FRA10B) minisatellite sequence
4346	GM_89_A1_C02_MR	g1142700	BLASTN	775	2e-28	86	Glycine max satellite STR120-A.2.
4347	GM_89_A1_C04_T7	g4006838	BLASTN	413	1e-11	62	Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence [Homo sapiens]
4348	GM_89_A1_C05_MR	g2522230	BLASTX	248	2e-27	41	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4349	GM_89_A1_C07_MR	g4063770	BLASTX	151	7e-09	33	(AB004906) transposase [Ipomoea purpurea]
4350	GM_89_A1_C08_MR	g905361	BLASTX	730	2e-71	96	(U22103) gag-protease polyprotein [Glycine max]
4351	GM_89_A1_C10_MR	g905361	BLASTX	701	2e-68	92	(U22103) gag-protease polyprotein [Glycine max]

4352	GM_89_A1_D01_T7	g4115365	BLASTX	223	3e-16	38	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
4353	GM_89_A1_D03_T7	g4038056	BLASTX	297	2e-24	46	(AC005897) putative transposon [Arabidopsis thaliana]
4354	GM_89_A1_D04_T7	g507910	BLASTN	419	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4355	GM_89_A1_D05_T7	g3142328	BLASTN	1002	2e-38	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4356	GM_89_A1_D06_MR	g3142328	BLASTN	603	3e-20	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4357	GM_89_A1_D07_MR	g1514643	BLASTX	120	1e-14	85	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
4358	GM_89_A1_D08_MR	g1255951	BLASTX	152	3e-09	40	(X96932) PS60 gene product [Nicotiana tabacum]
4359	GM_89_A1_D09_MR	g3777527	BLASTX	249	6e-19	58	(AF053008) gag-pol polyprotein [Glycine max]
4360	GM_89_A1_D11_MR	g18683	BLASTN	526	7e-17	79	G.max N-20t gene
4361	GM_89_A1_D12_MR	g507910	BLASTN	494	1e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
4362	GM_89_A1_E02_MR	g3935180	BLASTX	258	6e-20	47	(AC004557) F17L21.23 [Arabidopsis thaliana]
4363	GM_89_A1_E02_T7	g16056	BLASTN	385	2e-10	59	A. majus TAM1 gene for TNP1 and TNP2.
4364	GM_89_A1_E04_MR	g396249	BLASTN	435	6e-13	62	S.douglasii mitochondrial ATP subunit 9 gene, complete CDS
4365	GM_89_A1_E05_MR	g1480927	BLASTN	1143	2e-45	83	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
4366	GM_89_A1_E05_T7	g1769897	BLASTX	213	8e-16	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4367	GM_89_A1_E06_T7	g559278	BLASTN	451	2e-13	61	Saccharomyces cerevisiae mitochondrion origin of replication (ori3 and ori4).
4368	GM_89_A1_E08_MR	g3319362	BLASTX	192	3e-13	41	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
4369	GM_89_A1_E09_T7	g3097320	BLASTN	532	5e-17	70	Glycine max gene for Bd 30K, complete cds
4370	GM_89_A1_F05_MR	g4140712	BLASTX	318	8e-28	47	(AF110183) putative integrase [Oryza sativa]
4371	GM_89_A1_F07_MR	g2995405	BLASTX	443	4e-40	55	(Y12432) polyprotein [Ananas comosus]
4372	GM_89_A1_G02_MR	g1666236	BLASTX	146	7e-14	31	(U76261) unknown [Hordeum vulgare]
4373	GM_89_A1_G10_MR	g4063760	BLASTX	361	5e-31	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4374	GM_89_A1_H01_MR	g18559	BLASTN	1428	9e-58	87	G.max gene for catalase
4375	GM_89_A1_H01_T7	g2462936	BLASTX	245	5e-25	48	(Y12321) open reading frame 2 [Brassica oleracea]
4376	GM_89_A1_H06_MR	g507910	BLASTN	557	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4377	GM_89_A1_H08_MR	g629693	BLASTX	157	4e-10	52	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
4378	GM_89_A1_H08_T7	g2443320	BLASTX	241	7e-22	48	(D85597) polyprotein [Oryza australiensis]
4379	GM_89_A1_H09_MR	g4050011	BLASTN	581	3e-19	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
4380	GM_89_A1_H10_MR	g3582436	BLASTX	153	1e-21	68	(AB017502) beta-D-glucan exohydrolase [Nicotiana tabacum]
4381	GM_89_A1_H12_T7	g4126312	BLASTN	416	9e-12	64	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]

4382	GM_89_A2_A05_T7	g18702	BLASTN	365	3e-10	68	Soybean nodulin-24 gene 5' end
4383	GM_89_A2_A06_MR	g1666236	BLASTX	302	4e-26	34	(U76261) unknown [Hordeum vulgare]
4384	GM_89_A2_A07_MR	g3096930	BLASTX	216	4e-16	67	(AL023094) Homeodomain - like protein [Arabidopsis thaliana]
4385	GM_89_A2_A09_T7	g18559	BLASTN	1345	5e-54	74	G.max gene for catalase
4386	GM_89_A2_B02_MR	g2522230	BLASTX	267	4e-29	41	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4387	GM_89_A2_B02_T7	g3142379	BLASTX	291	7e-25	85	(AF053008) envelope-like [Glycine max]
4388	GM_89_A2_B06_MR	g130582	BLASTX	353	4e-30	45	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
4389	GM_89_A2_B10_MR	g2213632	BLASTX	164	1e-10	50	(AC000103) F21J9.24 [Arabidopsis thaliana]
4390	GM_89_A2_B11_MR	g130582	BLASTX	163	7e-10	41	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
4391	GM_89_A2_B12_MR	g2924653	BLASTN	396	2e-11	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]
4392	GM_89_A2_C01_MR	g507910	BLASTN	684	3e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
4393	GM_89_A2_C03_T7	g1666236	BLASTX	212	2e-16	30	(U76261) unknown [Hordeum vulgare]
4394	GM_89_A2_C08_T7	g2982452	BLASTX	132	8e-11	70	(AL022223) receptor protein kinase - like protein [Arabidopsis thaliana]
4395	GM_89_A2_D02_MR	g2443320	BLASTX	177	2e-18	32	(D85597) polyprotein [Oryza australiensis]
4396	GM_89_A2_D05_MR	g2995405	BLASTX	485	1e-44	65	(Y12432) polyprotein [Ananas comosus]
4397	GM_89_A2_D07_T7	g2104945	BLASTN	562	2e-34	71	Glycine max copia-like retrotransposon Tgmr, complete sequence
4398	GM_89_A2_D08_MR	g3142328	BLASTN	1240	3e-77	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4399	GM_89_A2_D12_T7	g3426334	BLASTN	375	6e-10	65	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
4400	GM_89_A2_E01_T7	g4050011	BLASTN	444	5e-13	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
4401	GM_89_A2_E05_MR	g3201608	BLASTN	360	3e-09	67	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence.
4402	GM_89_A2_E06_T7	g905361	BLASTX	619	2e-62	85	(U22103) gag-protease polyprotein [Glycine max]
4403	GM_89_A2_E10_T7	g18559	BLASTN	544	1e-17	66	G.max gene for catalase
4404	GM_89_A2_E11_MR	g3777527	BLASTX	744	9e-72	95	(AF053008) gag-pol polyprotein [Glycine max]
4405	GM_89_A2_F01_MR	g3777527	BLASTX	450	2e-40	80	(AF053008) gag-pol polyprotein [Glycine max]
4406	GM_89_A2_F03_T7	g18559	BLASTN	349	9e-09	69	G.max gene for catalase

4407	GM_89_A2_F07_MR	g170605	BLASTN	575	2e-19	64	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
4408	GM_89_A2_G01_T7	g3377802	BLASTX	203	3e-20	74	(AF075597) Similar to sucrose synthase; T2H3.8 [Arabidopsis thaliana]
4409	GM_89_A2_G03_T7	g2244950	BLASTN	356	8e-18	84	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 5
4410	GM_89_A2_G04_MR	g1619300	BLASTX	119	2e-09	40	(X95269) LRR protein [Lycopersicon esculentum]
4411	GM_89_A2_G04_T7	g3033389	BLASTX	186	2e-12	30	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
4412	GM_89_A2_G05_T7	g2501766	BLASTX	172	2e-11	77	(U69174) calmodulin-like domain protein kinase isoenzyme gamma [Glycine max]
4413	GM_89_A2_G07_MR	g4115365	BLASTX	252	2e-19	38	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
4414	GM_89_A2_G09_T7	g421955	BLASTX	342	2e-30	62	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
4415	GM_89_A2_H01_MR	g303900	BLASTN	425	3e-12	69	Soybean gene for ubiquitin, complete cds
4416	GM_89_A2_H07_MR	g3250687	BLASTX	246	3e-25	43	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
4417	GM_90_A1_A04_MR	g507910	BLASTN	580	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4418	GM_90_A1_A04_T7	g905361	BLASTX	527	5e-50	70	(U22103) gag-protease polyprotein [Glycine max]
4419	GM_90_A1_A05_T7	g4063770	BLASTX	202	3e-14	39	(AB004906) transposase [Ipomoea purpurea]
4420	GM_90_A1_A08_T7	g100484	BLASTX	244	7e-19	44	hypothetical protein - garden snapdragon
4421	GM_90_A1_A10_T7	g3193284	BLASTX	294	3e-24	40	(AF069298) No definition line found [Arabidopsis thaliana]
4422	GM_90_A1_A12_MR	g3142328	BLASTN	723	9e-26	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4423	GM_90_A1_A12_T7	g507910	BLASTN	356	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4424	GM_90_A1_B02_T7	g3157938	BLASTX	162	3e-10	62	(AC002131) Similar to seryl-tRNA synthetase gb U10400 from S cerevisiae. EST gb N96627 comes from this gene. [Arabidopsis thaliana]
4425	GM_90_A1_B03_MR	g507910	BLASTN	539	1e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
4426	GM_90_A1_B03_T7	g507910	BLASTN	536	1e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
4427	GM_90_A1_B04_MR	g2760172	BLASTN	444	5e-13	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUB3, complete sequence [Arabidopsis thaliana]
4428	GM_90_A1_B07_MR	g2995405	BLASTX	357	7e-31	64	(Y12432) polyprotein [Ananas comosus]
4429	GM_90_A1_C07_MR	g3894383	BLASTX	166	3e-15	41	(AF053993) disease resistance protein [Lycopersicon esculentum]
4430	GM_90_A1_D01_MR	g3928097	BLASTX	146	3e-09	50	(AC005770) unknown protein, 5' partial [Arabidopsis thaliana]
4431	GM_90_A1_D01_T7	g2522228	BLASTX	157	5e-10	29	(AB007466) reverse transcriptase-like protein [Vicia faba]
4432	GM_90_A1_D03_MR	g3695395	BLASTX	248	2e-19	48	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
4433	GM_90_A1_D04_MR	g3193221	BLASTN	583	2e-19	92	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
4434	GM_90_A1_D10_MR	g18559	BLASTN	450	2e-13	70	G.max gene for catalase

4435	GM_90_A1_E01_T7	g3426047	BLASTX	134	3e-10	51	(AC005168) putative DNA-binding protein [Arabidopsis thaliana]
4436	GM_90_A1_E06_T7	g3426334	BLASTN	351	7e-09	63	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
4437	GM_90_A1_E09_T7	g4063760	BLASTX	419	3e-37	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4438	GM_90_A1_E10_T7	g4063760	BLASTX	543	2e-50	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4439	GM_90_A1_F01_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
4440	GM_90_A1_F01_T7	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4441	GM_90_A1_F05_T7	g4139266	BLASTX	151	1e-09	55	(AF112444) L-asparaginase [Lupinus luteus]
4442	GM_90_A1_F07_T7	g1294787	BLASTN	387	1e-10	65	Meloidogyne javanica mitochondrial transfer RNA His, 16S ribosomal RNA (16S rRNA) genes, ND3 gene, complete cds, and cytochrome b gene, 5' end of CDS.
4443	GM_90_A1_F09_MR	g507910	BLASTN	486	2e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
4444	GM_90_A1_F11_T7	g4038056	BLASTX	330	6e-28	46	(AC005897) putative transposon [Arabidopsis thaliana]
4445	GM_90_A1_G01_T7	g1769897	BLASTX	455	6e-47	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4446	GM_90_A1_G02_T7	g2129618	BLASTX	211	4e-15	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4447	GM_90_A1_G03_MR	g3777527	BLASTX	318	3e-26	86	(AF053008) gag-pol polyprotein [Glycine max]
4448	GM_90_A1_G04_T7	g99922	BLASTX	511	3e-48	70	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
4449	GM_90_A1_G09_MR	g3779023	BLASTX	155	1e-10	36	(AC005171) probable splicing factor [Arabidopsis thaliana]
4450	GM_90_A1_H03_T7	g4140712	BLASTX	200	3e-15	36	(AF110183) putative integrase [Oryza sativa]
4451	GM_90_A1_H04_T7	g2129618	BLASTX	247	5e-19	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4452	GM_90_A1_H06_MR	g2522228	BLASTX	198	2e-14	78	(AB007466) reverse transcriptase-like protein [Vicia faba]
4453	GM_90_A1_H08_MR	g3777527	BLASTX	220	7e-16	53	(AF053008) gag-pol polyprotein [Glycine max]
4454	GM_90_A1_H09_T7	g2129618	BLASTX	198	8e-14	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4455	GM_90_A2_A02_MR	g1769898	BLASTX	104	6e-10	69	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4456	GM_90_A2_A05_T7	g4063760	BLASTX	132	5e-11	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4457	GM_90_A2_A06_MR	g2367675	BLASTX	233	2e-17	35	(AF017040) Pol [Dictyostelium discoideum]
4458	GM_90_A2_A11_MR	g3810596	BLASTX	184	3e-12	38	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4459	GM_90_A2_B01_MR	g3236259	BLASTX	161	7e-11	65	(AC004684) putative alcohol dehydrogenase [Arabidopsis thaliana]
4460	GM_90_A2_B03_MR	g2146735	BLASTX	268	6e-22	84	glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49) (clone E5) - Arabidopsis thaliana (fragment) gi 1166405 (X84229) glucose-6-phosphate 1-dehydrogenase [Arabidopsis thaliana]
4461	GM_90_A2_B05_T7	g505129	BLASTN	350	7e-09	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
4462	GM_90_A2_B07_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
4463	GM_90_A2_B10_MR	g3142328	BLASTN	2447	3e-105	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

4464	GM_90_A2_C01_T7	g3645899	BLASTX	206	1e-14	45	(U68408) 5' end not determined experimentally [Zea mays]
4465	GM_90_A2_C02_MR	g2252836	BLASTX	287	2e-23	41	(AF013293) contains weak similarity to S. cerevisiae BOB1 protein (PIR:S45444) [Arabidopsis thaliana]
4466	GM_90_A2_C07_MR	g18559	BLASTN	1053	1e-40	75	G.max gene for catalase
4467	GM_90_A2_C09_MR	g507910	BLASTN	462	3e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.
4468	GM_90_A2_C10_T7	g4063760	BLASTX	221	4e-16	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4469	GM_90_A2_D03_MR	g4063760	BLASTX	266	6e-21	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4470	GM_90_A2_D06_T7	g3047068	BLASTX	204	2e-14	35	(AF058825) similar to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
4471	GM_90_A2_D07_T7	g3142328	BLASTN	744	1e-26	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4472	GM_90_A2_D09_T7	g507910	BLASTN	407	9e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4473	GM_90_A2_D10_T7	g1666236	BLASTX	163	7e-11	29	(U76261) unknown [Hordeum vulgare]
4474	GM_90_A2_D11_MR	g3097320	BLASTN	657	1e-22	74	Glycine max gene for Bd 30K, complete cds
4475	GM_90_A2_D11_T7	g3282250	BLASTX	142	9e-11	55	(AF009337) CDPK-related protein kinase [Tradescantia virginiana]
4476	GM_90_A2_E02_MR	g340797	BLASTN	500	1e-16	64	Figure 6. DNA sequence of three 3' apoB VNTR alleles.
4477	GM_90_A2_E06_MR	g3482916	BLASTX	162	7e-12	43	(AC003970) Hypothetical protein [Arabidopsis thaliana]
4478	GM_90_A2_F01_T7	g4063760	BLASTX	249	3e-21	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4479	GM_90_A2_F02_T7	g3080427	BLASTX	166	1e-20	61	(AL022604) putative protein [Arabidopsis thaliana]
4480	GM_90_A2_F08_T7	g531389	BLASTX	102	5e-09	42	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
4481	GM_90_A2_G06_T7	g3021409	BLASTX	157	2e-12	60	(Y12781) transducin (beta) like 1 protein [Homo sapiens]
4482	GM_90_A2_G08_MR	g431164	BLASTX	127	4e-13	86	(D21823) ORF [Lilium longiflorum]
4483	GM_90_A2_G11_MR	g905361	BLASTX	428	3e-39	96	(U22103) gag-protease polyprotein [Glycine max]
4484	GM_90_A2_G12_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4485	GM_90_A2_H04_MR	g507910	BLASTN	515	1e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4486	GM_90_A2_H04_T7	g507910	BLASTN	579	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4487	GM_90_A2_H06_MR	g1769898	BLASTX	190	4e-26	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4488	GM_90_A2_H09_MR	g4063760	BLASTX	202	5e-15	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4489	GM_90_A2_H11_MR	g1142703	BLASTN	267	1e-11	72	Glycine max satellite STR120-B.1.
4490	GM_90_B1_A03_MR	g3204107	BLASTN	508	5e-17	69	Cicer arietinum mRNA for putative cytidine or deoxycytidylate deaminase, partial.
4491	GM_90_B1_A03_T7	g4063760	BLASTX	273	1e-21	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4492	GM_90_B1_A10_MR	g3777527	BLASTX	343	6e-29	71	(AF053008) gag-pol polyprotein [Glycine max]
4493	GM_90_B1_A11_MR	g4063770	BLASTX	188	2e-15	34	(AB004906) transposase [Ipomoea purpurea]
4494	GM_90_B1_A12_MR	g905361	BLASTX	266	2e-21	94	(U22103) gag-protease polyprotein [Glycine max]
4495	GM_90_B1_B02_MR	g4063760	BLASTX	457	3e-43	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4496	GM_90_B1_B02_T7	g1871192	BLASTX	378	2e-33	50	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]

4497	GM_90_B1_B05_T7	g3142328	BLASTN	1832	3e-76	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4498	GM_90_B1_B07_T7	g2828827	BLASTN	491	4e-15	61	Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) g...
4499	GM_90_B1_B09_T7	g4063760	BLASTX	255	9e-20	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4500	GM_90_B1_C03_MR	g3289984	BLASTN	359	3e-09	63	Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence [Homo sapiens]
4501	GM_90_B1_C05_MR	g507910	BLASTN	484	3e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
4502	GM_90_B1_C05_T7	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4503	GM_90_B1_C10_MR	g4063756	BLASTN	601	4e-20	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
4504	GM_90_B1_C10_T7	g3142379	BLASTX	298	1e-25	46	(AF053008) envelope-like [Glycine max]
4505	GM_90_B1_D02_T7	g1769898	BLASTX	460	7e-43	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4506	GM_90_B1_D10_MR	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4507	GM_90_B1_D10_T7	g507910	BLASTN	368	5e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4508	GM_90_B1_D11_MR	g3777527	BLASTX	251	3e-19	35	(AF053008) gag-pol polyprotein [Glycine max]
4509	GM_90_B1_D12_T7	g2586082	BLASTX	136	3e-10	50	(U72725) retrofit [Oryza longistaminata]
4510	GM_90_B1_E01_T7	g18559	BLASTN	1664	1e-68	90	G.max gene for catalase
4511	GM_90_B1_E02_T7	g507910	BLASTN	341	8e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4512	GM_90_B1_E03_MR	g13767	BLASTN	358	5e-10	63	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
4513	GM_90_B1_E03_T7	g3746069	BLASTX	205	2e-14	31	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
4514	GM_90_B1_E04_T7	g1142703	BLASTN	317	1e-17	78	Glycine max satellite STR120-B.1.
4515	GM_90_B1_E10_MR	g18559	BLASTN	1191	5e-47	72	G.max gene for catalase
4516	GM_90_B1_E11_T7	g2979574	BLASTN	419	7e-12	61	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence [Homo sapiens]
4517	GM_90_B1_E12_T7	g1666236	BLASTX	174	4e-12	29	(U76261) unknown [Hordeum vulgare]
4518	GM_90_B1_F10_T7	g18559	BLASTN	997	3e-38	70	G.max gene for catalase
4519	GM_90_B1_F12_MR	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4520	GM_90_B1_F12_T7	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4521	GM_90_B1_G06_MR	g3645899	BLASTX	228	4e-21	45	(U68408) 5' end not determined experimentally [Zea mays]
4522	GM_90_B1_G08_MR	g507910	BLASTN	486	2e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
4523	GM_90_B1_G10_MR	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4524	GM_90_B1_G10_T7	g4063760	BLASTX	288	3e-23	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4525	GM_90_B1_H02_MR	g3461846	BLASTX	356	9e-40	56	(AC005315) putative zinc-finger protein [Arabidopsis thaliana]

4526	GM_90_B1_H12_MR	g3142328	BLASTN	887	3e-33	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4527	GM_90_B2_A02_MR	g3777527	BLASTX	739	3e-71	95	(AF053008) gag-pol polyprotein [Glycine max]
4528	GM_90_B2_A04_T7	g4038056	BLASTX	347	9e-30	46	(AC005897) putative transposon [Arabidopsis thaliana]
4529	GM_90_B2_A06_MR	g3645899	BLASTX	374	2e-32	60	(U68408) 5' end not determined experimentally [Zea mays]
4530	GM_90_B2_A08_MR	g629693	BLASTX	363	1e-32	61	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
4531	GM_90_B2_A10_MR	g18737	BLASTN	368	1e-09	69	Glycine max RPRP3 gene for repetitive proline-rich protein 3
4532	GM_90_B2_A12_T7	g2911048	BLASTX	201	7e-15	54	(AL021961) hypothetical protein [Arabidopsis thaliana]
4533	GM_90_B2_B02_MR	g507910	BLASTN	435	5e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
4534	GM_90_B2_B02_T7	g507910	BLASTN	555	2e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
4535	GM_90_B2_C10_MR	g3810596	BLASTX	139	1e-13	33	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4536	GM_90_B2_D04_T7	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4537	GM_90_B2_D05_MR	g505129	BLASTN	363	2e-09	71	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
4538	GM_90_B2_D05_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
4539	GM_90_B2_D06_MR	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4540	GM_90_B2_D06_T7	g4063760	BLASTX	481	7e-44	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4541	GM_90_B2_D08_MR	g4063760	BLASTX	303	7e-25	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4542	GM_90_B2_D09_T7	g2959736	BLASTX	306	1e-26	80	(Y13651) homologous to GATA-binding transcription factors [Arabidopsis thaliana]
4543	GM_90_B2_D12_T7	g4038056	BLASTX	379	3e-33	52	(AC005897) putative transposon [Arabidopsis thaliana]
4544	GM_90_B2_E01_MR	g1628038	BLASTN	400	5e-11	62	Caenorhabditis elegans cosmid K09G1, complete sequence [Caenorhabditis elegans]
4545	GM_90_B2_E06_MR	g507910	BLASTN	413	5e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
4546	GM_90_B2_E06_T7	g3097320	BLASTN	509	5e-16	80	Glycine max gene for Bd 30K, complete cds
4547	GM_90_B2_E07_T7	g3549661	BLASTX	344	1e-30	51	(AL031394) hypothetical protein [Arabidopsis thaliana]
4548	GM_90_B2_F05_MR	g1652066	BLASTX	188	2e-13	45	(D90902) Na/H antiporter [Synechocystis sp.]
4549	GM_90_B2_F05_T7	g170083	BLASTN	388	8e-11	69	Soybean (clone E15) urease (ure) gene, exons 2,3 and 4 and partial cds.
4550	GM_90_B2_F06_T7	g18559	BLASTN	463	6e-14	75	G.max gene for catalase
4551	GM_90_B2_G01_MR	g3810596	BLASTX	159	1e-09	36	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4552	GM_90_B2_G01_T7	g340697	BLASTN	464	2e-19	71	Soybean chloroplast 16S/23S ribosomal intergenic spacer DNA.
4553	GM_90_B2_G08_MR	g3930515	BLASTX	122	4e-12	38	(AF059674) putative gag protein [Nicotiana tabacum]
4554	GM_90_B2_G09_MR	g2995405	BLASTX	477	8e-44	66	(Y12432) polyprotein [Ananas comosus]
4555	GM_90_B2_G09_T7	g3452140	BLASTX	231	1e-18	47	(AJ004901) resistance protein [Glycine max]
4556	GM_90_B2_G12_MR	g507910	BLASTN	561	1e-18	83	Glycine max BSR-101 satellite SB92 genomic sequence.
4557	GM_90_B2_H05_MR	g18559	BLASTN	974	4e-37	76	G.max gene for catalase
4558	GM_90_B2_H06_T7	g905361	BLASTX	694	1e-67	95	(U22103) gag-protease polyprotein [Glycine max]

4559	GM_90_B2_H07_MR	g507910	BLASTN	353	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4560	GM_90_B2_H08_T7	g4092471	BLASTN	446	4e-13	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
4561	GM_90_B2_H10_MR	g1076755	BLASTX	411	8e-37	78	protein kinase - rice gi 450300 (L27821) protein kinase [Oryza sativa]
4562	GM_91_A1_A09_T7	g3157910	BLASTX	196	6e-19	67	(AF003551) lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Zea mays]
4563	GM_91_A1_A12_T7	g3142328	BLASTN	1094	1e-42	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4564	GM_91_A1_B03_T7	g3695395	BLASTX	211	2e-15	45	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
4565	GM_91_A1_B06_MR	g2598589	BLASTX	250	3e-20	48	(Y15367) MtN19 [Medicago truncatula]
4566	GM_91_A1_B08_T7	g18559	BLASTN	972	5e-37	75	G.max gene for catalase
4567	GM_91_A1_C04_T7	g1877279	BLASTX	121	9e-09	58	(Z92770) fadE2 [Mycobacterium tuberculosis]
4568	GM_91_A1_C10_T7	g4063760	BLASTX	300	2e-24	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4569	GM_91_A1_D05_T7	g85105	BLASTX	177	2e-11	38	pol polyprotein - fruit fly (Drosophila melanogaster) transposon 1731 gi 8702 (X07656) pol polypeptide (AA 1-982) [Drosophila melanogaster]
4570	GM_91_A1_D09_MR	g507910	BLASTN	349	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4571	GM_91_A1_D09_T7	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
4572	GM_91_A1_E02_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4573	GM_91_A1_E07_T7	g1666236	BLASTX	224	7e-18	32	(U76261) unknown [Hordeum vulgare]
4574	GM_91_A1_E10_T7	g2522228	BLASTX	566	4e-54	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
4575	GM_91_A1_E11_T7	g1785739	BLASTX	149	2e-12	43	(Y08502) orf240b [Arabidopsis thaliana]
4576	GM_91_A1_F05_MR	g3510505	BLASTX	116	6e-10	41	(AF030881) pol polyprotein [Fugu rubripes]
4577	GM_91_A1_F06_MR	g3777527	BLASTX	415	1e-36	100	(AF053008) gag-pol polyprotein [Glycine max]
4578	GM_91_A1_F10_T7	g2129618	BLASTX	212	3e-15	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4579	GM_91_A1_F11_T7	g3645899	BLASTX	203	2e-19	53	(U68408) 5' end not determined experimentally [Zea mays]
4580	GM_91_A1_G02_MR	g100484	BLASTX	221	2e-16	42	hypothetical protein - garden snapdragon
4581	GM_91_A1_G09_MR	g2961349	BLASTX	153	7e-09	50	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
4582	GM_91_A1_G09_T7	g1369955	BLASTN	383	3e-10	63	Caenorhabditis elegans cosmid B0564, complete sequence [Caenorhabditis elegans]
4583	GM_91_A1_H01_T7	g507910	BLASTN	715	1e-25	88	Glycine max BSR-101 satellite SB92 genomic sequence.
4584	GM_91_A1_H02_MR	g4159704	BLASTN	437	1e-12	71	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence [Arabidopsis thaliana]
4585	GM_91_A1_H05_T7	g3695395	BLASTX	155	2e-14	44	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]

4586	GM_91_A1_H08_MR	g3327389	BLASTX	165	8e-22	79	(AC004483) putative DNA replication licensing factor, mcm5 [Arabidopsis thaliana]
4587	GM_91_A1_H08_T7	g557882	BLASTX	343	2e-30	62	(U13923) putative serine/threonine protein kinase; similar to product encoded by Lycopersicon pimpinellifolium Pto gene, GenBank Accession Number U02271; Fen is a member of the Pto gene family [Solanum pimpinellifolium] gi 1809263 (U59317) serine/threonine protein kinase Fen [Lycopersicon pimpinellifolium] gi 1096880 prf 2112354B Fen gene [Lycopersicon esculentum] gi 1098334 prf 2115395A Fen gene [Lycopersicon esculentum]
4588	GM_91_B1_A02_T7	g1769899	BLASTX	311	4e-27	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4589	GM_91_B1_A04_T7	g505129	BLASTN	453	1e-13	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
4590	GM_91_B1_A06_T7	g3097320	BLASTN	488	5e-15	72	Glycine max gene for Bd 30K, complete cds
4591	GM_91_B1_A07_T7	g505129	BLASTN	353	5e-09	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
4592	GM_91_B1_A10_T7	g4063760	BLASTX	254	1e-31	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4593	GM_91_B1_B01_T7	g2764526	BLASTN	398	7e-16	65	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
4594	GM_91_B1_B11_T7	g531389	BLASTX	227	4e-26	49	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
4595	GM_91_B1_C01_T7	g2586082	BLASTX	236	1e-25	47	(U72725) retrofit [Oryza longistaminata]
4596	GM_91_B1_C08_T7	g507910	BLASTN	686	2e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
4597	GM_91_B1_C09_T7	g2522230	BLASTX	134	1e-10	36	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4598	GM_91_B1_C12_T7	g4063760	BLASTX	249	4e-19	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4599	GM_91_B1_D05_T7	g2443320	BLASTX	218	1e-15	40	(D85597) polyprotein [Oryza australiensis]
4600	GM_91_B1_D08_T7	g3810596	BLASTX	158	1e-09	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4601	GM_91_B1_E10_T7	g1769898	BLASTX	402	2e-36	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4602	GM_91_B1_F10_T7	g4038056	BLASTX	266	4e-21	46	(AC005897) putative transposon [Arabidopsis thaliana]
4603	GM_91_B1_F12_T7	g4063760	BLASTX	495	2e-45	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4604	GM_91_B1_H12_T7	g1946279	BLASTX	270	5e-26	51	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
4605	GM_91_B2_A02_MR	g3549672	BLASTX	158	2e-18	91	(AL031394) putative protein [Arabidopsis thaliana]
4606	GM_91_B2_A03_T7	g2443320	BLASTX	269	3e-21	37	(D85597) polyprotein [Oryza australiensis]
4607	GM_91_B2_A05_MR	g3063464	BLASTX	248	6e-20	80	(AC003981) F22O13.26 [Arabidopsis thaliana]
4608	GM_91_B2_A08_MR	g2073447	BLASTN	369	1e-09	63	L.japonicus gln1, pge1 & krm genes
4609	GM_91_B2_B06_MR	g3319362	BLASTX	267	4e-21	47	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
4610	GM_91_B2_B07_MR	g1142702	BLASTN	1080	3e-42	95	Glycine max satellite STR120-A.4.

4611	GM_91_B2_B08_T7	g3777527	BLASTX	304	8e-25	43	(AF053008) gag-pol polyprotein [Glycine max]
4612	GM_91_B2_B09_MR	g3645899	BLASTX	272	1e-21	46	(U68408) 5' end not determined experimentally [Zea mays]
4613	GM_91_B2_B11_T7	g3645899	BLASTX	214	2e-15	48	(U68408) 5' end not determined experimentally [Zea mays]
4614	GM_91_B2_C06_MR	g3962377	BLASTX	663	2e-64	96	(AJ002551) heat shock protein 70 [Arabidopsis thaliana]
4615	GM_91_B2_C07_MR	g1142701	BLASTN	1351	1e-54	87	Glycine max satellite STR120-A.3.
4616	GM_91_B2_C08_MR	g2129618	BLASTX	238	4e-18	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4617	GM_91_B2_D01_MR	g3097320	BLASTN	1149	5e-45	79	Glycine max gene for Bd 30K, complete cds
4618	GM_91_B2_D03_T7	g508442	BLASTN	365	1e-09	60	Cucurbita maxima (clone gPC13-1B) phloem protein 2 (PP2) gene, complete cds.
4619	GM_91_B2_D06_MR	g507910	BLASTN	384	9e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
4620	GM_91_B2_D06_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4621	GM_91_B2_D07_MR	g128771	BLASTX	99	3e-11	59	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 5, CHLOROPLAST gi 100110 pir S08494 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - fava bean chloroplast gi 11555 (X14804) ndhF gene product (AA 1-746) [Vicia faba] gi 12390 (X51471) NADH dehydrogenase [Vicia faba] gi 552971 (M36832) NADH dehydrogenase (ndhF) [Vicia faba]
4622	GM_91_B2_D08_T7	g4063760	BLASTX	449	2e-40	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4623	GM_91_B2_D09_T7	g3641837	BLASTX	183	3e-12	46	(AL023094) Nonclathrin coat protein gamma - like protein [Arabidopsis thaliana]
4624	GM_91_B2_D10_MR	g1769898	BLASTX	363	5e-32	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4625	GM_91_B2_E08_MR	g3142328	BLASTN	2018	7e-85	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4626	GM_91_B2_E09_T7	g3513745	BLASTX	252	3e-19	34	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
4627	GM_91_B2_F03_MR	g3845197	BLASTN	467	4e-14	63	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
4628	GM_91_B2_F03_T7	g3894157	BLASTX	251	2e-19	38	(AC005312) putative protein kinase, 3' partial [Arabidopsis thaliana]
4629	GM_91_B2_F05_T7	g507910	BLASTN	619	2e-21	85	Glycine max BSR-101 satellite SB92 genomic sequence.
4630	GM_91_B2_F07_T7	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4631	GM_91_B2_F11_MR	g3097836	BLASTN	407	2e-11	62	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
4632	GM_91_B2_G04_MR	g3426334	BLASTN	350	8e-09	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
4633	GM_91_B2_G05_T7	g4092471	BLASTN	381	4e-10	64	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]

4634	GM_91_B2_G06_MR	g117519	BLASTX	489	6e-46	94	PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE) gi 99945 pir A39597 phytoene dehydrogenase (EC 1.3.-.-) - soybean gi 170044 (M64704) phytoene desaturase [Glycine max]
4635	GM_91_B2_G08_MR	g2764526	BLASTN	655	1e-22	68	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
4636	GM_91_B2_G08_T7	g100484	BLASTX	228	8e-24	52	hypothetical protein - garden snapdragon
4637	GM_91_B2_G09_T7	g2564051	BLASTN	380	7e-11	75	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]
4638	GM_91_B2_G11_T7	g3142328	BLASTN	1794	1e-74	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4639	GM_91_B2_H01_MR	g3777527	BLASTX	773	7e-75	96	(AF053008) gag-pol polyprotein [Glycine max]
4640	GM_91_B2_H03_T7	g559718	BLASTN	354	6e-09	62	Pneumocystis carinii genes for MSG99 and MSG100, complete cds
4641	GM_91_B2_H04_MR	g3785989	BLASTX	190	3e-13	63	(AC005560) unknown protein [Arabidopsis thaliana]
4642	GM_91_B2_H07_MR	g505129	BLASTN	371	8e-10	71	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
4643	GM_91_B2_H08_MR	g3650039	BLASTX	301	4e-25	43	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
4644	GM_91_B2_H10_MR	g4063760	BLASTX	174	4e-11	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4645	GM_91_B2_H11_MR	g3142328	BLASTN	794	5e-29	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4646	GM_92_A2_A07_MR	g3097320	BLASTN	1330	3e-53	83	Glycine max gene for Bd 30K, complete cds
4647	GM_92_A2_A09_MR	g3914007	BLASTX	157	5e-11	85	MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi 1848291 (U88087) LON protease homolog [Arabidopsis thaliana]
4648	GM_92_A2_A10_MR	g2735745	BLASTN	344	7e-09	60	Oncorhynchus kisutch growth hormone 1 gene, intron C, complete sequence
4649	GM_92_A2_B04_MR	g18559	BLASTN	467	4e-14	67	G.max gene for catalase
4650	GM_92_A2_B04_T7	g464900	BLASTX	221	6e-18	39	PUTATIVE KINASE-LIKE PROTEIN TMKL1 PRECURSOR gi 539008 pir S39476 kinase-like transmembrane protein TMKL1 precursor - Arabidopsis thaliana gi 313190 (X72863) TMKL1 gene product [Arabidopsis thaliana]
4651	GM_92_A2_B05_T7	g3142328	BLASTN	1205	1e-47	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4652	GM_92_A2_B06_T7	g2190544	BLASTX	158	4e-10	72	(AC001229) Similar to Saccharomyces hypothetical protein P9642.2 (gb U40828). [Arabidopsis thaliana]
4653	GM_92_A2_B08_MR	g170602	BLASTN	490	3e-16	67	Broad bean (V.faba) BamHI repetitive element, 900 bp family.
4654	GM_92_A2_C05_MR	g4049647	BLASTN	398	6e-11	63	Melanoplus sanguinipes entomopoxvirus, complete genome
4655	GM_92_A2_C08_MR	g2326340	BLASTN	351	8e-09	61	A.thaliana RH1, TC1, G14587-5, G14587-6, and PRL1 genes

4656	GM_92_A2_C11_MR	g4182	BLASTN	588	1e-19	85	2 micron plasmid of yeast (circularly closed). >gi 172190 gb J01347 YSCPLASM S.cerevisiae 2 micron circle plasmid, complete genome.
4657	GM_92_A2_D01_MR	g1666236	BLASTX	151	1e-09	32	(U76261) unknown [Hordeum vulgare]
4658	GM_92_A2_D08_T7	g905361	BLASTX	545	7e-52	82	(U22103) gag-protease polyprotein [Glycine max]
4659	GM_92_A2_D09_T7	g840618	BLASTN	348	7e-09	65	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
4660	GM_92_A2_D10_T7	g1769898	BLASTX	228	4e-32	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4661	GM_92_A2_D11_MR	g1167523	BLASTX	266	8e-21	40	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
4662	GM_92_A2_E02_T7	g3097320	BLASTN	367	1e-09	75	Glycine max gene for Bd 30K, complete cds
4663	GM_92_A2_E07_T7	g3142328	BLASTN	1971	1e-82	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4664	GM_92_A2_E08_MR	g2947063	BLASTX	151	4e-13	35	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]
4665	GM_92_A2_F05_MR	g3097320	BLASTN	916	2e-34	70	Glycine max gene for Bd 30K, complete cds
4666	GM_92_A2_F09_MR	g3097320	BLASTN	423	4e-12	69	Glycine max gene for Bd 30K, complete cds
4667	GM_92_A2_G02_MR	g3777527	BLASTX	179	2e-11	32	(AF053008) gag-pol polyprotein [Glycine max]
4668	GM_92_A2_G03_T7	g3142328	BLASTN	1391	4e-56	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4669	GM_92_A2_G05_MR	g18559	BLASTN	542	2e-17	74	G.max gene for catalase
4670	GM_92_A2_G08_MR	g3142328	BLASTN	898	1e-33	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4671	GM_92_A2_H01_T7	g2522227	BLASTX	151	1e-09	46	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
4672	GM_92_A2_H03_T7	g3377834	BLASTX	192	2e-13	33	(AF075598) No definition line found [Arabidopsis thaliana]
4673	GM_92_A2_H05_MR	g507910	BLASTN	346	5e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4674	GM_92_A2_H06_MR	g3763929	BLASTX	268	1e-21	70	(AC004450) hypothetical protein [Arabidopsis thaliana]
4675	GM_92_A2_H10_MR	g2995405	BLASTX	319	8e-27	51	(Y12432) polyprotein [Ananas comosus]
4676	GM_92_B1_A01_T7	g2961377	BLASTX	163	6e-10	34	(AL022141) putative receptor protein kinase [Arabidopsis thaliana]
4677	GM_92_B1_A02_T7	g507910	BLASTN	455	6e-14	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4678	GM_92_B1_A11_T7	g3142328	BLASTN	1185	9e-47	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4679	GM_92_B1_B01_T7	g4038056	BLASTX	377	5e-33	48	(AC005897) putative transposon [Arabidopsis thaliana]
4680	GM_92_B1_B03_MR	g18559	BLASTN	1027	2e-39	73	G.max gene for catalase
4681	GM_92_B1_B05_MR	g2129618	BLASTX	179	9e-12	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4682	GM_92_B1_C04_MR	g226407	BLASTX	339	1e-28	45	retrotransposon del1-46 [Lilium henryi]
4683	GM_92_B1_C05_MR	g2522230	BLASTX	171	3e-12	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4684	GM_92_B1_C05_T7	g2522228	BLASTX	366	7e-33	53	(AB007466) reverse transcriptase-like protein [Vicia faba]
4685	GM_92_B1_C12_T7	g4097587	BLASTX	185	1e-13	65	(U64926) NTGP5 [Nicotiana tabacum]
4686	GM_92_B1_D02_MR	g1769898	BLASTX	226	4e-17	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

4687	GM_92_B1_D03_MR	g1890143	BLASTN	347	1e-08	64	A.aegypti DNA, copia-like transposable element ZebedeeII
4688	GM_92_B1_D05_T7	g2462936	BLASTX	253	2e-23	41	(Y12321) open reading frame 2 [Brassica oleracea]
4689	GM_92_B1_D09_T7	g18695	BLASTN	370	7e-10	68	Soybean nodulin 22 gene
4690	GM_92_B1_D11_MR	g18559	BLASTN	913	2e-34	75	G.max gene for catalase
4691	GM_92_B1_D11_T7	g2961349	BLASTX	197	1e-28	52	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
4692	GM_92_B1_E01_T7	g3097320	BLASTN	1221	3e-48	84	Glycine max gene for Bd 30K, complete cds
4693	GM_92_B1_E02_T7	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
4694	GM_92_B1_E04_T7	g507910	BLASTN	353	2e-09	84	Glycine max BSR-101 satellite SB92 genomic sequence.
4695	GM_92_B1_E06_T7	g507910	BLASTN	410	6e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4696	GM_92_B1_F01_T7	g508826	BLASTN	415	9e-12	60	Drosophila melanogaster Oregon-R mitochondrial A+T region.
4697	GM_92_B1_F07_T7	g99922	BLASTX	693	1e-67	85	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
4698	GM_92_B1_F10_MR	g3212869	BLASTX	335	6e-29	77	(AC004005) unknown protein [Arabidopsis thaliana]
4699	GM_92_B1_G02_MR	g3142289	BLASTX	234	4e-18	55	(AC002411) Strong similarity to beta-keto-Coa synthase gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
4700	GM_92_B1_G02_T7	g3142328	BLASTN	1094	1e-42	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4701	GM_92_B1_G04_MR	g2367675	BLASTX	194	2e-13	33	(AF017040) Pol [Dictyostelium discoideum]
4702	GM_92_B1_G05_MR	g3560170	BLASTX	230	3e-24	71	(AL031525) 26s protease regulatory subunit S10b [Schizosaccharomyces pombe]
4703	GM_92_B1_G05_T7	g102489	BLASTX	114	4e-14	54	vacuolar proton pump homolog - Caenorhabditis elegans gi 6961 (Z11115) cDNA EST yk307a1.5 comes from this gene; cDNA EST yk469d12.5 comes from this gene; cDNA EST yk499g12.5 comes from this gene [Caenorhabditis elegans]
4704	GM_92_B1_G08_MR	g3377855	BLASTX	278	6e-35	59	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
4705	GM_92_B1_H03_T7	g18559	BLASTN	320	4e-10	76	G.max gene for catalase
4706	GM_92_B1_H05_T7	g2129618	BLASTX	171	6e-11	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4707	GM_92_B1_H09_MR	g2746847	BLASTX	179	2e-13	38	(AF040649) contains similarity to helicases [Caenorhabditis elegans]
4708	GM_92_B1_H09_T7	g18559	BLASTN	544	1e-17	71	G.max gene for catalase
4709	GM_94_A1_B08_T7	g3142328	BLASTN	948	5e-36	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4710	GM_94_A1_B09_T7	g3560029	BLASTN	427	2e-12	65	Schistosoma intercalatum ribosomal intergenic spacer DNA (2169 bp)
4711	GM_94_A1_C03_MR	g507910	BLASTN	366	6e-10	79	Glycine max BSR-101 satellite SB92 genomic sequence.
4712	GM_94_A1_C04_T7	g3777527	BLASTX	520	8e-48	91	(AF053008) gag-pol polyprotein [Glycine max]
4713	GM_94_A1_C07_MR	g507910	BLASTN	387	7e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.

4714	GM_94_A1_C07_T7	g507910	BLASTN	363	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4715	GM_94_A1_C12_MR	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4716	GM_94_A1_D03_T7	g2462134	BLASTX	323	5e-28	45	(Y13368) reverse transcriptase [Beta vulgaris]
4717	GM_94_A1_E02_MR	g2244747	BLASTN	355	5e-09	72	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 0
4718	GM_94_A1_E08_MR	g18559	BLASTN	399	5e-11	73	G.max gene for catalase
4719	GM_94_A1_F08_MR	g4063760	BLASTX	175	3e-11	36	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4720	GM_94_A1_H12_MR	g18559	BLASTN	631	1e-21	74	G.max gene for catalase
4721	GM_94_A2_A01_MR	g4050011	BLASTN	559	3e-18	70	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
4722	GM_94_A2_A03_T7	g3142328	BLASTN	471	3e-14	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4723	GM_94_A2_A06_MR	g3777527	BLASTX	665	3e-63	90	(AF053008) gag-pol polyprotein [Glycine max]
4724	GM_94_A2_A11_MR	g3777527	BLASTX	679	8e-65	92	(AF053008) gag-pol polyprotein [Glycine max]
4725	GM_94_A2_A11_T7	g1769898	BLASTX	241	4e-28	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4726	GM_94_A2_A12_T7	g2522227	BLASTX	160	1e-10	43	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
4727	GM_94_A2_B03_T7	g18559	BLASTN	966	9e-37	75	G.max gene for catalase
4728	GM_94_A2_B06_MR	g507910	BLASTN	557	1e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
4729	GM_94_A2_B06_T7	g507910	BLASTN	615	4e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
4730	GM_94_A2_B08_MR	g507910	BLASTN	362	9e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4731	GM_94_A2_B09_MR	g4092471	BLASTN	520	2e-16	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
4732	GM_94_A2_B11_MR	g3930515	BLASTX	115	4e-09	46	(AF059674) putative gag protein [Nicotiana tabacum]
4733	GM_94_A2_C01_T7	g2522228	BLASTX	442	6e-41	57	(AB007466) reverse transcriptase-like protein [Vicia faba]
4734	GM_94_A2_C02_MR	g1916643	BLASTX	269	1e-22	54	(U71604) desacetoxyvindoline 4-hydroxylase [Catharanthus roseus]
4735	GM_94_A2_C03_MR	g2443320	BLASTX	369	8e-32	45	(D85597) polyprotein [Oryza australiensis]
4736	GM_94_A2_C03_T7	g18559	BLASTN	607	2e-20	71	G.max gene for catalase
4737	GM_94_A2_C05_T7	g99922	BLASTX	279	1e-23	62	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
4738	GM_94_A2_C06_MR	g2708743	BLASTX	258	6e-20	43	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
4739	GM_94_A2_C08_MR	g2443320	BLASTX	351	7e-30	58	(D85597) polyprotein [Oryza australiensis]
4740	GM_94_A2_C12_MR	g320565	BLASTX	298	1e-25	55	transposon TA1-1 KAS-1 - Arabidopsis thaliana (fragment)
4741	GM_94_A2_D03_MR	g2129618	BLASTX	265	6e-21	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4742	GM_94_A2_D04_MR	g1769898	BLASTX	399	4e-42	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4743	GM_94_A2_D07_T7	g3142379	BLASTX	304	2e-26	67	(AF053008) envelope-like [Glycine max]
4744	GM_94_A2_D09_MR	g4006829	BLASTX	270	3e-22	70	(AC005970) putative protein kinase [Arabidopsis thaliana]

4745	GM_94_A2_D10_T7	g1666236	BLASTX	170	1e-11	28	(U76261) unknown [Hordeum vulgare]
4746	GM_94_A2_D12_MR	g100484	BLASTX	379	2e-33	62	hypothetical protein - garden snapdragon
4747	GM_94_A2_E07_MR	g505129	BLASTN	380	3e-10	71	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
4748	GM_94_A2_F02_MR	g13767	BLASTN	367	2e-10	59	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
4749	GM_94_A2_F02_T7	g3763998	BLASTN	344	4e-10	63	Plasmodium falciparum MAL3P4, complete sequence [Plasmodium falciparum]
4750	GM_94_A2_F05_T7	g2129618	BLASTX	196	1e-13	37	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4751	GM_94_A2_F06_MR	g1781040	BLASTX	172	3e-12	78	(X98422) delta-1-pyrroline-5-carboxylate synthase [Medicago sativa]
4752	GM_94_A2_F06_T7	g130582	BLASTX	178	2e-11	32	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
4753	GM_94_A2_F07_MR	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
4754	GM_94_A2_F07_T7	g507910	BLASTN	416	3e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
4755	GM_94_A2_F10_MR	g2500199	BLASTX	130	1e-16	93	RAC-LIKE GTP BINDING PROTEIN RHO1 gi 477010 pir A47525 ras-related small GTP-binding protein Rho1Ps - garden pea gi 1263170 (L19093) GTP-binding protein [Pisum sativum]
4756	GM_94_A2_F11_MR	g1171046	BLASTX	180	3e-13	60	METALLOTHIONEIN-LIKE PROTEIN B gi 480753 pir S37240 metallothionein-like protein - white clover gi 403329 (Z26493) metallothionein-like protein [Trifolium repens]
4757	GM_94_A2_G02_T7	g3845307	BLASTN	350	9e-09	63	Plasmodium falciparum chromosome 2, section 61 of 73 of the complete sequence
4758	GM_94_A2_G03_MR	g1174621	BLASTX	219	8e-22	54	T-COMPLEX PROTEIN 1, THETA SUBUNIT (TCP-1-THETA) (CCT-THETA) gi 1083259 pir JC4073 TCP-1 containing cytosolic chaperonin (CCT) theta chain - mouse gi 695625 (Z37164) CCTtheta, theta subunit of the chaperonin containing TCP-1 (CCT) [Mus musculus]
4759	GM_94_A2_G03_T7	g3894211	BLASTN	483	9e-15	65	Homo sapiens PAC clone DJ0888A21 from 7q31, complete sequence [Homo sapiens]
4760	GM_94_A2_G08_MR	g731675	BLASTX	101	2e-11	58	HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION gi 626631 pir S46811 hypothetical protein YHR074w - yeast (Saccharomyces cerevisiae) gi 500832 (U10556) Yhr074wp [Saccharomyces cerevisiae]

4761	GM_94_A2_G12_MR	g507910	BLASTN	579	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4762	GM_94_A2_H02_T7	g4063760	BLASTX	125	3e-11	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4763	GM_94_A2_H11_T7	g4038056	BLASTX	191	4e-13	42	(AC005897) putative transposon [Arabidopsis thaliana]
4764	GM_94_B2_B01_MR	g100484	BLASTX	300	6e-25	60	hypothetical protein - garden snapdragon
4765	GM_94_B2_B06_MR	g2443320	BLASTX	237	2e-21	52	(D85597) polyprotein [Oryza australiensis]
4766	GM_94_B2_B10_MR	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
4767	GM_94_B2_C03_T7	g905361	BLASTX	209	3e-15	38	(U22103) gag-protease polyprotein [Glycine max]
4768	GM_94_B2_C06_T7	g2997694	BLASTX	182	2e-13	43	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
4769	GM_94_B2_C08_T7	g507910	BLASTN	621	2e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4770	GM_94_B2_D03_T7	g2995405	BLASTX	278	2e-22	45	(Y12432) polyprotein [Ananas comosus]
4771	GM_94_B2_D08_MR	g507910	BLASTN	410	6e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4772	GM_94_B2_D10_T7	g3097320	BLASTN	1185	1e-46	82	Glycine max gene for Bd 30K, complete cds
4773	GM_94_B2_D11_T7	g4038056	BLASTX	298	1e-24	54	(AC005897) putative transposon [Arabidopsis thaliana]
4774	GM_94_B2_E05_T7	g3097320	BLASTN	610	1e-20	74	Glycine max gene for Bd 30K, complete cds
4775	GM_94_B2_F05_MR	g130582	BLASTX	292	1e-23	56	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
4776	GM_94_B2_F09_MR	g3142328	BLASTN	1054	8e-41	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4777	GM_94_B2_G04_T7	g2275215	BLASTX	219	2e-17	65	(AC002337) hypothetical protein [Arabidopsis thaliana]
4778	GM_94_B2_G11_T7	g4063760	BLASTX	299	3e-26	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4779	GM_94_B2_H05_MR	g2995405	BLASTX	161	7e-10	39	(Y12432) polyprotein [Ananas comosus]
4780	GM_94_B2_H05_T7	g3688328	BLASTX	112	2e-14	44	(AJ228325) reverse transcriptase [Ginkgo biloba]
4781	GM_95_A2_A06_T7	g4006833	BLASTX	200	8e-14	38	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
4782	GM_95_A2_B10_T7	g3645899	BLASTX	225	2e-28	63	(U68408) 5' end not determined experimentally [Zea mays]
4783	GM_95_A2_C05_MR	g3287465	BLASTN	372	9e-10	66	Homo sapiens chromosome 17, clone hRPK.1003_J_3, complete sequence [Homo sapiens]
4784	GM_95_A2_D06_MR	g1769898	BLASTX	300	3e-33	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4785	GM_95_A2_E05_MR	g2586082	BLASTX	152	6e-12	42	(U72725) retrofit [Oryza longistaminata]
4786	GM_95_A2_E07_MR	g2462936	BLASTX	277	2e-23	38	(Y12321) open reading frame 2 [Brassica oleracea]
4787	GM_95_A2_G04_T7	g507910	BLASTN	547	4e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
4788	GM_95_B1_A01_T7	g2522228	BLASTX	329	6e-29	74	(AB007466) reverse transcriptase-like protein [Vicia faba]
4789	GM_95_B1_A02_T7	g3337381	BLASTN	361	3e-09	67	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-952F10, complete sequence [Homo sapiens]
4790	GM_95_B1_A03_MR	g3599418	BLASTN	1038	4e-40	88	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds

4791	GM_95_B1_B03_T7	g3080452	BLASTX	163	2e-10	57	(AL022605) putative L-ascorbate oxidase [Arabidopsis thaliana]
4792	GM_95_B1_B05_T7	g2443320	BLASTX	364	3e-31	50	(D85597) polyprotein [Oryza australiensis]
4793	GM_95_B1_B11_T7	g3777527	BLASTX	168	3e-10	31	(AF053008) gag-pol polyprotein [Glycine max]
4794	GM_95_B1_C01_T7	g209638	BLASTN	346	8e-09	63	Amsacta entomopoxvirus thymidine kinase gene, complete cds; Q1 ORF, complete cds; Q3 ORF, 5'end. >gi 1251579 gb I16671 I16671 Sequence 8 from patent US 5476781 >gi 3409364 gb I89424 I89424 Sequence 8 from patent US 5721352
4795	GM_95_B1_C02_MR	g4063760	BLASTX	129	2e-11	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4796	GM_95_B1_C02_T7	g18559	BLASTN	414	1e-11	66	G.max gene for catalase
4797	GM_95_B1_C04_MR	g2245115	BLASTX	160	8e-10	57	(Z97343) unnamed protein product [Arabidopsis thaliana]
4798	GM_95_B1_C05_MR	g2522228	BLASTX	107	9e-09	27	(AB007466) reverse transcriptase-like protein [Vicia faba]
4799	GM_95_B1_C11_T7	g13773	BLASTN	441	7e-14	67	Torulopsis glabrata mitochondrial genes for tRNAs -Tyr, -Asn, -Ala, -Ile -Trp (from Var1-LrRNA intergenic region) >gi 343959 gb M11906 YSLMTIG09 Yeast (T.glabrata) mitochondrial DNA between var1 and L rRNA genes.
4800	GM_95_B1_C12_T7	g20854	BLASTN	419	4e-12	68	Pea rbcS-3A gene for ribulose 1.5-bisphosphate carboxylase (RBC) small subunit
4801	GM_95_B1_D01_MR	g3006135	BLASTN	421	6e-12	70	Homo sapiens DNA sequence from BAC 363A12 on chromosome 22q11.2-12.2, complete sequence [Homo sapiens]
4802	GM_95_B1_D06_MR	g1169534	BLASTX	141	5e-16	96	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) gi 542019 pir S39203 phosphopyruvate hydratase (EC 4.2.1.11) - castor bean gi 433609 (Z28386) enolase [Ricinus communis]
4803	GM_95_B1_E01_MR	g3777527	BLASTX	123	4e-09	28	(AF053008) gag-pol polyprotein [Glycine max]
4804	GM_95_B1_E02_T7	g3264544	BLASTN	490	4e-15	64	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
4805	GM_95_B1_E04_T7	g1666236	BLASTX	219	3e-17	31	(U76261) unknown [Hordeum vulgare]
4806	GM_95_B1_E05_MR	g1173285	BLASTX	288	9e-25	68	40S RIBOSOMAL PROTEIN S9 gi 1362936 pir S55917 ribosomal protein S9 - human gi 550023 (U14971) ribosomal protein S9 [Homo sapiens] gi 1096943 prf 2113200F ribosomal protein S9 [Homo sapiens]
4807	GM_95_B1_F01_T7	g3142328	BLASTN	923	8e-41	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4808	GM_95_B1_F03_T7	g2464905	BLASTX	164	2e-11	58	(Z99708) minor allergen [Arabidopsis thaliana]
4809	GM_95_B1_F04_T7	g1514643	BLASTX	232	2e-25	62	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
4810	GM_95_B1_F07_T7	g18768	BLASTN	370	2e-10	73	Soybean Tgm6 transposable element 3' end
4811	GM_95_B1_F08_T7	g99922	BLASTX	164	2e-23	82	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]

4812	GM_95_B1_G06_T7	g3142328	BLASTN	909	3e-34	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4813	GM_95_B1_G11_T7	g507910	BLASTN	348	4e-09	75	Glycine max BSR-101 satellite SB92 genomic sequence.
4814	GM_95_B1_H02_MR	g2558662	BLASTX	176	2e-13	59	(AC002354) No definition line found [Arabidopsis thaliana]
4815	GM_95_B1_H06_T7	g4063760	BLASTX	337	2e-28	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4816	GM_95_B1_H10_T7	g288378	BLASTN	372	7e-10	68	Z.mays gene PG for polygalacturonase.
4817	GM_95_B1_H11_MR	g2208908	BLASTX	327	2e-28	54	(AB004809) phosphate transporter [Catharanthus roseus]
4818	GM_95_B2_A09_MR	g3777527	BLASTX	162	1e-09	35	(AF053008) gag-pol polyprotein [Glycine max]
4819	GM_95_B2_A09_T7	g3097320	BLASTN	403	3e-11	76	Glycine max gene for Bd 30K, complete cds
4820	GM_95_B2_A10_MR	g3096945	BLASTX	160	5e-11	58	(AL023094) putative auxin-regulated protein [Arabidopsis thaliana]
4821	GM_95_B2_A10_T7	g1944188	BLASTN	346	8e-09	72	Soybean DNA for nodulin 35, partial cds
4822	GM_95_B2_A12_T7	g3142328	BLASTN	1171	4e-46	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4823	GM_95_B2_B01_MR	g507910	BLASTN	446	1e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
4824	GM_95_B2_B02_MR	g1813979	BLASTX	238	4e-32	70	(Y10860) hypothetical protein [Musa acuminata]
4825	GM_95_B2_B04_MR	g507910	BLASTN	582	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4826	GM_95_B2_B04_T7	g4063760	BLASTX	267	2e-36	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4827	GM_95_B2_B10_MR	g2129618	BLASTX	180	7e-12	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4828	GM_95_B2_B11_T7	g3264565	BLASTN	358	4e-09	62	Homo sapiens chromosome 17, clone hRPC.1037_O_7, complete sequence [Homo sapiens]
4829	GM_95_B2_B12_MR	g2443320	BLASTX	379	7e-33	48	(D85597) polyprotein [Oryza australiensis]
4830	GM_95_B2_C02_MR	g20854	BLASTN	468	3e-14	71	Pea rbcS-3A gene for ribulose 1.5-bisphosphate carboxylase (RBC) small subunit
4831	GM_95_B2_C02_T7	g18559	BLASTN	1046	2e-40	76	G.max gene for catalase
4832	GM_95_B2_C06_MR	g507910	BLASTN	343	7e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4833	GM_95_B2_D04_MR	g507910	BLASTN	591	4e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4834	GM_95_B2_D06_T7	g18559	BLASTN	527	7e-17	66	G.max gene for catalase
4835	GM_95_B2_D10_MR	g507910	BLASTN	556	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4836	GM_95_B2_D10_T7	g507910	BLASTN	553	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4837	GM_95_B2_D11_T7	g1171583	BLASTN	415	1e-11	64	P.falciparum complete gene map of plastid-like DNA (IR-A)
4838	GM_95_B2_E01_T7	g1769898	BLASTX	233	7e-18	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4839	GM_95_B2_E04_MR	g507910	BLASTN	540	8e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4840	GM_95_B2_E04_T7	g507910	BLASTN	495	9e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
4841	GM_95_B2_E06_T7	g3212846	BLASTN	451	2e-13	78	Arabidopsis thaliana chromosome II BAC F6E13 genomic sequence, complete sequence [Arabidopsis thaliana]
4842	GM_95_B2_E10_MR	g1769898	BLASTX	222	7e-20	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4843	GM_95_B2_E11_T7	g2462134	BLASTX	150	5e-11	42	(Y13368) reverse transcriptase [Beta vulgaris]
4844	GM_95_B2_F01_T7	g507910	BLASTN	423	2e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.

4845	GM_95_B2_F03_T7	g2464905	BLASTX	220	2e-17	56	(Z99708) minor allergen [Arabidopsis thaliana]
4846	GM_95_B2_F06_T7	g18767	BLASTN	458	2e-14	73	Soybean Tgm6 transposable element 5' end
4847	GM_95_B2_F07_MR	g3402755	BLASTX	245	1e-18	36	(AL031187) putative transposable element [Arabidopsis thaliana]
4848	GM_95_B2_F09_MR	g2104945	BLASTN	536	3e-17	80	Glycine max copia-like retrotransposon Tgmr, complete sequence
4849	GM_95_B2_H02_T7	g130405	BLASTX	220	5e-16	39	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 17.6) gi 74642 pir GNFF17 retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) transposon 17.6 gi 1335613 gnl PID e1849 (X01472) ORF 2, pot. reverse transcriptase [Drosophila melanogaster] gi 224319 prf 1101404B ORF 2 [Drosophila melanogaster]
4850	GM_95_B2_H04_T7	g1184075	BLASTX	174	4e-11	34	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
4851	GM_95_B2_H05_T7	g3650039	BLASTX	210	2e-15	36	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
4852	GM_95_B2_H08_MR	g2160154	BLASTX	248	2e-19	34	(AC000375) F19K23.18 gene product [Arabidopsis thaliana]
4853	GM_95_B2_H08_T7	g342952	BLASTN	430	2e-13	60	paramecium species 1,168 mt dna dimer: replication init. region.
4854	GM_98_A2_A01_MR	g4063760	BLASTX	524	2e-48	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4855	GM_98_A2_A02_MR	g507910	BLASTN	501	5e-16	79	Glycine max BSR-101 satellite SB92 genomic sequence.
4856	GM_98_A2_A02_T7	g507910	BLASTN	474	8e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
4857	GM_98_A2_A10_MR	g70616	BLASTX	157	9e-11	81	leghemoglobin c3 - soybean
4858	GM_98_A2_A12_MR	g3777527	BLASTX	480	2e-43	91	(AF053008) gag-pol polyprotein [Glycine max]
4859	GM_98_A2_B02_T7	g507910	BLASTN	588	6e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
4860	GM_98_A2_B03_T7	g3142328	BLASTN	1139	1e-44	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4861	GM_98_A2_B04_MR	g507910	BLASTN	673	8e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
4862	GM_98_A2_B08_MR	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4863	GM_98_A2_B08_T7	g507910	BLASTN	600	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4864	GM_98_A2_B12_T7	g2459440	BLASTX	131	8e-12	41	(AC002332) putative receptor kinase [Arabidopsis thaliana]
4865	GM_98_A2_C02_T7	g2588617	BLASTN	372	9e-10	65	Human BAC clone RG119H12 from 7p15, complete sequence [Homo sapiens]
4866	GM_98_A2_C03_T7	g4115365	BLASTX	192	6e-13	42	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
4867	GM_98_A2_C04_MR	g507910	BLASTN	577	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4868	GM_98_A2_C04_T7	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4869	GM_98_A2_C06_MR	g3097320	BLASTN	757	3e-34	82	Glycine max gene for Bd 30K, complete cds
4870	GM_98_A2_C07_MR	g3327389	BLASTX	119	3e-11	66	(AC004483) putative DNA replication licensing factor, mcm5 [Arabidopsis thaliana]
4871	GM_98_A2_C08_T7	g3820757	BLASTN	380	2e-10	64	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]

4872	GM_98_A2_C10_T7	g3777527	BLASTX	178	2e-11	55	(AF053008) gag-pol polyprotein [Glycine max]
4873	GM_98_A2_C11_T7	g4049332	BLASTN	362	5e-10	71	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)
4874	GM_98_A2_C12_MR	g1769898	BLASTX	200	2e-14	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4875	GM_98_A2_D03_MR	g218269	BLASTX	197	5e-15	87	(D12839) reverse transcriptase [Glycine max]
4876	GM_98_A2_D04_MR	g507910	BLASTN	348	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4877	GM_98_A2_D04_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4878	GM_98_A2_D06_MR	g531389	BLASTX	371	6e-32	53	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
4879	GM_98_A2_D11_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4880	GM_98_A2_D11_T7	g507910	BLASTN	369	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
4881	GM_98_A2_D12_T7	g507910	BLASTN	347	4e-09	75	Glycine max BSR-101 satellite SB92 genomic sequence.
4882	GM_98_A2_E06_MR	g507910	BLASTN	364	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4883	GM_98_A2_E09_T7	g507910	BLASTN	494	1e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
4884	GM_98_A2_E10_MR	g3947839	BLASTN	375	7e-10	60	Human DNA sequence from clone 569D19 on chromosome 22q13.1. Contains a novel gene similar to mouse Ras, Dexamethasone-induced 1 (Ras-related protein, RASD1, DEXRAS1) and the last exon of the MB gene for Myoglobin. Cont...
4885	GM_98_A2_F08_MR	g507910	BLASTN	657	4e-23	84	Glycine max BSR-101 satellite SB92 genomic sequence.
4886	GM_98_A2_F10_MR	g4063760	BLASTX	436	5e-39	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4887	GM_98_A2_G01_MR	g3097320	BLASTN	369	1e-09	75	Glycine max gene for Bd 30K, complete cds
4888	GM_98_A2_G03_MR	g3810596	BLASTX	125	6e-12	61	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
4889	GM_98_A2_G04_MR	g2832611	BLASTN	288	7e-10	74	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)
4890	GM_98_A2_G08_T7	g3777527	BLASTX	590	3e-55	95	(AF053008) gag-pol polyprotein [Glycine max]
4891	GM_98_A2_G09_MR	g1769898	BLASTX	537	5e-51	80	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4892	GM_98_A2_G12_MR	g3142328	BLASTN	755	3e-27	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4893	GM_98_A2_H03_MR	g130582	BLASTX	422	2e-37	52	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
4894	GM_98_A2_H09_MR	g3142328	BLASTN	802	2e-29	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4895	GM_98_A2_H10_T7	g3063438	BLASTN	482	1e-14	71	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]
4896	GM_98_A2_H11_T7	g507910	BLASTN	394	3e-11	78	Glycine max BSR-101 satellite SB92 genomic sequence.

4897	GM_98_B1_A01_MR	g3142328	BLASTN	785	1e-28	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4898	GM_98_B1_A08_MR	g3056594	BLASTX	199	5e-14	56	(AC004255) T1F9.15 [Arabidopsis thaliana]
4899	GM_98_B1_B03_MR	g1419120	BLASTX	233	8e-19	58	(Z75513) reverse transcriptase [Oryza sativa]
4900	GM_98_B1_B05_MR	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
4901	GM_98_B1_B05_T7	g507910	BLASTN	370	4e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
4902	GM_98_B1_B09_T7	g507910	BLASTN	514	1e-16	83	Glycine max BSR-101 satellite SB92 genomic sequence.
4903	GM_98_B1_C01_MR	g2244952	BLASTX	224	9e-25	76	(Z97340) strong similarity to ZK688.3 protein - Caenorhabditis elegans [Arabidopsis thaliana]
4904	GM_98_B1_C01_T7	g2642431	BLASTX	270	3e-21	50	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
4905	GM_98_B1_C03_MR	g3777527	BLASTX	318	6e-28	81	(AF053008) gag-pol polyprotein [Glycine max]
4906	GM_98_B1_C07_T7	g342964	BLASTN	535	4e-18	66	paramecium species 5,311 mt dna dimer: replication init. region.
4907	GM_98_B1_C09_MR	g3777527	BLASTX	177	3e-11	37	(AF053008) gag-pol polyprotein [Glycine max]
4908	GM_98_B1_D02_MR	g99922	BLASTX	391	1e-57	81	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
4909	GM_98_B1_D11_MR	g2982452	BLASTX	266	5e-21	43	(AL022223) receptor protein kinase - like protein [Arabidopsis thaliana]
4910	GM_98_B1_E02_MR	g2522230	BLASTX	171	3e-12	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4911	GM_98_B1_E02_T7	g2522230	BLASTX	190	3e-14	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4912	GM_98_B1_E03_MR	g3970803	BLASTX	117	3e-12	37	(AJ130841) caffeoyl-CoA 3-O-methyltransferase [Populus balsamifera subsp. trichocarpa]
4913	GM_98_B1_E05_T7	g4063760	BLASTX	152	9e-09	29	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4914	GM_98_B1_E08_MR	g342964	BLASTN	419	7e-13	63	paramecium species 5,311 mt dna dimer: replication init. region.
4915	GM_98_B1_E10_T7	g2522228	BLASTX	161	2e-10	51	(AB007466) reverse transcriptase-like protein [Vicia faba]
4916	GM_98_B1_G02_T7	g2160161	BLASTX	167	7e-11	36	(AC000132) F21M12.7 gene product [Arabidopsis thaliana]
4917	GM_98_B1_G04_T7	g2586082	BLASTX	179	6e-20	60	(U72725) retrofit [Oryza longistaminata]
4918	GM_98_B1_H06_MR	g2522230	BLASTX	200	3e-18	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4919	GM_98_B1_H09_T7	g1362091	BLASTX	178	4e-12	84	cellulase (EC 3.2.1.4) precursor - tomato gi 924622 (U20590) endo-1,4-beta-glucanase precursor [Solanum lycopersicum]
4920	GM_98_B2_A06_T7	g905361	BLASTX	893	9e-89	90	(U22103) gag-protease polyprotein [Glycine max]
4921	GM_98_B2_A08_T7	g507910	BLASTN	398	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4922	GM_98_B2_A10_T7	g507910	BLASTN	348	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.

4923	GM_98_B2_A12_T7	g130582	BLASTX	189	1e-19	51	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
4924	GM_98_B2_B03_T7	g3386598	BLASTX	404	5e-37	75	(AC004665) putative cytochrome p450 [Arabidopsis thaliana]
4925	GM_98_B2_B08_T7	g2129618	BLASTX	293	6e-24	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
4926	GM_98_B2_C07_T7	g4063760	BLASTX	310	2e-27	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4927	GM_98_B2_C08_T7	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
4928	GM_98_B2_C09_T7	g13581	BLASTN	331	9e-09	59	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTCG10 Saccharomyces cerevisiae mitochondrion DNA segment.
4929	GM_98_B2_C10_T7	g3142328	BLASTN	1730	1e-71	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4930	GM_98_B2_E01_T7	g4140712	BLASTX	164	2e-11	45	(AF110183) putative integrase [Oryza sativa]
4931	GM_98_B2_E07_T7	g976282	BLASTN	377	6e-11	60	Arabidopsis thaliana (clone NING6) reverse transcriptase (Ta27) pseudogene, partial cds
4932	GM_98_B2_F01_T7	g3283026	BLASTX	298	1e-24	37	putative transposase [Arabidopsis thaliana]
4933	GM_98_B2_F04_T7	g4063760	BLASTX	513	3e-47	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4934	GM_98_B2_F08_T7	g9837	BLASTN	446	3e-13	62	P.falciparum 3.8 gene for putative serine kinase (partial) and GBP130 gene for glycophorin binding protein (partial)
4935	GM_98_B2_F09_T7	g1617270	BLASTX	233	6e-32	68	(X94624) acyl-CoA synthetase [Brassica napus]
4936	GM_98_B2_F11_T7	g1402910	BLASTX	191	2e-25	76	(X98316) peroxidase [Arabidopsis thaliana] gi 1429223 gnl PID e252638 (X99096) peroxidase [Arabidopsis thaliana]
4937	GM_98_B2_F12_T7	g3777527	BLASTX	269	2e-24	45	(AF053008) gag-pol polyprotein [Glycine max]
4938	GM_98_B2_G07_T7	g2522228	BLASTX	168	3e-11	53	(AB007466) reverse transcriptase-like protein [Vicia faba]
4939	GM_98_B2_G08_T7	g2194136	BLASTX	234	2e-17	32	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
4940	GM_98_B2_H02_T7	g1305549	BLASTX	203	6e-27	74	(U55874) asparagine synthetase [Glycine max]
4941	GM_98_B2_H04_T7	g4160362	BLASTN	366	3e-13	68	Saccharomyces cerevisiae complete mitochondrial genome
4942	GM_98_B2_H08_T7	g1769897	BLASTX	219	7e-20	39	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4943	GM_99_A2_A03_MR	g18559	BLASTN	1027	2e-39	76	G.max gene for catalase
4944	GM_99_A2_A05_MR	g3142328	BLASTN	1102	5e-43	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4945	GM_99_A2_A05_T7	g3097320	BLASTN	412	1e-11	75	Glycine max gene for Bd 30K, complete cds
4946	GM_99_A2_A06_MR	g3650039	BLASTX	289	8e-24	44	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]

4947	GM_99_A2_A07_MR	g2894590	BLASTN	371	8e-10	60	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-115, complete sequence [Plasmodium falciparum]
4948	GM_99_A2_A09_MR	g548488	BLASTX	208	1e-18	67	POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) gi 166325 (L12019) polygalacturonase [Actinidia deliciosa]
4949	GM_99_A2_B03_T7	g2245073	BLASTN	403	4e-11	64	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8
4950	GM_99_A2_B10_MR	g1769898	BLASTX	362	2e-39	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
4951	GM_99_A2_B10_T7	g3142330	BLASTX	536	6e-51	80	(U96295) envelope-like [Glycine max]
4952	GM_99_A2_B11_T7	g4038056	BLASTX	315	2e-26	51	(AC005897) putative transposon [Arabidopsis thaliana]
4953	GM_99_A2_B12_T7	g2995405	BLASTX	421	8e-38	65	(Y12432) polyprotein [Ananas comosus]
4954	GM_99_A2_C02_T7	g4063760	BLASTX	571	2e-53	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4955	GM_99_A2_C03_T7	g4038056	BLASTX	314	3e-26	42	(AC005897) putative transposon [Arabidopsis thaliana]
4956	GM_99_A2_C08_MR	g421955	BLASTX	217	2e-26	60	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
4957	GM_99_A2_D01_MR	g1165321	BLASTN	634	1e-29	91	Glycine max extensin (SbHRGP3) gene, complete cds
4958	GM_99_A2_D01_T7	g2085783	BLASTN	359	3e-09	58	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
4959	GM_99_A2_D03_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
4960	GM_99_A2_D03_T7	g4063760	BLASTX	277	4e-22	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4961	GM_99_A2_D07_T7	g3142328	BLASTN	784	2e-28	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4962	GM_99_A2_D08_MR	g3299824	BLASTN	473	3e-14	60	Arabidopsis thaliana BAC F4C21 from chromosome IV, top arm, near 17 cM, complete sequence [Arabidopsis thaliana]
4963	GM_99_A2_D08_T7	g2244876	BLASTX	421	5e-37	68	(Z97338) hypothetical protein [Arabidopsis thaliana]
4964	GM_99_A2_E01_MR	g3777527	BLASTX	223	4e-16	53	(AF053008) gag-pol polyprotein [Glycine max]
4965	GM_99_A2_E08_T7	g507910	BLASTN	575	2e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4966	GM_99_A2_E10_MR	g905361	BLASTX	181	3e-12	28	(U22103) gag-protease polyprotein [Glycine max]
4967	GM_99_A2_E11_MR	g1480927	BLASTN	462	5e-14	74	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
4968	GM_99_A2_F10_T7	g1480927	BLASTN	635	6e-22	96	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
4969	GM_99_A2_F12_MR	g507910	BLASTN	662	3e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
4970	GM_99_A2_G01_MR	g170029	BLASTN	388	1e-10	80	Glycine max cv. Dare nodulin 26 gene fragment.
4971	GM_99_A2_G01_T7	g2522230	BLASTX	297	1e-25	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
4972	GM_99_A2_G02_MR	g4063760	BLASTX	176	3e-11	32	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4973	GM_99_A2_G03_MR	g2351064	BLASTN	676	2e-23	73	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22
4974	GM_99_A2_G04_MR	g3097320	BLASTN	982	2e-37	77	Glycine max gene for Bd 30K, complete cds

4975	GM_99_A2_G05_MR	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
4976	GM_99_A2_G05_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
4977	GM_99_A2_G08_MR	g4115365	BLASTX	117	1e-13	36	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
4978	GM_99_A2_G09_MR	g3426334	BLASTN	535	3e-17	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
4979	GM_99_A2_G10_MR	g507910	BLASTN	545	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
4980	GM_99_A2_G11_MR	g1084429	BLASTX	235	5e-19	53	pectin esterase - Petunia inflata
4981	GM_99_A2_H05_T7	g100484	BLASTX	260	1e-20	46	hypothetical protein - garden snapdragon
4982	GM_99_A2_H07_MR	g507910	BLASTN	575	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
4983	GM_99_A2_H07_T7	g507910	BLASTN	559	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
4984	GM_99_A2_H08_MR	g4063760	BLASTX	364	7e-41	78	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4985	GM_99_A2_H09_MR	g4063760	BLASTX	191	5e-14	36	(AC005561) putative POL3 protein [Arabidopsis thaliana]
4986	GM_99_A2_H11_MR	g507910	BLASTN	492	1e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
4987	GM_99_A2_H11_T7	g507910	BLASTN	604	1e-20	84	Glycine max BSR-101 satellite SB92 genomic sequence.
4988	GM_99_A2_H12_T7	g3283026	BLASTX	158	1e-09	34	putative transposase [Arabidopsis thaliana]
4989	GM_99_B1_C03_MR	g3142328	BLASTN	710	4e-25	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
4990	GM_99_B1_C04_MR	g509768	BLASTN	410	1e-11	62	Glycine max seed-specific low molecular weight sulfur-rich protein.
4991	GM_99_B1_D08_MR	g507910	BLASTN	605	1e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
4992	GM_99_B1_D12_T7	g1666236	BLASTX	207	8e-16	30	(U76261) unknown [Hordeum vulgare]
4993	GM_99_B1_E01_T7	g2673901	BLASTN	351	8e-09	66	Arabidopsis thaliana chromosome II BAC T24P15 genomic sequence, complete sequence.
4994	GM_99_B1_E02_MR	g3097320	BLASTN	390	1e-10	68	Glycine max gene for Bd 30K, complete cds
4995	GM_99_B1_E06_T7	g3097320	BLASTN	710	4e-25	75	Glycine max gene for Bd 30K, complete cds
4996	GM_99_B1_F01_T7	g3021511	BLASTN	354	4e-09	67	N.tabacum mRNA for NADP-dependent isocitrate dehydrogenase
4997	GM_99_B1_F03_MR	g1217967	BLASTX	230	2e-17	72	(X96431) high affinity sulphate transporter [Hordeum vulgare]
4998	GM_99_B1_F03_T7	g2995405	BLASTX	359	4e-31	52	(Y12432) polyprotein [Ananas comosus]
4999	GM_99_B1_G02_T7	g3047066	BLASTX	134	2e-12	48	(AF058825) contains similarity to retrovirus-related POL polyproteins [Arabidopsis thaliana]
5000	GM_99_B1_G06_T7	g282964	BLASTX	230	5e-18	81	transforming protein (myb) homolog (clone myb.Ph3) - garden petunia gi 20563 (Z13996) protein 1 [Petunia hybrida]
5001	GM_99_B1_G07_MR	g3319362	BLASTX	186	2e-12	41	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
5002	GM_99_B1_G07_T7	g99755	BLASTX	346	3e-30	51	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
5003	GM_99_B1_G08_T7	g2443320	BLASTX	179	1e-11	33	(D85597) polyprotein [Oryza australiensis]
5004	GM_99_B1_G10_MR	g4063760	BLASTX	268	4e-21	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5005	GM_99_B1_H01_MR	g3176777	BLASTN	485	6e-16	63	Homo sapiens allele 4 fragile site locus (FRA10B) minisatellite, 3' sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5006	GM_99_B1_H08_MR	g507910	BLASTN	375	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5007	GM_99_B2_A02_MR	g2829133	BLASTX	179	3e-19	75	(AF043351) adenosine-5'-phosphosulfate-kinase [Arabidopsis thaliana]
5008	GM_99_B2_A08_T7	g3250687	BLASTX	317	1e-27	39	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
5009	GM_99_B2_A12_T7	g4063760	BLASTX	427	2e-39	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5010	GM_99_B2_B03_MR	g2264320	BLASTN	979	3e-37	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
5011	GM_99_B2_B05_T7	g3777526	BLASTN	478	1e-14	67	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
5012	GM_99_B2_B07_MR	g507910	BLASTN	581	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5013	GM_99_B2_B07_T7	g507910	BLASTN	492	1e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5014	GM_99_B2_B08_MR	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5015	GM_99_B2_B08_T7	g507910	BLASTN	552	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5016	GM_99_B2_B09_T7	g3377824	BLASTX	125	3e-11	32	(AF075598) contains similarity to reverse transcriptases [Arabidopsis thaliana]
5017	GM_99_B2_B11_T7	g905361	BLASTX	218	3e-16	30	(U22103) gag-protease polyprotein [Glycine max]
5018	GM_99_B2_C01_MR	g905361	BLASTX	432	1e-39	97	(U22103) gag-protease polyprotein [Glycine max]
5019	GM_99_B2_C02_MR	g3142328	BLASTN	1271	1e-50	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5020	GM_99_B2_C03_MR	g4063760	BLASTX	290	2e-52	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5021	GM_99_B2_C04_T7	g100484	BLASTX	152	5e-09	60	hypothetical protein - garden snapdragon
5022	GM_99_B2_C05_T7	g3142328	BLASTN	718	2e-25	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5023	GM_99_B2_C06_MR	g3097320	BLASTN	479	1e-14	71	Glycine max gene for Bd 30K, complete cds
5024	GM_99_B2_C06_T7	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5025	GM_99_B2_C08_MR	g4049647	BLASTN	420	6e-12	61	Melanoplus sanguinipes entomopoxvirus, complete genome
5026	GM_99_B2_C09_MR	g505129	BLASTN	347	1e-08	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5027	GM_99_B2_C11_MR	g1666236	BLASTX	260	1e-21	33	(U76261) unknown [Hordeum vulgare]
5028	GM_99_B2_C11_T7	g3097320	BLASTN	1037	6e-40	76	Glycine max gene for Bd 30K, complete cds
5029	GM_99_B2_C12_MR	g3193221	BLASTN	455	1e-13	76	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
5030	GM_99_B2_D01_T7	g3645899	BLASTX	319	1e-35	44	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5031	GM_99_B2_D02_T7	g4049647	BLASTN	387	2e-10	60	Melanoplus sanguinipes entomopoxvirus, complete genome
5032	GM_99_B2_D04_MR	g507910	BLASTN	387	7e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5033	GM_99_B2_D04_T7	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5034	GM_99_B2_D08_T7	g507910	BLASTN	598	2e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
5035	GM_99_B2_D09_T7	g2586082	BLASTX	195	5e-32	55	(U72725) retrofit [Oryza longistaminata]
5036	GM_99_B2_D11_MR	g2708743	BLASTX	168	2e-10	33	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
5037	GM_99_B2_E01_MR	g3599418	BLASTN	568	1e-18	91	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
5038	GM_99_B2_E02_MR	g3777527	BLASTX	163	9e-10	57	(AF053008) gag-pol polyprotein [Glycine max]
5039	GM_99_B2_E04_T7	g4063760	BLASTX	163	6e-10	32	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5040	GM_99_B2_E05_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5041	GM_99_B2_E05_T7	g507910	BLASTN	367	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5042	GM_99_B2_E06_MR	g2961349	BLASTX	414	1e-46	44	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
5043	GM_99_B2_E06_T7	g3688328	BLASTX	147	7e-13	45	(AJ228325) reverse transcriptase [Ginkgo biloba]
5044	GM_99_B2_E08_MR	g4160362	BLASTN	350	9e-09	64	Saccharomyces cerevisiae complete mitochondrial genome
5045	GM_99_B2_E08_T7	g4115365	BLASTX	159	1e-11	56	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
5046	GM_99_B2_E12_T7	g3097320	BLASTN	1002	2e-38	76	Glycine max gene for Bd 30K, complete cds
5047	GM_99_B2_F03_MR	g3142328	BLASTN	690	3e-24	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5048	GM_99_B2_F04_MR	g507910	BLASTN	403	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5049	GM_99_B2_F04_T7	g507910	BLASTN	368	5e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5050	GM_99_B2_F06_T7	g1769899	BLASTX	401	1e-36	67	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5051	GM_99_B2_F10_MR	g1769897	BLASTX	366	8e-33	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5052	GM_99_B2_G01_MR	g3599418	BLASTN	457	1e-13	91	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
5053	GM_99_B2_G03_T7	g4063756	BLASTN	432	2e-12	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
5054	GM_99_B2_G04_MR	g507910	BLASTN	625	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
5055	GM_99_B2_G08_MR	g18559	BLASTN	1360	1e-54	76	G.max gene for catalase
5056	GM_99_B2_G09_MR	g2088653	BLASTX	219	8e-17	67	(AF002109) Hs1pro-1 related protein isolog [Arabidopsis thaliana]
5057	GM_99_B2_G10_T7	g3777527	BLASTX	761	1e-73	94	(AF053008) gag-pol polyprotein [Glycine max]
5058	GM_99_B2_G11_MR	g18559	BLASTN	1213	5e-48	75	G.max gene for catalase
5059	GM_99_B2_G12_MR	g3435286	BLASTX	148	4e-18	93	(AF082597) cytosolic glyceraldehyde-3-phosphate dehydrogenase [Leavenworthia crassa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5060	GM_99_B2_H03_MR	g507910	BLASTN	358	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5061	GM_99_B2_H03_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5062	GM_99_B2_H04_T7	g905361	BLASTX	851	3e-84	96	(U22103) gag-protease polyprotein [Glycine max]
5063	GM_99_B2_H06_MR	g170029	BLASTN	540	2e-17	66	Glycine max cv. Dare nodulin 26 gene fragment.
5064	GM_99_B2_H06_T7	g905361	BLASTX	750	1e-73	86	(U22103) gag-protease polyprotein [Glycine max]
5065	GM_99_B2_H08_T7	g1769898	BLASTX	223	1e-37	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5066	GM_99_B2_H11_MR	g3913366	BLASTX	387	4e-34	47	PUTATIVE RECEPTOR PROTEIN KINASE CRINKLY4 PRECURSOR >gi 1597723 (U67422) CRINKLY4 precursor [Zea mays]
5067	GM_99_B2_H12_MR	g3777527	BLASTX	944	3e-93	96	(AF053008) gag-pol polyprotein [Glycine max]
5068	GM_100_A1_A03_MR	g3142328	BLASTN	442	5e-13	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5069	GM_100_A1_A07_MR	g100484	BLASTX	212	2e-15	51	hypothetical protein - garden snapdragon
5070	GM_100_A1_B04_MR	g3294511	BLASTN	420	6e-12	64	Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
5071	GM_100_A1_C01_MR	g2316016	BLASTX	160	2e-09	42	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
5072	GM_100_A1_C03_MR	g507910	BLASTN	361	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5073	GM_100_A1_C05_MR	g507910	BLASTN	558	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5074	GM_100_A1_D09_T7	g18559	BLASTN	684	6e-24	75	G.max gene for catalase
5075	GM_100_A1_E03_MR	g2995405	BLASTX	153	2e-16	61	(Y12432) polyprotein [Ananas comosus]
5076	GM_100_A1_E04_MR	g2369714	BLASTX	376	6e-33	86	(Z97178) elongation factor 2 [Beta vulgaris]
5077	GM_100_A1_E05_T7	g22490	BLASTX	154	2e-10	58	(X01380) ORF1 [Zea mays]
5078	GM_100_A1_F09_MR	g507910	BLASTN	340	9e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5079	GM_100_A1_F12_MR	g2769655	BLASTN	364	2e-09	61	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
5080	GM_100_A1_G09_MR	g2909782	BLASTN	382	3e-10	70	Arabidopsis thaliana MgATP-energized glutathione S-conjugate pump (MRP2) gene, complete cds
5081	GM_100_A1_H07_MR	g3047098	BLASTX	186	3e-25	86	(AF058826) similar to eukaryotic protein kinase domains (Pfam: pkinase.hmm, score: 171.43) [Arabidopsis thaliana]
5082	GM_100_A1_H09_MR	g3777527	BLASTX	466	4e-42	85	(AF053008) gag-pol polyprotein [Glycine max]
5083	GM_100_A2_A03_T7	g3097320	BLASTN	824	3e-30	79	Glycine max gene for Bd 30K, complete cds
5084	GM_100_A2_A05_T7	g2995405	BLASTX	416	3e-37	54	(Y12432) polyprotein [Ananas comosus]
5085	GM_100_A2_A07_MR	g2443320	BLASTX	404	1e-35	52	(D85597) polyprotein [Oryza australiensis]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5086	GM_100_A2_A07_T7	g3979928	BLASTN	369	1e-09	61	Caenorhabditis elegans cosmid Y18D10A, complete sequence [Caenorhabditis elegans]
5087	GM_100_A2_A08_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
5088	GM_100_A2_A08_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
5089	GM_100_A2_A09_T7	g1142701	BLASTN	1090	6e-43	82	Glycine max satellite STR120-A.3.
5090	GM_100_A2_A10_T7	g507910	BLASTN	501	5e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
5091	GM_100_A2_A11_MR	g3985949	BLASTN	412	1e-11	69	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MOB24, complete sequence [Arabidopsis thaliana]
5092	GM_100_A2_A12_MR	g100484	BLASTX	409	9e-37	54	hypothetical protein - garden snapdragon
5093	GM_100_A2_B02_MR	g3176798	BLASTN	473	4e-15	65	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite, 5' sequence
5094	GM_100_A2_B03_T7	g3645899	BLASTX	294	6e-24	56	(U68408) 5' end not determined experimentally [Zea mays]
5095	GM_100_A2_B04_MR	g3645899	BLASTX	249	3e-19	45	(U68408) 5' end not determined experimentally [Zea mays]
5096	GM_100_A2_B08_MR	g3142330	BLASTX	623	4e-60	87	(U96295) envelope-like [Glycine max]
5097	GM_100_A2_C02_T7	g3645899	BLASTX	290	1e-23	49	(U68408) 5' end not determined experimentally [Zea mays]
5098	GM_100_A2_C03_MR	g1171046	BLASTX	176	8e-13	58	METALLOTHIONEIN-LIKE PROTEIN B gi 480753 pir S37240 metallothionein-like protein - white clover gi 403329 (Z26493) metallothionein-like protein [Trifolium repens]
5099	GM_100_A2_C05_MR	g3935150	BLASTX	255	2e-20	62	(AC005106) T25N20.14 [Arabidopsis thaliana]
5100	GM_100_A2_C06_T7	g1666236	BLASTX	190	7e-14	33	(U76261) unknown [Hordeum vulgare]
5101	GM_100_A2_C07_T7	g1076634	BLASTX	292	5e-25	45	protein-serine/threonine kinase NPK15 - common tobacco gi 505146 gnl PID d1007109 (D31737) protein-serine/threonine kinase [Nicotiana tabacum]
5102	GM_100_A2_C08_T7	g3386621	BLASTX	236	4e-19	75	(AC004665) unknown protein [Arabidopsis thaliana]
5103	GM_100_A2_C10_MR	g2864621	BLASTX	149	3e-18	54	hypothetical protein [Arabidopsis thaliana]
5104	GM_100_A2_C11_T7	g4115365	BLASTX	133	4e-10	36	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
5105	GM_100_A2_D04_T7	g3169170	BLASTX	465	2e-43	67	(AC004401) putative chloroplast envelope Ca2+-ATPase, 5' partial [Arabidopsis thaliana]
5106	GM_100_A2_D05_MR	g507910	BLASTN	675	7e-24	85	Glycine max BSR-101 satellite SB92 genomic sequence.
5107	GM_100_A2_D07_MR	g3650035	BLASTX	190	7e-13	47	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
5108	GM_100_A2_E01_MR	g99726	BLASTX	128	3e-17	53	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976) orf 3 [Arabidopsis thaliana]
5109	GM_100_A2_E05_MR	g1335861	BLASTN	359	3e-09	78	Glycine max clathrin heavy chain mRNA, complete cds
5110	GM_100_A2_E10_T7	g1666236	BLASTX	206	1e-15	32	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5111	GM_100_A2_F02_T7	g507910	BLASTN	412	5e-12	79	Glycine max BSR-101 satellite SB92 genomic sequence.
5112	GM_100_A2_F03_T7	g2129618	BLASTX	257	4e-20	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5113	GM_100_A2_F06_MR	g905361	BLASTX	252	7e-20	41	(U22103) gag-protease polyprotein [Glycine max]
5114	GM_100_A2_F07_T7	g100484	BLASTX	254	6e-20	60	hypothetical protein - garden snapdragon
5115	GM_100_A2_F12_T7	g905361	BLASTX	223	9e-17	43	(U22103) gag-protease polyprotein [Glycine max]
5116	GM_100_A2_G01_T7	g3695395	BLASTX	265	3e-21	62	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
5117	GM_100_A2_G04_MR	g4038056	BLASTX	151	7e-09	42	(AC005897) putative transposon [Arabidopsis thaliana]
5118	GM_100_A2_G04_T7	g629693	BLASTX	128	2e-13	42	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
5119	GM_100_A2_G07_T7	g2842490	BLASTX	380	2e-34	55	(AL021749) heat-shock protein [Arabidopsis thaliana]
5120	GM_100_A2_G10_MR	g3142328	BLASTN	831	1e-30	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5121	GM_100_A2_H03_T7	g3449319	BLASTN	401	9e-13	62	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQP15, complete sequence [Arabidopsis thaliana]
5122	GM_100_A2_H05_MR	g3935148	BLASTX	188	1e-29	70	(AC005106) T25N20.12 [Arabidopsis thaliana]
5123	GM_100_A2_H05_T7	g3142328	BLASTN	841	4e-31	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5124	GM_100_A2_H11_T7	g4063760	BLASTX	197	1e-13	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5125	GM_100_A2_H12_MR	g2146731	BLASTX	197	4e-14	88	FK506-binding protein - Arabidopsis thaliana gi 1354207 (U49453) rof1 [Arabidopsis thaliana]
5126	GM_100_B1_A02_T7	g3426334	BLASTN	383	3e-10	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
5127	GM_100_B1_A03_MR	g2407790	BLASTX	154	3e-09	79	(AF019910) grr1 [Glycine max]
5128	GM_100_B1_A04_MR	g905361	BLASTX	432	1e-39	97	(U22103) gag-protease polyprotein [Glycine max]
5129	GM_100_B1_A05_T7	g1277164	BLASTX	213	1e-16	93	(U51853) cysteine proteinase inhibitor [Glycine max]
5130	GM_100_B1_A06_MR	g3142328	BLASTN	722	5e-52	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5131	GM_100_B1_A07_MR	g100484	BLASTX	365	6e-32	51	hypothetical protein - garden snapdragon
5132	GM_100_B1_A12_MR	g1666236	BLASTX	192	4e-14	30	(U76261) unknown [Hordeum vulgare]
5133	GM_100_B1_B01_MR	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5134	GM_100_B1_B03_MR	g2522227	BLASTX	192	2e-14	53	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
5135	GM_100_B1_B04_MR	g507910	BLASTN	382	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5136	GM_100_B1_B04_T7	g4063760	BLASTX	238	6e-18	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5137	GM_100_B1_B06_T7	g1769897	BLASTX	311	2e-26	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5138	GM_100_B1_C01_T7	g1769899	BLASTX	361	2e-32	70	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5139	GM_100_B1_C05_MR	g507910	BLASTN	386	8e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5140	GM_100_B1_C07_MR	g3645899	BLASTX	242	1e-20	46	(U68408) 5' end not determined experimentally [Zea mays]
5141	GM_100_B1_D01_MR	g507910	BLASTN	604	1e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5142	GM_100_B1_D03_MR	g2129709	BLASTX	156	4e-09	34	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
5143	GM_100_B1_D04_T7	g4140712	BLASTX	194	1e-14	45	(AF110183) putative integrase [Oryza sativa]
5144	GM_100_B1_D05_MR	g507910	BLASTN	549	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
5145	GM_100_B1_D05_T7	g507910	BLASTN	545	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
5146	GM_100_B1_D08_MR	g3021285	BLASTX	137	5e-16	63	(AL022347) hypothetical protein [Arabidopsis thaliana] gi 3451058 gnl PID e1316745 (AL031326) hypothetical protein [Arabidopsis thaliana]
5147	GM_100_B1_D09_MR	g3171159	BLASTN	518	2e-16	65	Homo sapiens chromosome 21q22.3 PAC 21L13, complete sequence [Homo sapiens]
5148	GM_100_B1_D09_T7	g1769898	BLASTX	100	2e-11	72	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5149	GM_100_B1_E03_T7	g2842490	BLASTX	387	4e-35	56	(AL021749) heat-shock protein [Arabidopsis thaliana]
5150	GM_100_B1_E04_T7	g3142328	BLASTN	622	4e-21	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5151	GM_100_B1_E06_MR	g3426334	BLASTN	358	3e-09	66	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
5152	GM_100_B1_E06_T7	g2522230	BLASTX	206	6e-16	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
5153	GM_100_B1_E08_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5154	GM_100_B1_E08_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5155	GM_100_B1_F03_T7	g2443320	BLASTX	372	4e-32	52	(D85597) polyprotein [Oryza australiensis]
5156	GM_100_B1_F04_T7	g3426334	BLASTN	469	3e-14	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
5157	GM_100_B1_F06_MR	g130582	BLASTX	231	4e-17	49	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
5158	GM_100_B1_F07_MR	g3777527	BLASTX	690	6e-66	95	(AF053008) gag-pol polyprotein [Glycine max]
5159	GM_100_B1_F11_MR	g1769897	BLASTX	203	4e-18	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5160	GM_100_B1_F12_T7	g18559	BLASTN	793	6e-29	74	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5161	GM_100_B1_G01_T7	g2564750	BLASTN	428	3e-12	64	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
5162	GM_100_B1_G02_MR	g1091678	BLASTX	274	5e-22	43	activator-like transposable element [Pennisetum glaucum]
5163	GM_100_B1_G03_MR	g13581	BLASTN	350	1e-09	60	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTCG10 Saccharomyces cerevisiae mitochondrion DNA segment.
5164	GM_100_B1_G04_MR	g4063760	BLASTX	551	2e-51	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5165	GM_100_B1_G04_T7	g507910	BLASTN	564	7e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5166	GM_100_B1_G05_T7	g3080401	BLASTX	351	3e-31	71	(AL022603) putative protein [Arabidopsis thaliana]
5167	GM_100_B1_G06_MR	g3860246	BLASTX	195	1e-14	36	(AC005824) putative reverse-transcriptase protein [Arabidopsis thaliana]
5168	GM_100_B1_G06_T7	g3777526	BLASTN	1531	3e-62	89	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
5169	GM_100_B1_G08_T7	g2896804	BLASTN	394	9e-11	64	Human Chromosome 16 BAC clone CIT987SK-A-598D4, complete sequence [Homo sapiens]
5170	GM_100_B1_G11_MR	g3777527	BLASTX	269	5e-21	44	(AF053008) gag-pol polyprotein [Glycine max]
5171	GM_100_B1_G12_MR	g1142699	BLASTN	1450	3e-59	88	Glycine max satellite STR120-A.1.
5172	GM_100_B1_H04_MR	g2245104	BLASTX	185	3e-12	40	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
5173	GM_100_B1_H06_MR	g2443320	BLASTX	203	4e-14	41	(D85597) polyprotein [Oryza australiensis]
5174	GM_100_B1_H08_MR	g2462134	BLASTX	181	2e-12	31	(Y13368) reverse transcriptase [Beta vulgaris]
5175	GM_100_B1_H08_T7	g3328126	BLASTX	222	1e-17	67	(AF072691) putative basic helix-loop-helix DNA binding protein TCP2 [Arabidopsis thaliana]
5176	GM_100_B1_H12_T7	g3687234	BLASTX	201	5e-14	30	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
5177	GM_100_B2_A01_MR	g3142328	BLASTN	1414	3e-57	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5178	GM_100_B2_A03_MR	g505129	BLASTN	324	7e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5179	GM_100_B2_A08_MR	g2924781	BLASTX	283	8e-23	60	(AC002334) putative cellulose synthase [Arabidopsis thaliana]
5180	GM_100_B2_A10_T7	g2245104	BLASTX	168	1e-11	35	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
5181	GM_100_B2_A11_T7	g3695387	BLASTX	249	4e-19	63	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
5182	GM_100_B2_B02_MR	g3097320	BLASTN	658	9e-23	66	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5183	GM_100_B2_B05_T7	g3695393	BLASTX	233	2e-17	31	(AF096371) contains similarity to retroviral aspartyl proteases (Pfam: rvp.hmm, score: 11.80) [Arabidopsis thaliana]
5184	GM_100_B2_B06_MR	g3777527	BLASTX	117	8e-10	58	(AF053008) gag-pol polyprotein [Glycine max]
5185	GM_100_B2_B07_MR	g3097320	BLASTN	1271	2e-50	75	Glycine max gene for Bd 30K, complete cds
5186	GM_100_B2_B11_T7	g1170619	BLASTX	144	1e-13	62	KINESIN-LIKE PROTEIN A gi 479594 pir S34830 kinesin-related protein katA - Arabidopsis thaliana gi 303502 gnl PID d1002453 (D11371) kinesin-like motor protein heavy chain [Arabidopsis thaliana] gi 2911084 gnl PID e1253323 (AL021960) kinesin-related protein katA [Arabidopsis thaliana]
5187	GM_100_B2_B12_MR	g3142328	BLASTN	1379	1e-55	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5188	GM_100_B2_C01_MR	g3777527	BLASTX	381	5e-33	94	(AF053008) gag-pol polyprotein [Glycine max]
5189	GM_100_B2_C01_T7	g507910	BLASTN	380	1e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
5190	GM_100_B2_C02_MR	g2895632	BLASTN	388	7e-11	58	Speyeria mormonia large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
5191	GM_100_B2_C06_MR	g3097320	BLASTN	432	2e-12	70	Glycine max gene for Bd 30K, complete cds
5192	GM_100_B2_C06_T7	g3142379	BLASTX	337	7e-30	66	(AF053008) envelope-like [Glycine max]
5193	GM_100_B2_C07_MR	g3097320	BLASTN	469	3e-14	69	Glycine max gene for Bd 30K, complete cds
5194	GM_100_B2_C09_T7	g18634	BLASTN	349	8e-09	74	Soybean Gy1 gene for glycinin subunit G1
5195	GM_100_B2_C10_MR	g3097320	BLASTN	449	3e-13	71	Glycine max gene for Bd 30K, complete cds
5196	GM_100_B2_C10_T7	g3142328	BLASTN	615	7e-21	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5197	GM_100_B2_C11_T7	g421955	BLASTX	152	1e-27	58	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
5198	GM_100_B2_D01_MR	g2735017	BLASTX	241	4e-22	66	(U82481) KI domain interacting kinase 1 [Zea mays]
5199	GM_100_B2_D02_T7	g3335226	BLASTX	175	9e-13	39	(AF077374) small proline-rich protein [Homo sapiens]
5200	GM_100_B2_D03_T7	g4063760	BLASTX	667	8e-64	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5201	GM_100_B2_D05_MR	g3800955	BLASTN	394	9e-11	62	Caenorhabditis elegans cosmid F58E2
5202	GM_100_B2_D08_T7	g160298	BLASTN	483	6e-15	60	P.falciparum glutamic acid-rich protein gnen, complete cds.
5203	GM_100_B2_D09_MR	g3777527	BLASTX	790	1e-76	98	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5204	GM_100_B2_D10_T7	g3059060	BLASTN	467	5e-14	60	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
5205	GM_100_B2_D12_MR	g507910	BLASTN	413	5e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5206	GM_100_B2_D12_T7	g2995405	BLASTX	312	4e-26	51	(Y12432) polyprotein [Ananas comosus]
5207	GM_100_B2_E03_MR	g4140712	BLASTX	597	2e-57	53	(AF110183) putative integrase [Oryza sativa]
5208	GM_100_B2_E05_T7	g2781364	BLASTX	149	2e-09	26	(AC003113) F24O1.20 [Arabidopsis thaliana]
5209	GM_100_B2_E06_T7	g3097320	BLASTN	920	1e-34	78	Glycine max gene for Bd 30K, complete cds
5210	GM_100_B2_E08_MR	g507910	BLASTN	352	3e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5211	GM_100_B2_E08_T7	g4063756	BLASTN	508	7e-16	70	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
5212	GM_100_B2_E09_T7	g3378224	BLASTX	176	9e-13	73	(AJ001213) reverse transcriptase [Lycopersicon chilense]
5213	GM_100_B2_E11_T7	g3142328	BLASTN	2496	2e-107	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5214	GM_100_B2_E12_T7	g3142328	BLASTN	1186	8e-47	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5215	GM_100_B2_F02_MR	g3869063	BLASTN	367	1e-09	63	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17O22, complete sequence [Arabidopsis thaliana]
5216	GM_100_B2_F02_T7	g4038056	BLASTX	343	2e-29	38	(AC005897) putative transposon [Arabidopsis thaliana]
5217	GM_100_B2_F03_T7	g2688264	BLASTN	360	3e-09	60	Borrelia burgdorferi (section 28 of 70) of the complete genome
5218	GM_100_B2_F05_MR	g3845197	BLASTN	345	2e-10	65	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
5219	GM_100_B2_F06_MR	g1666236	BLASTX	298	1e-25	34	(U76261) unknown [Hordeum vulgare]
5220	GM_100_B2_F09_T7	g4063760	BLASTX	509	5e-48	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5221	GM_100_B2_F11_T7	g2995405	BLASTX	295	9e-50	61	(Y12432) polyprotein [Ananas comosus]
5222	GM_100_B2_F12_MR	g3142328	BLASTN	1514	9e-62	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5223	GM_100_B2_G02_MR	g1666236	BLASTX	298	1e-25	34	(U76261) unknown [Hordeum vulgare]
5224	GM_100_B2_G03_T7	g99922	BLASTX	422	4e-60	82	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
5225	GM_100_B2_G05_T7	g3142328	BLASTN	1164	8e-46	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5226	GM_100_B2_G09_MR	g3738114	BLASTN	577	5e-19	66	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5227	GM_100_B2_G09_T7	g3941472	BLASTX	116	3e-13	47	(AF062890) putative transcription factor [Arabidopsis thaliana]
5228	GM_100_B2_G10_MR	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5229	GM_100_B2_G12_MR	g2522228	BLASTX	459	1e-42	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
5230	GM_100_B2_H02_MR	g2245015	BLASTX	439	1e-40	56	(Z97341) unnamed protein product [Arabidopsis thaliana]
5231	GM_100_B2_H07_T7	g2995405	BLASTX	458	9e-42	72	(Y12432) polyprotein [Ananas comosus]
5232	GM_101_A1_B03_T7	g905361	BLASTX	168	8e-11	31	(U22103) gag-protease polyprotein [Glycine max]
5233	GM_101_A1_C04_T7	g226407	BLASTX	175	3e-24	46	retrotransposon del1-46 [Lilium henryi]
5234	GM_101_A1_E02_T7	g3142328	BLASTN	464	5e-14	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5235	GM_101_A1_E03_T7	g3142328	BLASTN	878	8e-33	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5236	GM_101_A1_E12_T7	g507910	BLASTN	578	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
5237	GM_101_A1_F03_T7	g507910	BLASTN	610	6e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5238	GM_101_A1_F05_T7	g4063760	BLASTX	174	4e-11	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5239	GM_101_A1_F06_T7	g2462936	BLASTX	170	2e-23	48	(Y12321) open reading frame 2 [Brassica oleracea]
5240	GM_101_A1_F07_T7	g507910	BLASTN	358	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5241	GM_101_A1_F11_T7	g507910	BLASTN	352	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5242	GM_101_A1_G03_T7	g3548806	BLASTX	171	5e-11	42	(AC005313) unknown protein [Arabidopsis thaliana]
5243	GM_101_A1_G06_T7	g3142328	BLASTN	1441	2e-58	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5244	GM_101_B1_A01_T7	g2264320	BLASTN	546	1e-17	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
5245	GM_101_B1_A06_MR	g3777527	BLASTX	619	3e-67	93	(AF053008) gag-pol polyprotein [Glycine max]
5246	GM_101_B1_A09_MR	g507910	BLASTN	383	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5247	GM_101_B1_A09_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5248	GM_101_B1_A12_MR	g507910	BLASTN	356	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5249	GM_101_B1_B03_MR	g505129	BLASTN	395	7e-11	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5250	GM_101_B1_B07_T7	g18559	BLASTN	1046	2e-40	75	G.max gene for catalase
5251	GM_101_B1_B08_MR	g2462134	BLASTX	246	1e-29	49	(Y13368) reverse transcriptase [Beta vulgaris]
5252	GM_101_B1_B08_T7	g629693	BLASTX	195	2e-18	41	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
5253	GM_101_B1_B09_MR	g3979928	BLASTN	373	8e-10	59	Caenorhabditis elegans cosmid Y18D10A, complete sequence [Caenorhabditis elegans]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5254	GM_101_B1_B09_T7	g3513747	BLASTX	188	2e-12	46	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
5255	GM_101_B1_C02_MR	g2462134	BLASTX	343	2e-30	52	(Y13368) reverse transcriptase [Beta vulgaris]
5256	GM_101_B1_C02_T7	g2315153	BLASTX	264	2e-30	82	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
5257	GM_101_B1_C03_T7	g3193306	BLASTX	229	9e-19	31	(AF069300) contains similarity to Arabidopsis membrane-associated salt-inducible-like protein (GB:AL021637) [Arabidopsis thaliana]
5258	GM_101_B1_C10_MR	g2351073	BLASTN	461	9e-14	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24
5259	GM_101_B1_C12_MR	g3687828	BLASTN	380	4e-10	66	Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence [Homo sapiens]
5260	GM_101_B1_C12_T7	g1170878	BLASTX	176	7e-24	88	MALATE SYNTHASE, GLYOXYSOMAL (MS) gi 170026 (L01629) malate synthase [Glycine max]
5261	GM_101_B1_D01_MR	g3142328	BLASTN	493	2e-15	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5262	GM_101_B1_D03_T7	g507910	BLASTN	600	2e-20	84	Glycine max BSR-101 satellite SB92 genomic sequence.
5263	GM_101_B1_D04_T7	g4039114	BLASTN	625	2e-21	70	Glycine max alcohol-dehydrogenase (Adh-2) gene, partial cds
5264	GM_101_B1_D06_T7	g3643603	BLASTX	413	9e-37	63	(AC005395) unknown protein [Arabidopsis thaliana]
5265	GM_101_B1_D07_MR	g1666236	BLASTX	256	3e-21	34	(U76261) unknown [Hordeum vulgare]
5266	GM_101_B1_D09_T7	g3097320	BLASTN	924	8e-35	78	Glycine max gene for Bd 30K, complete cds
5267	GM_101_B1_D10_T7	g18559	BLASTN	918	8e-55	90	G.max gene for catalase
5268	GM_101_B1_D11_MR	g3142379	BLASTX	236	1e-18	55	(AF053008) envelope-like [Glycine max]
5269	GM_101_B1_D11_T7	g421955	BLASTX	145	4e-18	52	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
5270	GM_101_B1_E01_T7	g507910	BLASTN	557	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5271	GM_101_B1_E02_T7	g1488267	BLASTX	149	4e-09	75	(U57412) low affinity calcium antiporter CAX2 [Arabidopsis thaliana]
5272	GM_101_B1_E03_MR	g3319362	BLASTX	228	5e-23	55	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
5273	GM_101_B1_E04_MR	g3777527	BLASTX	725	1e-69	91	(AF053008) gag-pol polyprotein [Glycine max]
5274	GM_101_B1_E07_MR	g4150930	BLASTN	329	1e-08	61	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5275	GM_101_B1_E08_MR	g1755156	BLASTX	473	3e-44	69	(U75189) germin-like protein [Arabidopsis thaliana] gi 1755158 (U75190) germin-like protein [Arabidopsis thaliana] gi 1755170 (U75196) germin-like protein [Arabidopsis thaliana] gi 1755172 (U75197) germin-like protein [Arabidopsis thaliana] gi 1755180 (U75201) germin-like protein [Arabidopsis thaliana] gi 1755190 (U75206) germin-like protein [Arabidopsis thaliana] gi 1934728 (U95035) germin-like protein [Arabidopsis thaliana]
5276	GM_101_B1_E08_T7	g2351069	BLASTN	577	5e-19	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12
5277	GM_101_B1_E09_MR	g905361	BLASTX	129	7e-14	41	(U22103) gag-protease polyprotein [Glycine max]
5278	GM_101_B1_E11_MR	g4115365	BLASTX	179	6e-15	47	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
5279	GM_101_B1_E11_T7	g130582	BLASTX	283	1e-22	33	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
5280	GM_101_B1_F01_T7	g507910	BLASTN	385	9e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5281	GM_101_B1_F04_MR	g2924257	BLASTN	372	3e-18	70	Tobacco chloroplast genome DNA
5282	GM_101_B1_F04_T7	g12212	BLASTN	1241	4e-67	89	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
5283	GM_101_B1_F05_MR	g2579859	BLASTN	334	9e-09	63	Homo sapiens genomic DNA, 21q region, clone: S39BG29
5284	GM_101_B1_F07_T7	g4038056	BLASTX	269	2e-21	50	(AC005897) putative transposon [Arabidopsis thaliana]
5285	GM_101_B1_F08_MR	g3097320	BLASTN	1343	8e-54	81	Glycine max gene for Bd 30K, complete cds
5286	GM_101_B1_F09_MR	g507910	BLASTN	370	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5287	GM_101_B1_F10_T7	g2656028	BLASTN	432	2e-12	61	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNF13
5288	GM_101_B1_F12_MR	g2995405	BLASTX	533	6e-50	60	(Y12432) polyprotein [Ananas comosus]
5289	GM_101_B1_G01_T7	g4063760	BLASTX	569	3e-53	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5290	GM_101_B1_G03_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5291	GM_101_B1_G04_MR	g3645899	BLASTX	187	2e-12	60	(U68408) 5' end not determined experimentally [Zea mays]
5292	GM_101_B1_G05_MR	g3426334	BLASTN	372	8e-10	66	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
5293	GM_101_B1_G07_T7	g3650039	BLASTX	105	4e-10	46	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
5294	GM_101_B1_G09_MR	g1666236	BLASTX	107	7e-10	35	(U76261) unknown [Hordeum vulgare]
5295	GM_101_B1_G10_MR	g2618689	BLASTX	149	6e-11	73	(AC002510) unknown protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5296	GM_101_B1_G11_T7	g3142379	BLASTX	310	6e-27	67	(AF053008) envelope-like [Glycine max]
5297	GM_101_B1_G12_T7	g3176690	BLASTX	157	9e-18	76	(AC003671) Similar to ubiquitin ligase gb D63905 from S. cerevisiae. EST gb R65295 comes from this gene. [Arabidopsis thaliana]
5298	GM_102_A1_A05_T7	g2462134	BLASTX	179	3e-12	35	(Y13368) reverse transcriptase [Beta vulgaris]
5299	GM_102_A1_A12_T7	g1771160	BLASTX	222	7e-22	55	(X98929) SBT1 [Lycopersicon esculentum] gi 3687305 gnl PID e1299610 (AJ006378) subtilisin-like protease [Lycopersicon esculentum]
5300	GM_102_A1_B07_MR	g3142328	BLASTN	798	4e-29	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5301	GM_102_A1_B11_MR	g2522228	BLASTX	204	4e-15	78	(AB007466) reverse transcriptase-like protein [Vicia faba]
5302	GM_102_A1_C05_MR	g413725	BLASTN	410	1e-11	67	Medicago sativa aspartate aminotransferase (AAT1) gene, complete cds
5303	GM_102_A1_C06_MR	g2245104	BLASTX	335	3e-29	58	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
5304	GM_102_A1_E03_T7	g507910	BLASTN	367	6e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5305	GM_102_A1_E04_T7	g226407	BLASTX	342	6e-29	54	retrotransposon del1-46 [Lilium henryi]
5306	GM_102_A1_E10_MR	g507910	BLASTN	521	6e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
5307	GM_102_A1_F03_T7	g2245104	BLASTX	164	6e-10	33	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
5308	GM_102_A1_F11_T7	g3142328	BLASTN	1085	3e-42	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5309	GM_102_A1_G02_T7	g507910	BLASTN	353	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
5310	GM_102_A1_G12_T7	g3093293	BLASTN	350	7e-09	76	Arabidopsis thaliana mRNA for putative villin.
5311	GM_102_A1_H02_MR	g2522228	BLASTX	153	1e-09	42	(AB007466) reverse transcriptase-like protein [Vicia faba]
5312	GM_102_A1_H10_MR	g3645899	BLASTX	156	3e-09	43	(U68408) 5' end not determined experimentally [Zea mays]
5313	GM_102_A1_H12_T7	g3171875	BLASTN	454	2e-13	64	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.1...
5314	GM_102_A2_A03_T7	g3319345	BLASTX	169	1e-10	33	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
5315	GM_102_A2_A04_T7	g4063760	BLASTX	491	6e-45	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5316	GM_102_A2_A06_T7	g3337395	BLASTN	356	5e-09	60	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
5317	GM_102_A2_A12_MR	g507910	BLASTN	619	2e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
5318	GM_102_A2_B04_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5319	GM_102_A2_B10_MR	g2522227	BLASTX	189	9e-17	34	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
5320	GM_102_A2_C01_MR	g2462058	BLASTX	196	1e-18	56	(Y13389) reverse transcriptase [Antirrhinum majus]
5321	GM_102_A2_C02_T7	g507910	BLASTN	409	7e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5322	GM_102_A2_C05_MR	g3142328	BLASTN	756	3e-27	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5323	GM_102_A2_C05_T7	g3599418	BLASTN	381	3e-10	87	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
5324	GM_102_A2_C07_MR	g507910	BLASTN	367	6e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5325	GM_102_A2_C07_T7	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5326	GM_102_A2_C10_MR	g1419118	BLASTX	68	6e-11	81	(Z75512) reverse transcriptase [Oryza sativa]
5327	GM_102_A2_D04_MR	g18768	BLASTN	493	6e-16	74	Soybean Tgm6 transposable element 3' end
5328	GM_102_A2_D06_MR	g2443320	BLASTX	252	4e-20	39	(D85597) polyprotein [Oryza australiensis]
5329	GM_102_A2_D08_MR	g2522228	BLASTX	186	4e-13	51	(AB007466) reverse transcriptase-like protein [Vicia faba]
5330	GM_102_A2_D11_T7	g1666236	BLASTX	148	3e-09	26	(U76261) unknown [Hordeum vulgare]
5331	GM_102_A2_E01_MR	g99729	BLASTX	256	3e-21	45	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
5332	GM_102_A2_E01_T7	g3777527	BLASTX	107	8e-10	38	(AF053008) gag-pol polyprotein [Glycine max]
5333	GM_102_A2_E06_MR	g905361	BLASTX	390	6e-35	90	(U22103) gag-protease polyprotein [Glycine max]
5334	GM_102_A2_E08_MR	g408793	BLASTN	423	3e-12	72	Glycine soja chloroplast 3-omega faty acid desaturase (Fad3) mRNA, complete cds.
5335	GM_102_A2_E10_MR	g3522939	BLASTX	185	9e-14	62	(AC004411) putative squamosa-promoter binding protein [Arabidopsis thaliana]
5336	GM_102_A2_F01_T7	g99730	BLASTX	362	2e-32	50	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
5337	GM_102_A2_F05_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5338	GM_102_A2_F06_MR	g3142328	BLASTN	833	9e-31	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5339	GM_102_A2_F10_T7	g507910	BLASTN	583	1e-19	83	Glycine max BSR-101 satellite SB92 genomic sequence.
5340	GM_102_A2_F11_MR	g1142699	BLASTN	734	7e-27	83	Glycine max satellite STR120-A.1.
5341	GM_102_A2_F12_T7	g1490417	BLASTX	197	1e-13	49	(U45025) 89B helicase [Drosophila melanogaster]
5342	GM_102_A2_G07_T7	g2443320	BLASTX	354	3e-30	51	(D85597) polyprotein [Oryza australiensis]
5343	GM_102_A2_G11_T7	g3097320	BLASTN	467	4e-14	71	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5344	GM_102_A2_H02_T7	g507910	BLASTN	415	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5345	GM_102_A2_H05_MR	g507910	BLASTN	367	6e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5346	GM_102_A2_H06_T7	g3645899	BLASTX	273	9e-22	37	(U68408) 5' end not determined experimentally [Zea mays]
5347	GM_102_A2_H07_MR	g1167523	BLASTX	261	2e-20	53	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
5348	GM_102_A2_H08_T7	g3548808	BLASTX	457	1e-42	58	(AC005313) unknown protein [Arabidopsis thaliana]
5349	GM_102_A2_H10_T7	g4050011	BLASTN	561	2e-18	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
5350	GM_102_B1_A01_MR	g3097320	BLASTN	473	2e-14	71	Glycine max gene for Bd 30K, complete cds
5351	GM_102_B1_A02_MR	g905361	BLASTX	241	1e-18	34	(U22103) gag-protease polyprotein [Glycine max]
5352	GM_102_B1_A04_T7	g2194136	BLASTX	482	7e-44	55	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
5353	GM_102_B1_A06_MR	g1946355	BLASTX	138	1e-09	32	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] gi 2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]
5354	GM_102_B1_A06_T7	g3426334	BLASTN	404	3e-11	59	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
5355	GM_102_B1_A07_MR	g4160362	BLASTN	411	2e-11	60	Saccharomyces cerevisiae complete mitochondrial genome
5356	GM_102_B1_A08_T7	g1326016	BLASTX	309	3e-28	38	TY3-2 orfB
5357	GM_102_B1_A11_T7	g4038056	BLASTX	373	1e-32	49	(AC005897) putative transposon [Arabidopsis thaliana]
5358	GM_102_B1_A12_MR	g3845100	BLASTN	278	1e-09	66	Plasmodium falciparum chromosome 2, section 11 of 73 of the complete sequence
5359	GM_102_B1_B02_MR	g507910	BLASTN	701	5e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
5360	GM_102_B1_B03_MR	g1769898	BLASTX	160	2e-11	52	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5361	GM_102_B1_B10_T7	g2995405	BLASTX	166	2e-10	36	(Y12432) polyprotein [Ananas comosus]
5362	GM_102_B1_B11_T7	g505129	BLASTN	472	2e-14	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5363	GM_102_B1_B12_T7	g282881	BLASTX	398	2e-35	45	receptor-like protein kinase precursor - Arabidopsis thaliana gi 166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]
5364	GM_102_B1_C01_T7	g508826	BLASTN	310	1e-15	62	Drosophila melanogaster Oregon-R mitochondrial A+T region.
5365	GM_102_B1_C11_MR	g505129	BLASTN	287	2e-10	68	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5366	GM_102_B1_C12_T7	g3142328	BLASTN	1786	3e-74	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5367	GM_102_B1_D02_MR	g3097320	BLASTN	1066	3e-41	79	Glycine max gene for Bd 30K, complete cds
5368	GM_102_B1_D09_MR	g3894176	BLASTX	368	4e-33	85	(AC005312) putative NAM (no apical meristem) protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5369	GM_102_B1_D09_T7	g3377517	BLASTX	287	1e-28	50	(AF073361) nitrate transporter NTL1 [Arabidopsis thaliana]
5370	GM_102_B1_D10_MR	g2129618	BLASTX	234	1e-17	37	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5371	GM_102_B1_E02_T7	g99729	BLASTX	178	1e-21	40	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
5372	GM_102_B1_E04_MR	g130398	BLASTX	155	4e-09	53	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 297) gi 85089 pir B24872 retrovirus-related pol polyprotein homolog - fruit fly (Drosophila melanogaster) transposon 297
5373	GM_102_B1_E05_T7	g4063760	BLASTX	377	7e-35	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5374	GM_102_B1_E11_MR	g3097320	BLASTN	881	7e-33	72	Glycine max gene for Bd 30K, complete cds
5375	GM_102_B1_E12_MR	g320564	BLASTX	99	9e-09	48	transposon copia - Arabidopsis thaliana (fragment)
5376	GM_102_B1_F01_MR	g2129618	BLASTX	210	4e-15	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5377	GM_102_B1_F01_T7	g3599418	BLASTN	622	4e-21	82	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
5378	GM_102_B1_F03_T7	g2443320	BLASTX	239	5e-18	40	(D85597) polyprotein [Oryza australiensis]
5379	GM_102_B1_F04_MR	g2052383	BLASTX	252	2e-20	75	(U66345) calreticulin [Arabidopsis thaliana]
5380	GM_102_B1_F04_T7	g3047086	BLASTX	412	9e-37	45	(AF058914) similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31) [Arabidopsis thaliana]
5381	GM_102_B1_F07_T7	g3142328	BLASTN	1455	4e-59	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5382	GM_102_B1_F12_MR	g507910	BLASTN	371	4e-10	76	Glycine max BSR-101 satellite SB92 genomic sequence.
5383	GM_102_B1_G01_MR	g2970554	BLASTN	378	5e-10	64	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
5384	GM_102_B1_G01_T7	g3273127	BLASTN	360	3e-09	61	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-54, complete sequence [Plasmodium falciparum]
5385	GM_102_B1_G02_MR	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5386	GM_102_B1_G02_T7	g507910	BLASTN	394	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5387	GM_102_B1_G04_T7	g3273123	BLASTN	370	1e-09	59	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-58, complete sequence [Plasmodium falciparum]
5388	GM_102_B1_G05_T7	g559268	BLASTN	337	9e-09	64	Saccharomyces cerevisiae mitochondrion DNA segment.
5389	GM_102_B1_G12_T7	g1091678	BLASTX	174	2e-23	47	activator-like transposable element [Pennisetum glaucum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5390	GM_102_B1_H07_MR	g3808101	BLASTX	241	9e-24	84	(AJ012165) chloroplast protease [Capsicum annuum]
5391	GM_102_B1_H09_MR	g4063760	BLASTX	157	2e-09	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5392	GM_102_B1_H09_T7	g507910	BLASTN	574	3e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5393	GM_102_B2_A01_T7	g2505865	BLASTX	301	3e-25	44	(Y12227) putative topoisomerase [Arabidopsis thaliana]
5394	GM_102_B2_A04_T7	g2764526	BLASTN	489	4e-15	61	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
5395	GM_102_B2_A07_MR	g3128138	BLASTN	681	1e-23	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFO20, complete sequence [Arabidopsis thaliana]
5396	GM_102_B2_A12_MR	g18559	BLASTN	1404	1e-56	81	G.max gene for catalase
5397	GM_102_B2_B02_MR	g3461840	BLASTX	154	7e-09	34	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
5398	GM_102_B2_B03_MR	g3319362	BLASTX	159	1e-09	36	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
5399	GM_102_B2_B04_T7	g2522228	BLASTX	619	5e-62	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
5400	GM_102_B2_B08_T7	g3845108	BLASTN	398	6e-11	63	Plasmodium falciparum chromosome 2, section 13 of 73 of the complete sequence
5401	GM_102_B2_B11_MR	g3142328	BLASTN	512	3e-16	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5402	GM_102_B2_B11_T7	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
5403	GM_102_B2_C01_MR	g3142328	BLASTN	2385	2e-102	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5404	GM_102_B2_C01_T7	g505129	BLASTN	324	2e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5405	GM_102_B2_C02_MR	g18559	BLASTN	397	6e-11	66	G.max gene for catalase
5406	GM_102_B2_C04_MR	g18559	BLASTN	1105	4e-43	74	G.max gene for catalase
5407	GM_102_B2_C05_T7	g4063760	BLASTX	262	2e-20	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5408	GM_102_B2_C08_T7	g3097320	BLASTN	464	6e-14	70	Glycine max gene for Bd 30K, complete cds
5409	GM_102_B2_C09_T7	g3201541	BLASTX	152	2e-24	74	(AJ005077) TCTR2 protein [Lycopersicon esculentum]
5410	GM_102_B2_C10_MR	g3845079	BLASTN	352	7e-09	59	Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence
5411	GM_102_B2_C10_T7	g2995405	BLASTX	367	1e-34	43	(Y12432) polyprotein [Ananas comosus]
5412	GM_102_B2_D02_MR	g2501498	BLASTX	203	9e-17	37	FLAVONOL 3-O-GLUCOSYLTRANSFERASE (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE) gi 1076656 pir S51767 glycosyl transferase - eggplant gi 607192 (X77369) glycosyl transferase [Solanum melongena]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5413	GM_102_B2_D02_T7	g2982576	BLASTN	439	8e-13	56	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-105, complete sequence [Plasmodium falciparum]
5414	GM_102_B2_D03_T7	g343624	BLASTN	453	1e-13	61	Leptomonas sp. 9S and 12S ribosomal RNA genes.
5415	GM_102_B2_D05_T7	g1045530	BLASTN	395	6e-11	64	Magnaporthe grisea host-species specificity (Pwl1) gene, complete cds.
5416	GM_102_B2_D08_T7	g4038056	BLASTX	397	4e-35	51	(AC005897) putative transposon [Arabidopsis thaliana]
5417	GM_102_B2_D09_MR	g245310	BLASTX	221	2e-17	67	reverse transcriptase [Solanum tuberosum=potatoes, cv. Pentland Squire, Peptide Transposon Partial, 78 aa]
5418	GM_102_B2_D10_T7	g3845197	BLASTN	437	1e-12	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
5419	GM_102_B2_D12_MR	g421955	BLASTX	208	2e-28	38	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
5420	GM_102_B2_D12_T7	g2970556	BLASTX	204	2e-14	83	(AF049708) aspartokinase-homoserine dehydrogenase [Glycine max]
5421	GM_102_B2_E03_T7	g2947070	BLASTX	156	7e-10	47	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]
5422	GM_102_B2_E05_T7	g3645899	BLASTX	196	1e-15	50	(U68408) 5' end not determined experimentally [Zea mays]
5423	GM_102_B2_E06_MR	g3599418	BLASTN	774	4e-28	73	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
5424	GM_102_B2_E06_T7	g629693	BLASTX	560	2e-53	55	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
5425	GM_102_B2_E07_T7	g507910	BLASTN	401	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5426	GM_102_B2_E09_T7	g3461846	BLASTX	323	6e-27	42	(AC005315) putative zinc-finger protein [Arabidopsis thaliana]
5427	GM_102_B2_E12_MR	g3367750	BLASTX	171	3e-11	61	(AL031155) putative amidase [Streptomyces coelicolor]
5428	GM_102_B2_E12_T7	g18559	BLASTN	403	3e-11	67	G.max gene for catalase
5429	GM_102_B2_F01_MR	g507910	BLASTN	585	8e-20	84	Glycine max BSR-101 satellite SB92 genomic sequence.
5430	GM_102_B2_F03_MR	g1666236	BLASTX	112	2e-13	30	(U76261) unknown [Hordeum vulgare]
5431	GM_102_B2_F04_T7	g507910	BLASTN	394	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5432	GM_102_B2_F06_MR	g507910	BLASTN	399	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5433	GM_102_B2_F06_T7	g507910	BLASTN	387	7e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5434	GM_102_B2_F07_MR	g3645899	BLASTX	146	3e-12	58	(U68408) 5' end not determined experimentally [Zea mays]
5435	GM_102_B2_F07_T7	g507910	BLASTN	438	4e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5436	GM_102_B2_F08_MR	g584825	BLASTX	171	3e-16	44	B2 PROTEIN gi 322726 pir S32124 B2 protein - carrot gi 297889 (X72385) B2 protein [Daucus carota]
5437	GM_102_B2_F08_T7	g3845068	BLASTN	418	7e-12	63	Plasmodium falciparum chromosome 2, section 1 of 73 of the complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5438	GM_102_B2_F10_T7	g3319362	BLASTX	270	2e-21	41	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
5439	GM_102_B2_G04_MR	g3810596	BLASTX	162	6e-10	36	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
5440	GM_102_B2_G06_MR	g2213540	BLASTX	228	2e-21	59	(X98744) chloroplast DNA-binding protein PD3 [Pisum sativum]
5441	GM_102_B2_G06_T7	g2564048	BLASTN	378	5e-10	80	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]
5442	GM_102_B2_G10_MR	g1173055	BLASTX	316	1e-27	85	60S RIBOSOMAL PROTEIN L11 (L5) gi 541961 pir S42497 ribosomal protein L11.e - alfalfa gi 1076504 pir S51819 RL5 ribosomal protein - alfalfa gi 463252 (X78284) RL5 ribosomal protein [Medicago sativa]
5443	GM_102_B2_G10_T7	g18768	BLASTN	351	2e-09	69	Soybean Tgm6 transposable element 3' end
5444	GM_102_B2_H01_MR	g2995405	BLASTX	303	4e-25	46	(Y12432) polyprotein [Ananas comosus]
5445	GM_102_B2_H01_T7	g3845197	BLASTN	546	1e-17	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
5446	GM_102_B2_H02_T7	g3377834	BLASTX	161	5e-10	27	(AF075598) No definition line found [Arabidopsis thaliana]
5447	GM_102_B2_H03_MR	g1666236	BLASTX	279	1e-23	34	(U76261) unknown [Hordeum vulgare]
5448	GM_102_B2_H04_T7	g2996647	BLASTN	519	2e-16	62	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
5449	GM_102_B2_H05_T7	g3779026	BLASTX	167	7e-24	50	(AC005171) putative retrotransposon [Arabidopsis thaliana]
5450	GM_102_B2_H06_MR	g507910	BLASTN	520	7e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
5451	GM_102_B2_H06_T7	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5452	GM_102_B2_H09_MR	g3645899	BLASTX	180	2e-26	38	(U68408) 5' end not determined experimentally [Zea mays]
5453	GM_102_B2_H09_T7	g3449317	BLASTN	351	8e-09	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKM21, complete sequence [Arabidopsis thaliana]
5454	GM_102_B2_H11_MR	g100484	BLASTX	433	2e-43	55	hypothetical protein - garden snapdragon
5455	GM_102_B2_H11_T7	g905361	BLASTX	167	9e-11	30	(U22103) gag-protease polyprotein [Glycine max]
5456	GM_103_A1_A04_MR	g507910	BLASTN	367	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5457	GM_103_A1_A04_T7	g905361	BLASTX	300	4e-25	78	(U22103) gag-protease polyprotein [Glycine max]
5458	GM_103_A1_B06_T7	g905361	BLASTX	321	2e-27	88	(U22103) gag-protease polyprotein [Glycine max]
5459	GM_103_A1_D02_T7	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5460	GM_103_A1_D08_T7	g507910	BLASTN	495	9e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
5461	GM_103_A1_E02_T7	g4063760	BLASTX	182	6e-12	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5462	GM_103_A1_E05_T7	g507910	BLASTN	394	3e-11	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5463	GM_103_A1_F01_T7	g3097320	BLASTN	683	1e-39	82	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5464	GM_103_A1_F03_MR	g544018	BLASTX	192	2e-13	35	NITRATE/CHLORATE TRANSPORTER gi 1076359 pir A45772 nitrate-inducible nitrate transporter - Arabidopsis thaliana gi 166668 (L10357) CHL1 [Arabidopsis thaliana] gi 3157921 (AC002131) Identical to nitrate/chlorate transporter cDNA gb L10357 from A. thaliana. ESTs gb H37533 and gb R29790, gb T46117, gb T46068, gb T75688, gb R29817, gb R29862, gb Z34634 and gb Z34258 come from this gene. [Arabidopsis thaliana]
5465	GM_103_A1_F03_T7	g860800	BLASTN	355	4e-09	61	B.juncea Xle7-2EB gene
5466	GM_103_A1_G01_T7	g3004480	BLASTX	161	4e-11	52	(AJ228333) reverse transcriptase [Pinus elliottii]
5467	GM_103_A1_G05_MR	g2586082	BLASTX	150	4e-09	41	(U72725) retrofit [Oryza longistaminata]
5468	GM_103_A1_G08_T7	g100484	BLASTX	272	6e-22	57	hypothetical protein - garden snapdragon
5469	GM_103_B1_A02_T7	g18559	BLASTN	523	1e-16	68	G.max gene for catalase
5470	GM_103_B1_A04_T7	g507910	BLASTN	401	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5471	GM_103_B1_A06_MR	g3777527	BLASTX	183	5e-17	42	(AF053008) gag-pol polyprotein [Glycine max]
5472	GM_103_B1_A06_T7	g1256945	BLASTN	345	4e-10	65	Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete transcribed region and flanks.
5473	GM_103_B1_A07_MR	g505129	BLASTN	360	3e-09	68	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5474	GM_103_B1_A10_MR	g2864608	BLASTX	128	3e-10	45	(AL021811) ferredoxin--NADP+ reductase - like protein [Arabidopsis thaliana]
5475	GM_103_B1_B01_T7	g3779030	BLASTX	146	7e-15	35	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
5476	GM_103_B1_B03_T7	g3142328	BLASTN	2483	6e-107	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5477	GM_103_B1_B06_T7	g3845197	BLASTN	428	3e-12	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
5478	GM_103_B1_B08_MR	g3645899	BLASTX	277	3e-26	45	(U68408) 5' end not determined experimentally [Zea mays]
5479	GM_103_B1_B10_MR	g3645899	BLASTX	156	3e-09	40	(U68408) 5' end not determined experimentally [Zea mays]
5480	GM_103_B1_B12_MR	g3928090	BLASTX	150	5e-28	50	(AC005770) putative MTN3 protein [Arabidopsis thaliana]
5481	GM_103_B1_C01_MR	g508826	BLASTN	464	7e-20	65	Drosophila melanogaster Oregon-R mitochondrial A+T region.
5482	GM_103_B1_C07_T7	g2522230	BLASTX	335	1e-29	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
5483	GM_103_B1_C10_MR	g4063770	BLASTX	221	2e-16	37	(AB004906) transposase [Ipomoea purpurea]
5484	GM_103_B1_C10_T7	g4063760	BLASTX	508	9e-47	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5485	GM_103_B1_C11_MR	g3097320	BLASTN	493	3e-15	69	Glycine max gene for Bd 30K, complete cds
5486	GM_103_B1_C12_T7	g2245104	BLASTX	305	3e-37	55	(Z97343) LTR retrotransposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5487	GM_103_B1_D01_MR	g522302	BLASTX	183	6e-16	49	(L35053) endonuclease [Magnaporthe grisea]
5488	GM_103_B1_D02_T7	g3645899	BLASTX	239	4e-18	51	(U68408) 5' end not determined experimentally [Zea mays]
5489	GM_103_B1_D05_MR	g4138343	BLASTX	223	1e-16	69	(AJ011979) RNA-directed RNA polymerase [Petunia x hybrida]
5490	GM_103_B1_D08_T7	g4063760	BLASTX	633	1e-63	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5491	GM_103_B1_E01_MR	g342965	BLASTN	434	3e-13	64	paramecium species 7,227 mt dna dimer: replication init. region.
5492	GM_103_B1_E05_T7	g2864613	BLASTX	192	2e-18	54	(AL021811) S-receptor kinase -like protein [Arabidopsis thaliana]
5493	GM_103_B1_E08_T7	g1769898	BLASTX	498	7e-47	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5494	GM_103_B1_E10_T7	g2244916	BLASTX	186	1e-19	44	(Z97339) hypothetical protein [Arabidopsis thaliana]
5495	GM_103_B1_F04_T7	g3892061	BLASTX	163	7e-14	28	(AC002330) putative reverse transcriptase [Arabidopsis thaliana]
5496	GM_103_B1_F06_T7	g3142328	BLASTN	955	3e-36	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5497	GM_103_B1_F09_MR	g3319368	BLASTX	152	3e-09	32	(AF077409) similar to maize transposon MuDR mudrA protein (GB:AL021710) [Arabidopsis thaliana]
5498	GM_103_B1_F10_T7	g18559	BLASTN	420	5e-12	66	G.max gene for catalase
5499	GM_103_B1_F12_MR	g3777527	BLASTX	433	2e-38	86	(AF053008) gag-pol polyprotein [Glycine max]
5500	GM_103_B1_G01_T7	g905361	BLASTX	225	6e-17	33	(U22103) gag-protease polyprotein [Glycine max]
5501	GM_103_B1_G03_MR	g3777527	BLASTX	922	7e-91	95	(AF053008) gag-pol polyprotein [Glycine max]
5502	GM_103_B1_G08_MR	g3777526	BLASTN	715	3e-25	66	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
5503	GM_103_B1_G09_MR	g3599418	BLASTN	649	2e-22	84	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
5504	GM_103_B1_G09_T7	g1666236	BLASTX	172	7e-12	30	(U76261) unknown [Hordeum vulgare]
5505	GM_103_B1_G12_T7	g3777527	BLASTX	775	4e-75	94	(AF053008) gag-pol polyprotein [Glycine max]
5506	GM_103_B1_H02_T7	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5507	GM_103_B1_H04_MR	g13584	BLASTN	426	1e-12	60	Yeast mitochondrial oxi3 gene exon 1 for cytochrome c oxidase subunit I
5508	GM_103_B1_H04_T7	g3695395	BLASTX	221	2e-16	44	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
5509	GM_103_B1_H05_MR	g2673911	BLASTX	160	1e-13	40	(AC002561) putative squamosa-promoter binding protein [Arabidopsis thaliana]
5510	GM_103_B1_H07_T7	g3377848	BLASTX	142	8e-20	52	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
5511	GM_103_B1_H08_MR	g507910	BLASTN	343	7e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5512	GM_103_B1_H08_T7	g507910	BLASTN	368	5e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5513	GM_104_A1_A07_T7	g3510336	BLASTN	381	4e-10	67	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]
5514	GM_104_A1_A08_T7	g3810596	BLASTX	282	9e-23	41	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
5515	GM_104_A1_A10_T7	g629693	BLASTX	332	3e-29	54	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
5516	GM_104_A1_B03_T7	g3810596	BLASTX	109	4e-11	40	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
5517	GM_104_A1_B05_T7	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5518	GM_104_A1_B09_MR	g4063756	BLASTN	408	2e-11	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
5519	GM_104_A1_B12_T7	g3097320	BLASTN	711	4e-25	84	Glycine max gene for Bd 30K, complete cds
5520	GM_104_A1_C03_T7	g1142702	BLASTN	385	7e-11	79	Glycine max satellite STR120-A.4.
5521	GM_104_A1_C11_T7	g4038056	BLASTX	230	6e-20	51	(AC005897) putative transposon [Arabidopsis thaliana]
5522	GM_104_A1_D03_MR	g4038056	BLASTX	262	3e-23	43	(AC005897) putative transposon [Arabidopsis thaliana]
5523	GM_104_A1_D08_T7	g2924777	BLASTX	158	2e-09	42	(AC002334) putative receptor protein kinase [Arabidopsis thaliana]
5524	GM_104_A1_D11_MR	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
5525	GM_104_A1_D11_T7	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5526	GM_104_A1_D12_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
5527	GM_104_A1_E02_T7	g905361	BLASTX	207	5e-15	32	(U22103) gag-protease polyprotein [Glycine max]
5528	GM_104_A1_E07_T7	g4063760	BLASTX	145	5e-18	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5529	GM_104_A1_E10_T7	g2522228	BLASTX	519	4e-49	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
5530	GM_104_A1_E12_MR	g3645899	BLASTX	345	2e-29	49	(U68408) 5' end not determined experimentally [Zea mays]
5531	GM_104_A1_F02_T7	g3097320	BLASTN	506	7e-16	82	Glycine max gene for Bd 30K, complete cds
5532	GM_104_A1_F03_T7	g3142328	BLASTN	804	2e-29	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5533	GM_104_A1_F06_T7	g1431738	BLASTN	392	8e-11	92	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
5534	GM_104_A1_F08_MR	g3097320	BLASTN	700	1e-24	82	Glycine max gene for Bd 30K, complete cds
5535	GM_104_A1_G02_T7	g507910	BLASTN	360	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5536	GM_104_A1_G04_T7	g840618	BLASTN	347	7e-09	58	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
5537	GM_104_A1_G05_MR	g2583130	BLASTX	169	2e-10	36	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
5538	GM_104_A1_G06_T7	g100484	BLASTX	212	7e-25	49	hypothetical protein - garden snapdragon
5539	GM_104_A1_G09_MR	g1040936	BLASTN	352	9e-10	63	Anopheles konderi NADH dehydrogenase subunit 2 gene, mitochondrial gene encoding mitochondrial product, partial cds.
5540	GM_104_A1_H08_MR	g2522228	BLASTX	328	7e-29	66	(AB007466) reverse transcriptase-like protein [Vicia faba]
5541	GM_104_A1_H10_MR	g320569	BLASTX	138	2e-11	38	transposon TNT1 - Arabidopsis thaliana (fragment)

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5542	GM_104_A1_H11_T7	g905361	BLASTX	216	5e-16	63	(U22103) gag-protease polyprotein [Glycine max]
5543	GM_104_A2_A02_MR	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5544	GM_104_A2_A02_T7	g905361	BLASTX	429	2e-39	95	(U22103) gag-protease polyprotein [Glycine max]
5545	GM_104_A2_A04_MR	g3892061	BLASTX	138	3e-11	28	(AC002330) putative reverse transcriptase [Arabidopsis thaliana]
5546	GM_104_A2_A07_T7	g1345977	BLASTX	163	1e-10	88	OMEGA-6 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM ISOZYME 2 gi 904154 (L43921) microsomal omega-6 desaturase [Glycine max]
5547	GM_104_A2_A08_T7	g3097320	BLASTN	483	8e-15	70	Glycine max gene for Bd 30K, complete cds
5548	GM_104_A2_A09_T7	g1370204	BLASTN	375	1e-10	86	L.japonicus mRNA for small GTP-binding protein, RAN1B
5549	GM_104_A2_A10_T7	g3777527	BLASTX	768	3e-74	95	(AF053008) gag-pol polyprotein [Glycine max]
5550	GM_104_A2_A11_MR	g3241925	BLASTN	426	3e-12	61	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]
5551	GM_104_A2_B01_MR	g2264320	BLASTN	551	7e-18	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
5552	GM_104_A2_B03_T7	g1085922	BLASTX	201	2e-20	82	hypothetical protein 224 - evening primrose mitochondrion >gi 459533 (X78038) orf224; homology to ribosomal protein S1 of E. coli [Oenothera berteriana]
5553	GM_104_A2_B06_MR	g2522230	BLASTX	245	4e-20	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
5554	GM_104_A2_B06_T7	g454847	BLASTN	405	2e-11	70	Glycine max ribosomal protein S11 gene, complete cds
5555	GM_104_A2_B07_T7	g2245104	BLASTX	241	4e-18	42	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
5556	GM_104_A2_B10_T7	g18559	BLASTN	993	5e-38	80	G.max gene for catalase
5557	GM_104_A2_C01_MR	g3738114	BLASTN	419	2e-14	67	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
5558	GM_104_A2_C02_T7	g2688657	BLASTX	158	5e-10	73	(AE001172) pyrophosphate--fructose 6-phosphate 1-phosphotransferase (pfk) [Borrelia burgdorferi]
5559	GM_104_A2_C04_T7	g18559	BLASTN	681	8e-24	75	G.max gene for catalase
5560	GM_104_A2_C08_T7	g507910	BLASTN	477	6e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
5561	GM_104_A2_C09_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5562	GM_104_A2_C09_T7	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5563	GM_104_A2_D02_MR	g18559	BLASTN	1195	3e-47	87	G.max gene for catalase
5564	GM_104_A2_D02_T7	g3820976	BLASTN	406	3e-11	60	Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complet...

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5565	GM_104_A2_D04_T7	g3319362	BLASTX	229	4e-17	42	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
5566	GM_104_A2_D08_MR	g18559	BLASTN	682	7e-24	75	G.max gene for catalase
5567	GM_104_A2_D11_T7	g2522230	BLASTX	187	6e-14	46	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
5568	GM_104_A2_E07_MR	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
5569	GM_104_A2_E07_T7	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
5570	GM_104_A2_E08_MR	g4063760	BLASTX	439	2e-39	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5571	GM_104_A2_E09_T7	g2501460	BLASTX	159	9e-20	67	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) gi 1545952 gnl PID e244584 (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]
5572	GM_104_A2_E10_T7	g1345644	BLASTX	254	2e-20	54	CYTOCHROME P450 LXXXVI gi 940446 (X90458) cytochrome p450 [Arabidopsis thaliana]
5573	GM_104_A2_F08_MR	g507910	BLASTN	351	3e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5574	GM_104_A2_F09_T7	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5575	GM_104_A2_F11_MR	g2982320	BLASTX	221	2e-17	43	(AF051245) hypothetical protein [Picea mariana]
5576	GM_104_A2_G04_MR	g507910	BLASTN	352	3e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
5577	GM_104_A2_G04_T7	g507910	BLASTN	378	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5578	GM_104_A2_G08_MR	g4063760	BLASTX	286	5e-23	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5579	GM_104_A2_H01_T7	g3004545	BLASTX	190	1e-12	34	(AC003673) putative reverse transcriptase [Arabidopsis thaliana]
5580	GM_104_A2_H06_T7	g507910	BLASTN	598	2e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
5581	GM_104_A2_H09_T7	g1165321	BLASTN	484	7e-15	79	Glycine max extensin (SbHRGP3) gene, complete cds
5582	GM_104_A2_H10_MR	g4063760	BLASTX	273	1e-21	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5583	GM_104_B1_A09_T7	g3097320	BLASTN	542	2e-17	73	Glycine max gene for Bd 30K, complete cds
5584	GM_104_B1_A11_T7	g3386604	BLASTX	232	5e-19	56	(AC004665) putative protein kinase [Arabidopsis thaliana]
5585	GM_104_B1_C03_T7	g2493908	BLASTX	297	7e-25	55	CULLIN HOMOLOG 3 (CUL-3) gi 1381146 (U58089) Hs-CUL-3 [Homo sapiens]
5586	GM_104_B1_C04_T7	g100226	BLASTX	210	2e-15	43	hypothetical protein - tomato gi 19275 (Z12127) protein of unknown function [Lycopersicon esculentum] gi 445619 prf 1909366A Leu zipper protein [Lycopersicon esculentum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5587	GM_104_B1_C05_T7	g2129618	BLASTX	235	1e-17	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5588	GM_104_B1_C07_T7	g4160362	BLASTN	402	4e-11	63	Saccharomyces cerevisiae complete mitochondrial genome
5589	GM_104_B1_C08_T7	g905361	BLASTX	216	5e-16	35	(U22103) gag-protease polyprotein [Glycine max]
5590	GM_104_B1_C10_T7	g422418	BLASTX	208	7e-15	41	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
5591	GM_104_B1_D02_T7	g4063760	BLASTX	279	3e-22	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5592	GM_104_B1_D08_T7	g3142328	BLASTN	592	8e-20	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5593	GM_104_B1_D11_T7	g3021276	BLASTX	159	2e-18	64	(AL022347) serine/threonine kinase - like protein [Arabidopsis thaliana]
5594	GM_104_B1_E02_T7	g18559	BLASTN	1060	5e-41	78	G.max gene for catalase
5595	GM_104_B1_E04_T7	g507910	BLASTN	402	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5596	GM_104_B1_E06_T7	g3097320	BLASTN	443	5e-13	74	Glycine max gene for Bd 30K, complete cds
5597	GM_104_B1_E09_T7	g3851527	BLASTN	414	9e-12	65	Hordeum vulgare cultivar Bomi starch branching enzyme IIb (sbeIIb) gene, nuclear gene encoding plastid protein, partial cds
5598	GM_104_B1_F02_T7	g2896804	BLASTN	393	1e-10	63	Human Chromosome 16 BAC clone CIT987SK-A-598D4, complete sequence [Homo sapiens]
5599	GM_104_B1_F05_T7	g4063760	BLASTX	195	1e-14	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5600	GM_104_B1_G01_T7	g3319362	BLASTX	228	9e-22	56	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
5601	GM_104_B1_G04_T7	g2129618	BLASTX	171	7e-11	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5602	GM_104_B1_G05_T7	g2961390	BLASTX	138	1e-15	78	(AL022141) beta-galactosidase like protein [Arabidopsis thaliana]
5603	GM_104_B1_G09_T7	g507910	BLASTN	369	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5604	GM_104_B1_G11_T7	g4106666	BLASTX	180	3e-13	44	(AL035064) putative ubiquinone biosynthesis protein [Schizosaccharomyces pombe]
5605	GM_104_B1_H02_T7	g3608150	BLASTX	345	1e-30	60	(AC005314) putative peroxidase [Arabidopsis thaliana]
5606	GM_104_B1_H06_T7	g3250687	BLASTX	199	3e-15	36	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
5607	GM_104_B2_A02_MR	g1709919	BLASTX	378	3e-34	72	AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) (GPAT) gi 439105 (L23834) glutamine phosphoribosylpyrophosphate amidotransferase [Vigna aconitifolia]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5608	GM_104_B2_A03_T7	g2979574	BLASTN	366	2e-09	66	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence [Homo sapiens]
5609	GM_104_B2_A04_MR	g2522228	BLASTX	335	1e-29	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
5610	GM_104_B2_A08_T7	g226407	BLASTX	110	5e-09	44	retrotransposon del1-46 [Lilium henryi]
5611	GM_104_B2_A11_T7	g3645899	BLASTX	279	2e-22	50	(U68408) 5' end not determined experimentally [Zea mays]
5612	GM_104_B2_A12_MR	g1769897	BLASTX	153	2e-09	32	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5613	GM_104_B2_B06_T7	g166884	BLASTN	457	2e-14	76	A.thaliana telomeric DNA. >gi 589934 gb I07744 Sequence 1 from Patent EP 0338266
5614	GM_104_B2_B07_T7	g4063760	BLASTX	140	2e-10	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5615	GM_104_B2_B08_MR	g1568538	BLASTN	370	1e-09	65	Human DNA sequence from PAC 253J14 on chromosome X contains polymorphic CA repeat
5616	GM_104_B2_C01_MR	g4038056	BLASTX	187	1e-12	42	(AC005897) putative transposon [Arabidopsis thaliana]
5617	GM_104_B2_C05_T7	g3947733	BLASTX	217	1e-20	73	(AJ009719) NL25 [Solanum tuberosum]
5618	GM_104_B2_D01_MR	g3097320	BLASTN	380	4e-10	62	Glycine max gene for Bd 30K, complete cds
5619	GM_104_B2_D02_MR	g2735017	BLASTX	272	9e-22	72	(U82481) KI domain interacting kinase 1 [Zea mays]
5620	GM_104_B2_D03_MR	g3777527	BLASTX	536	2e-49	97	(AF053008) gag-pol polyprotein [Glycine max]
5621	GM_104_B2_D06_T7	g4063760	BLASTX	345	3e-29	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5622	GM_104_B2_D07_MR	g4063756	BLASTN	422	5e-12	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
5623	GM_104_B2_D07_T7	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5624	GM_104_B2_D11_MR	g3142328	BLASTN	691	3e-24	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5625	GM_104_B2_D11_T7	g4063760	BLASTX	177	2e-11	30	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5626	GM_104_B2_E06_T7	g3097320	BLASTN	577	4e-19	71	Glycine max gene for Bd 30K, complete cds
5627	GM_104_B2_E08_T7	g2791289	BLASTX	143	5e-15	40	(AJ000387) protease [Drosophila melanogaster]
5628	GM_104_B2_E09_MR	g2316016	BLASTX	296	6e-24	58	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
5629	GM_104_B2_E12_T7	g4063770	BLASTX	193	2e-13	37	(AB004906) transposase [Ipomoea purpurea]
5630	GM_104_B2_F01_MR	g905361	BLASTX	422	1e-38	95	(U22103) gag-protease polyprotein [Glycine max]
5631	GM_104_B2_F09_MR	g507910	BLASTN	569	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5632	GM_104_B2_F09_T7	g507910	BLASTN	591	4e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
5633	GM_104_B2_F12_MR	g3869069	BLASTN	365	2e-09	65	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]
5634	GM_104_B2_G01_T7	g18559	BLASTN	841	4e-31	76	G.max gene for catalase
5635	GM_104_B2_G03_MR	g18559	BLASTN	466	4e-14	67	G.max gene for catalase
5636	GM_104_B2_G04_MR	g4038056	BLASTX	266	4e-21	52	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5637	GM_104_B2_G05_T7	g2098709	BLASTX	202	1e-14	67	(U82975) pectinesterase [Citrus sinensis]
5638	GM_104_B2_G08_MR	g18559	BLASTN	698	1e-24	75	G.max gene for catalase
5639	GM_104_B2_G09_MR	g1769899	BLASTX	230	2e-20	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5640	GM_104_B2_G11_MR	g2522228	BLASTX	187	3e-13	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
5641	GM_104_B2_H01_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5642	GM_104_B2_H01_T7	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5643	GM_104_B2_H04_MR	g1588265	BLASTX	186	1e-12	84	100RNP protein [Spinacia oleracea]
5644	GM_104_B2_H05_MR	g3695395	BLASTX	183	5e-14	43	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
5645	GM_104_B2_H06_MR	g3695395	BLASTX	185	3e-14	43	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
5646	GM_104_B2_H08_MR	g3599418	BLASTN	396	6e-11	73	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
5647	GM_104_B2_H10_T7	g2565011	BLASTX	194	2e-13	50	(AC002983) putative mudrA-like retrotransposon-associated protein [Arabidopsis thaliana]
5648	GM_105_A1_A01_MR	g3337395	BLASTN	442	6e-13	65	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
5649	GM_105_A1_A04_MR	g322662	BLASTX	134	6e-18	69	S-receptor kinase-related protein - Chinese kale gi 17915 (Z18883) S-receptor kinase related protein [Brassica oleracea]
5650	GM_105_A1_A09_MR	g507910	BLASTN	519	8e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
5651	GM_105_A1_C04_MR	g3894210	BLASTN	352	7e-09	63	Homo sapiens PAC clone DJ0953B05 from 7p12-p14, complete sequence [Homo sapiens]
5652	GM_105_A1_C07_MR	g1142701	BLASTN	1188	2e-47	82	Glycine max satellite STR120-A.3.
5653	GM_105_A1_C11_MR	g3142328	BLASTN	1709	1e-70	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5654	GM_105_A1_D05_MR	g2522230	BLASTX	293	4e-25	44	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
5655	GM_105_A1_D10_MR	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
5656	GM_105_A1_E04_MR	g2160694	BLASTX	261	5e-21	67	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
5657	GM_105_A1_E07_MR	g2522227	BLASTX	181	4e-13	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
5658	GM_105_A1_E09_MR	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5659	GM_105_A1_F03_MR	g4063760	BLASTX	225	1e-16	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5660	GM_105_A1_F04_MR	g18559	BLASTN	794	1e-34	78	G.max gene for catalase
5661	GM_105_A1_G03_MR	g3097320	BLASTN	916	2e-34	77	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5662	GM_105_A1_G04_MR	g3930515	BLASTX	109	2e-09	43	(AF059674) putative gag protein [Nicotiana tabacum]
5663	GM_105_A1_G10_MR	g100484	BLASTX	394	4e-35	54	hypothetical protein - garden snapdragon
5664	GM_105_A1_H05_MR	g421953	BLASTX	174	4e-12	40	hypothetical protein 2 - potato transposon Tst1 gi 21432 (X52387) ORF2 [Solanum tuberosum]
5665	GM_105_A1_H09_MR	g1167523	BLASTX	279	3e-22	36	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
5666	GM_105_A1_H12_MR	g421954	BLASTX	211	5e-27	47	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
5667	GM_105_A2_A03_T7	g2995405	BLASTX	392	1e-34	54	(Y12432) polyprotein [Ananas comosus]
5668	GM_105_A2_A07_MR	g4063756	BLASTN	473	3e-14	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
5669	GM_105_A2_A07_T7	g3142379	BLASTX	213	5e-16	55	(AF053008) envelope-like [Glycine max]
5670	GM_105_A2_A09_MR	g3645899	BLASTX	190	8e-17	58	(U68408) 5' end not determined experimentally [Zea mays]
5671	GM_105_A2_A12_T7	g3142328	BLASTN	1179	2e-46	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5672	GM_105_A2_B04_MR	g1204057	BLASTN	416	9e-12	62	Caenorhabditis elegans cosmid C04B4, complete sequence [Caenorhabditis elegans]
5673	GM_105_A2_B04_T7	g2462936	BLASTX	389	3e-35	56	(Y12321) open reading frame 2 [Brassica oleracea]
5674	GM_105_A2_B09_T7	g1142699	BLASTN	1360	4e-55	88	Glycine max satellite STR120-A.1.
5675	GM_105_A2_B10_MR	g2244942	BLASTX	118	1e-09	44	(Z97339) similarity to hypothetical protein [Arabidopsis thaliana]
5676	GM_105_A2_B11_T7	g507910	BLASTN	459	4e-14	77	Glycine max BSR-101 satellite SB92 genomic sequence.
5677	GM_105_A2_C04_MR	g1769897	BLASTX	166	8e-11	27	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5678	GM_105_A2_C06_MR	g3777527	BLASTX	570	1e-54	89	(AF053008) gag-pol polyprotein [Glycine max]
5679	GM_105_A2_C06_T7	g4159703	BLASTN	350	9e-09	72	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence [Arabidopsis thaliana]
5680	GM_105_A2_C07_MR	g4063760	BLASTX	240	2e-19	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5681	GM_105_A2_C07_T7	g2995405	BLASTX	398	3e-35	52	(Y12432) polyprotein [Ananas comosus]
5682	GM_105_A2_C08_MR	g3600043	BLASTX	173	2e-21	49	(AF080119) No definition line found [Arabidopsis thaliana]
5683	GM_105_A2_C09_T7	g100484	BLASTX	337	6e-29	56	hypothetical protein - garden snapdragon
5684	GM_105_A2_C10_MR	g507910	BLASTN	567	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5685	GM_105_A2_C12_MR	g13773	BLASTN	404	6e-12	68	Torulopsis glabrata mitochondrial genes for tRNAs -Tyr, -Asn, -Ala, -Ile -Trp (from Var1-LrRNA intergenic region) >gi 343959 gb M11906 YSLMTIG09 Yeast (T.glabrata) mitochondrial DNA between var1 and L rRNA genes.
5686	GM_105_A2_C12_T7	g2827709	BLASTX	198	1e-13	53	(AL021684) predicted protein [Arabidopsis thaliana]
5687	GM_105_A2_D03_T7	g2160694	BLASTX	271	3e-22	83	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5688	GM_105_A2_D04_T7	g3142328	BLASTN	735	3e-26	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5689	GM_105_A2_E02_T7	g3037017	BLASTN	374	8e-11	66	Bodo saltans NADH dehydrogenase subunit 5 (ND5) mRNA, kinetoplast gene encoding kinetoplast protein, partial cds
5690	GM_105_A2_E04_T7	g2522227	BLASTX	223	9e-18	56	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
5691	GM_105_A2_F04_MR	g4063760	BLASTX	299	2e-24	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5692	GM_105_A2_F05_MR	g3097320	BLASTN	1040	4e-40	80	Glycine max gene for Bd 30K, complete cds
5693	GM_105_A2_F06_T7	g3142328	BLASTN	673	2e-23	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5694	GM_105_A2_F08_MR	g4063756	BLASTN	459	1e-13	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
5695	GM_105_A2_G06_T7	g2995405	BLASTX	368	4e-32	62	(Y12432) polyprotein [Ananas comosus]
5696	GM_105_A2_G07_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5697	GM_105_A2_G10_T7	g3461840	BLASTX	190	1e-12	34	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
5698	GM_105_A2_H03_MR	g3834313	BLASTX	327	7e-39	72	(AC005679) Strong similarity to T16B12.3 gi 3746060 unknown protein from Arabidopsis thaliana BAC gb AC005311. [Arabidopsis thaliana]
5699	GM_105_A2_H06_MR	g507910	BLASTN	410	6e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5700	GM_105_A2_H07_MR	g3860246	BLASTX	113	3e-09	47	(AC005824) putative reverse-transcriptase protein [Arabidopsis thaliana]
5701	GM_105_A2_H12_MR	g507910	BLASTN	702	4e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
5702	GM_106_A1_A06_MR	g2459431	BLASTX	215	4e-16	44	(AC002332) unknown protein [Arabidopsis thaliana]
5703	GM_106_A1_B02_T7	g2995405	BLASTX	346	1e-29	48	(Y12432) polyprotein [Ananas comosus]
5704	GM_106_A1_B07_T7	g3777527	BLASTX	189	2e-12	33	(AF053008) gag-pol polyprotein [Glycine max]
5705	GM_106_A1_B09_T7	g3033389	BLASTX	200	5e-14	42	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
5706	GM_106_A1_C01_T7	g2129618	BLASTX	163	6e-16	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5707	GM_106_A1_C03_MR	g2522230	BLASTX	244	6e-20	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
5708	GM_106_A1_C04_T7	g130582	BLASTX	241	1e-20	40	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5709	GM_106_A1_C06_MR	g2894587	BLASTN	378	4e-10	65	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-112, complete sequence [Plasmodium falciparum]
5710	GM_106_A1_C10_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5711	GM_106_A1_D04_T7	g840618	BLASTN	346	8e-09	58	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
5712	GM_106_A1_D05_MR	g178858	BLASTN	383	9e-11	62	Human restriction fragment length polymorphism 3' to the apolipoprotein B gene.
5713	GM_106_A1_D08_T7	g2129618	BLASTX	218	6e-16	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5714	GM_106_A1_D09_T7	g2121303	BLASTN	477	2e-14	66	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
5715	GM_106_A1_E01_T7	g421954	BLASTX	326	8e-28	50	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
5716	GM_106_A1_E04_T7	g342954	BLASTN	389	2e-11	60	paramecium species 4.51b mt dna dimer: replication init. region, clone-1.
5717	GM_106_A1_E06_T7	g3645899	BLASTX	201	2e-15	50	(U68408) 5' end not determined experimentally [Zea mays]
5718	GM_106_A1_E07_T7	g3777527	BLASTX	154	9e-21	45	(AF053008) gag-pol polyprotein [Glycine max]
5719	GM_106_A1_E09_T7	g4038056	BLASTX	267	2e-27	46	(AC005897) putative transposon [Arabidopsis thaliana]
5720	GM_106_A1_E12_MR	g387902	BLASTX	154	2e-16	51	(L23524) ORF [Hordeum vulgare]
5721	GM_106_A1_F02_T7	g505129	BLASTN	375	5e-10	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5722	GM_106_A1_F03_T7	g4063760	BLASTX	654	2e-62	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5723	GM_106_A1_F05_T7	g3785991	BLASTX	234	4e-18	82	(AC005560) putative MAP kinase [Arabidopsis thaliana]
5724	GM_106_A1_F11_T7	g2996647	BLASTN	407	2e-11	59	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
5725	GM_106_A1_F12_T7	g3097320	BLASTN	414	1e-11	73	Glycine max gene for Bd 30K, complete cds
5726	GM_106_A1_G01_T7	g905361	BLASTX	122	4e-12	33	(U22103) gag-protease polyprotein [Glycine max]
5727	GM_106_A1_G02_MR	g3097320	BLASTN	1048	2e-40	75	Glycine max gene for Bd 30K, complete cds
5728	GM_106_A1_G04_MR	g905361	BLASTX	197	6e-14	31	(U22103) gag-protease polyprotein [Glycine max]
5729	GM_106_A1_G09_T7	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5730	GM_106_A1_G11_T7	g18575	BLASTN	826	1e-30	89	Soybean ENOD2A gene for Ngm-75
5731	GM_106_A1_G12_MR	g1431738	BLASTN	696	1e-24	77	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
5732	GM_106_A1_G12_T7	g505129	BLASTN	410	1e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5733	GM_106_A1_H01_T7	g3777527	BLASTX	667	2e-63	84	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5734	GM_106_A1_H02_MR	g3695387	BLASTX	239	4e-18	58	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
5735	GM_106_A1_H05_T7	g3097320	BLASTN	1205	2e-47	77	Glycine max gene for Bd 30K, complete cds
5736	GM_106_A1_H07_T7	g3777527	BLASTX	461	2e-41	57	(AF053008) gag-pol polyprotein [Glycine max]
5737	GM_106_A1_H10_T7	g3687234	BLASTX	211	4e-15	39	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
5738	GM_106_A1_H11_T7	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5739	GM_106_A1_H12_MR	g3142328	BLASTN	682	7e-24	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5740	GM_106_B1_A01_MR	g1480927	BLASTN	718	1e-25	97	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
5741	GM_106_B1_A08_T7	g2522227	BLASTX	202	2e-15	53	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
5742	GM_106_B1_A09_T7	g3249105	BLASTX	230	6e-18	61	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
5743	GM_106_B1_B04_T7	g541951	BLASTX	441	7e-41	84	SPCP2 protein - soybean gi 310578 (L12258) nodulin-26 [Glycine max]
5744	GM_106_B1_B06_T7	g3695395	BLASTX	197	6e-14	43	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
5745	GM_106_B1_B07_T7	g3097320	BLASTN	564	2e-18	75	Glycine max gene for Bd 30K, complete cds
5746	GM_106_B1_B11_MR	g1730557	BLASTX	238	4e-18	69	ALPHA-GLUCAN PHOSPHORYLASE, L ISOZYME 2 PRECURSOR (STARCH PHOSPHORYLASE L-2) gi 421957 pir S34189 starch phosphorylase (EC 2.4.1.1) - potato gi 1084437 pir S53489 starch phosphorylase (EC 2.4.1.1) - potato gi 313349 (X73684) starch phosphorylase [Solanum tuberosum]
5747	GM_106_B1_B11_T7	g18559	BLASTN	428	2e-12	78	G.max gene for catalase
5748	GM_106_B1_B12_MR	g507910	BLASTN	398	2e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5749	GM_106_B1_B12_T7	g507910	BLASTN	381	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5750	GM_106_B1_C01_MR	g2982452	BLASTX	218	7e-16	45	(AL022223) receptor protein kinase - like protein [Arabidopsis thaliana]
5751	GM_106_B1_C01_T7	g541978	BLASTX	134	4e-17	96	guanine nucleotide regulatory protein - fava bean gi 303734 gnl PID d1002608 (D12550) GTP-binding protein [Pisum sativum] gi 452359 (Z29590) guanine nucleotide regulatory protein [Vicia faba] gi 738942 prf 2001457K GTP-binding protein [Pisum sativum] gi 1098293 prf 2115367A small GTP-binding protein [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5752	GM_106_B1_C04_T7	g2586083	BLASTX	193	3e-13	38	(U72725) receptor kinase-like protein [Oryza longistaminata]
5753	GM_106_B1_C09_MR	g1769898	BLASTX	195	1e-13	70	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5754	GM_106_B1_C12_MR	g507910	BLASTN	435	5e-13	78	Glycine max BSR-101 satellite SB92 genomic sequence.
5755	GM_106_B1_D01_T7	g4038056	BLASTX	194	6e-21	56	(AC005897) putative transposon [Arabidopsis thaliana]
5756	GM_106_B1_D02_T7	g531389	BLASTX	124	2e-14	44	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
5757	GM_106_B1_D04_T7	g3250687	BLASTX	203	1e-15	54	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
5758	GM_106_B1_E02_T7	g4106408	BLASTN	674	4e-24	76	Oryza sativa subsp. indica dispersed centromeric repeat family RCS1
5759	GM_106_B1_E05_MR	g1769897	BLASTX	333	6e-29	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5760	GM_106_B1_E11_T7	g531389	BLASTX	111	4e-13	48	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
5761	GM_106_B1_E12_T7	g1769898	BLASTX	350	1e-30	72	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5762	GM_106_B1_F03_T7	g2129618	BLASTX	183	4e-12	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5763	GM_106_B1_F04_T7	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5764	GM_106_B1_G04_MR	g4056613	BLASTX	177	2e-12	41	(AF067400) Scl1 protein [Zea mays]
5765	GM_106_B1_G05_MR	g507910	BLASTN	514	1e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
5766	GM_106_B1_G11_T7	g2522227	BLASTX	202	1e-15	52	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
5767	GM_106_B1_H05_MR	g4159707	BLASTN	515	3e-16	66	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence [Arabidopsis thaliana]
5768	GM_106_B1_H05_T7	g1708314	BLASTX	204	1e-14	69	HEAT SHOCK PROTEIN 83 gi 169296 (M99431) heat shock protein 83 [Pharbitis nil] gi 445625 prf 1909372A heat shock protein 83 [Ipomoea nil]
5769	GM_106_B1_H10_MR	g3777527	BLASTX	168	1e-14	52	(AF053008) gag-pol polyprotein [Glycine max]
5770	GM_106_B1_H12_T7	g2642431	BLASTX	284	1e-22	59	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
5771	GM_107_A1_A02_MR	g1840106	BLASTN	385	5e-11	65	Human fragile site locus (FRA16B) minisatellite repeat
5772	GM_107_A1_A05_T7	g4063760	BLASTX	168	2e-10	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5773	GM_107_A1_A06_T7	g304040	BLASTN	1515	1e-62	85	Alnus incana chloroplast 23S ribosomal RNA (23S rRNA) gene.
5774	GM_107_A1_A09_MR	g1171591	BLASTN	352	7e-09	62	P.falciparum complete gene map of plastid-like DNA (IR-B)
5775	GM_107_A1_A11_MR	g1813979	BLASTX	173	5e-35	71	(Y10860) hypothetical protein [Musa acuminata]
5776	GM_107_A1_B03_MR	g2443881	BLASTX	157	3e-09	51	(AC002294) contains beta-transducin motif [Arabidopsis thaliana]
5777	GM_107_A1_B06_MR	g4115373	BLASTX	156	3e-09	33	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5778	GM_107_A1_B10_MR	g3142328	BLASTN	661	6e-23	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5779	GM_107_A1_B11_MR	g1813979	BLASTX	170	8e-29	71	(Y10860) hypothetical protein [Musa acuminata]
5780	GM_107_A1_C02_T7	g3695395	BLASTX	187	7e-13	45	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
5781	GM_107_A1_C03_MR	g3319345	BLASTX	119	2e-10	32	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
5782	GM_107_A1_C06_MR	g3377855	BLASTX	209	7e-23	71	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
5783	GM_107_A1_C06_T7	g2462134	BLASTX	92	1e-09	43	(Y13368) reverse transcriptase [Beta vulgaris]
5784	GM_107_A1_C09_MR	g2499616	BLASTX	267	2e-30	84	MITOGEN-ACTIVATED PROTEIN KINASE HOMOLOG NTF6 (P43) gi 1076639 pir S51320 mitogen-activated protein kinase 6 (EC 2.7.1.-) - common tobacco gi 2129967 pir S68189 serine/threonine protein kinase p43 - common tobacco gi 634068 (X83879) p43Nft6 serine/threonine protein kinase [Nicotiana tabacum]
5785	GM_107_A1_D08_T7	g3645899	BLASTX	341	5e-29	50	(U68408) 5' end not determined experimentally [Zea mays]
5786	GM_107_A1_D10_T7	g2921625	BLASTN	524	1e-16	72	Lupinus luteus leghemoglobin (LbI) gene, complete cds
5787	GM_107_A1_E04_MR	g261221	BLASTN	352	6e-09	64	patatin A gene, patatin B gene [Solanum tuberosum=potatoes, HH578, tetraploid, Genomic, 4116 nt]
5788	GM_107_A1_E07_MR	g507910	BLASTN	340	9e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5789	GM_107_A1_E08_MR	g507910	BLASTN	647	1e-22	86	Glycine max BSR-101 satellite SB92 genomic sequence.
5790	GM_107_A1_E08_T7	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
5791	GM_107_A1_E10_MR	g1142701	BLASTN	1367	2e-55	86	Glycine max satellite STR120-A.3.
5792	GM_107_A1_E12_T7	g2073447	BLASTN	365	2e-09	64	L.japonicus gln1, pge1 & krm genes
5793	GM_107_A1_F01_T7	g3779030	BLASTX	113	2e-09	38	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
5794	GM_107_A1_F04_MR	g507910	BLASTN	407	9e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5795	GM_107_A1_F04_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5796	GM_107_A1_F07_MR	g4038056	BLASTX	330	4e-33	51	(AC005897) putative transposon [Arabidopsis thaliana]
5797	GM_107_A1_F08_T7	g1769898	BLASTX	280	6e-23	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5798	GM_107_A1_F11_T7	g2979574	BLASTN	352	7e-09	61	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence [Homo sapiens]
5799	GM_107_A1_G03_MR	g1747310	BLASTX	213	2e-15	91	(D58424) Myb-like DNA binding protein [Arabidopsis thaliana]
5800	GM_107_A1_G04_T7	g507910	BLASTN	414	4e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5801	GM_107_A1_G08_T7	g3075398	BLASTX	136	1e-16	66	(AC004484) unknown protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5802	GM_107_A1_H02_T7	g3142328	BLASTN	668	3e-23	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5803	GM_107_A1_H03_MR	g1666236	BLASTX	220	2e-17	30	(U76261) unknown [Hordeum vulgare]
5804	GM_107_A1_H07_T7	g3810596	BLASTX	185	2e-12	32	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
5805	GM_107_A1_H09_MR	g507910	BLASTN	461	3e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
5806	GM_107_A1_H09_T7	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5807	GM_107_A1_H12_MR	g507910	BLASTN	596	3e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
5808	GM_107_A1_H12_T7	g507910	BLASTN	545	5e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
5809	GM_107_B1_A06_T7	g3426334	BLASTN	374	7e-10	66	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
5810	GM_107_B1_A11_T7	g3445212	BLASTX	218	6e-16	51	(AC004786) putative chloroplast envelope Ca2+-ATPase [Arabidopsis thaliana]
5811	GM_107_B1_B10_T7	g3645899	BLASTX	265	7e-21	49	(U68408) 5' end not determined experimentally [Zea mays]
5812	GM_107_B1_C02_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5813	GM_107_B1_C07_T7	g2642431	BLASTX	286	7e-23	57	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
5814	GM_107_B1_D01_T7	g3810596	BLASTX	188	8e-13	36	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
5815	GM_107_B1_E01_T7	g905361	BLASTX	163	3e-10	39	(U22103) gag-protease polyprotein [Glycine max]
5816	GM_107_B1_E03_T7	g2462134	BLASTX	182	2e-12	46	(Y13368) reverse transcriptase [Beta vulgaris]
5817	GM_107_B1_E08_T7	g507910	BLASTN	378	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5818	GM_107_B1_E09_T7	g1872521	BLASTX	149	7e-10	71	(U87833) zinc-finger protein Lsd1 [Arabidopsis thaliana] gi 1872523 (U87834) zinc-finger protein Lsd1 [Arabidopsis thaliana]
5819	GM_107_B1_E12_T7	g4063760	BLASTX	294	6e-24	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5820	GM_107_B1_F07_T7	g2129618	BLASTX	96	1e-09	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5821	GM_107_B1_F09_T7	g170080	BLASTN	495	2e-15	74	Soybean seed lectin gene transposable element tgm1.
5822	GM_107_B1_G03_T7	g507910	BLASTN	610	6e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
5823	GM_107_B1_G07_T7	g18559	BLASTN	822	3e-30	76	G.max gene for catalase
5824	GM_107_B1_G12_T7	g4063760	BLASTX	253	1e-19	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5825	GM_107_B1_H03_T7	g1769897	BLASTX	268	2e-25	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5826	GM_107_B1_H05_T7	g507910	BLASTN	369	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5827	GM_107_B1_H07_T7	g2244839	BLASTX	141	2e-12	48	(Z97337) hypothetical protein [Arabidopsis thaliana]
5828	GM_107_B1_H08_T7	g1066859	BLASTX	185	9e-14	65	(L49020) acetyl-CoA carboxylase [Glycine max]
5829	GM_108_A1_A02_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5830	GM_108_A1_A03_MR	g3810596	BLASTX	311	7e-26	38	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5831	GM_108_A1_A03_T7	g3421038	BLASTN	377	5e-10	69	Human DNA sequence from clone 35C21 on chromosome 1q23-24. Contains STSs, complete sequence [Homo sapiens]
5832	GM_108_A1_A04_MR	g3334663	BLASTX	508	6e-48	67	(Y10491) putative cytochrome P450 [Glycine max]
5833	GM_108_A1_A05_T7	g507910	BLASTN	387	7e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5834	GM_108_A1_A06_T7	g507910	BLASTN	370	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5835	GM_108_A1_A08_MR	g1684913	BLASTX	480	8e-44	60	(U77888) receptor-like protein kinase [Ipomoea nil]
5836	GM_108_A1_A08_T7	g3779020	BLASTN	491	4e-15	63	Arabidopsis thaliana chromosome II BAC T4E14 genomic sequence, complete sequence [Arabidopsis thaliana]
5837	GM_108_A1_A11_MR	g130582	BLASTX	237	3e-19	40	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
5838	GM_108_A1_B03_MR	g18559	BLASTN	1150	4e-45	75	G.max gene for catalase
5839	GM_108_A1_B08_T7	g507910	BLASTN	380	1e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
5840	GM_108_A1_B10_MR	g4150933	BLASTN	393	1e-10	63	Homo sapiens BAC clone NH0520M18 from 7q31.1-q31.2, complete sequence [Homo sapiens]
5841	GM_108_A1_C04_MR	g3810596	BLASTX	345	2e-29	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
5842	GM_108_A1_C07_MR	g3777527	BLASTX	778	2e-75	97	(AF053008) gag-pol polyprotein [Glycine max]
5843	GM_108_A1_C10_MR	g3935187	BLASTX	498	7e-47	64	(AC004557) F17L21.30 [Arabidopsis thaliana]
5844	GM_108_A1_D03_MR	g3142328	BLASTN	1139	1e-44	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5845	GM_108_A1_D08_MR	g3645899	BLASTX	176	2e-16	42	(U68408) 5' end not determined experimentally [Zea mays]
5846	GM_108_A1_D08_T7	g3688328	BLASTX	304	2e-26	57	(AJ228325) reverse transcriptase [Ginkgo biloba]
5847	GM_108_A1_D12_MR	g3947735	BLASTX	89	6e-09	41	(AJ009720) NL27 [Solanum tuberosum]
5848	GM_108_A1_D12_T7	g3947733	BLASTX	202	1e-14	46	(AJ009719) NL25 [Solanum tuberosum]
5849	GM_108_A1_E01_T7	g3142328	BLASTN	635	9e-22	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5850	GM_108_A1_E02_MR	g2738982	BLASTX	311	1e-26	71	(AF022157) CYP71A10 [Glycine max]
5851	GM_108_A1_E04_MR	g1351856	BLASTX	631	7e-61	89	ACONITATE HYDRATASE, CYTOPLASMIC (CITRATE HYDRO-LYASE) (ACONITASE) gi 868003 gnl PID d1006662 (D29629) aconitase [Cucurbita sp.]
5852	GM_108_A1_E09_T7	g1666236	BLASTX	164	6e-11	35	(U76261) unknown [Hordeum vulgare]
5853	GM_108_A1_E10_MR	g2828294	BLASTX	178	2e-24	40	(AL021687) putatative protein [Arabidopsis thaliana]
5854	GM_108_A1_F01_MR	g507910	BLASTN	369	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5855	GM_108_A1_F01_T7	g507910	BLASTN	359	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
5856	GM_108_A1_F02_T7	g3142328	BLASTN	1018	4e-39	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5857	GM_108_A1_F03_MR	g1666236	BLASTX	144	9e-09	28	(U76261) unknown [Hordeum vulgare]
5858	GM_108_A1_F03_T7	g3097320	BLASTN	813	9e-30	75	Glycine max gene for Bd 30K, complete cds
5859	GM_108_A1_F06_T7	g2501353	BLASTX	496	9e-47	84	TRANSKETOLASE, CHLOROPLAST (TK) gi 1084440 pir S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) gi 664901 (Z46646) transketolase [Craterostigma plantagineum]
5860	GM_108_A1_F09_T7	g3687234	BLASTX	154	4e-10	31	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
5861	GM_108_A1_G01_T7	g3913420	BLASTX	450	8e-42	77	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi 1421752 (U60592) S-adenosylmethionine decarboxylase [Pisum sativum]
5862	GM_108_A1_G04_MR	g421955	BLASTX	444	3e-41	58	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
5863	GM_108_A1_G05_MR	g1929056	BLASTX	171	3e-11	64	(Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]
5864	GM_108_A1_G07_MR	g3845197	BLASTN	366	2e-09	59	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
5865	GM_108_A1_G09_T7	g1946279	BLASTX	159	5e-17	46	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
5866	GM_108_A1_H02_MR	g2129618	BLASTX	105	3e-12	46	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5867	GM_108_A1_H03_T7	g2522228	BLASTX	116	1e-12	54	(AB007466) reverse transcriptase-like protein [Vicia faba]
5868	GM_108_A1_H07_T7	g2522227	BLASTX	221	2e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
5869	GM_108_A1_H08_T7	g2708743	BLASTX	180	1e-11	35	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
5870	GM_108_A1_H10_MR	g3142328	BLASTN	901	7e-34	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5871	GM_108_A1_H11_MR	g4063760	BLASTX	340	7e-29	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5872	GM_108_A1_H12_MR	g2995405	BLASTX	337	1e-28	48	(Y12432) polyprotein [Ananas comosus]
5873	GM_109_A1_A03_MR	g1142699	BLASTN	264	8e-09	68	Glycine max satellite STR120-A.1.
5874	GM_109_A1_B02_T7	g100484	BLASTX	359	3e-31	52	hypothetical protein - garden snapdragon
5875	GM_109_A1_B03_MR	g2462058	BLASTX	396	4e-36	54	(Y13389) reverse transcriptase [Antirrhinum majus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5876	GM_109_A1_B06_T7	g3097320	BLASTN	723	1e-25	74	Glycine max gene for Bd 30K, complete cds
5877	GM_109_A1_B09_MR	g3142328	BLASTN	983	1e-37	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5878	GM_109_A1_C05_T7	g507910	BLASTN	396	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
5879	GM_109_A1_C12_MR	g2642431	BLASTX	214	3e-15	53	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
5880	GM_109_A1_D03_MR	g100484	BLASTX	270	1e-21	52	hypothetical protein - garden snapdragon
5881	GM_109_A1_E02_T7	g3810596	BLASTX	231	3e-17	61	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
5882	GM_109_A1_E03_MR	g1142703	BLASTN	839	2e-31	85	Glycine max satellite STR120-B.1.
5883	GM_109_A1_E09_T7	g2522228	BLASTX	232	3e-18	44	(AB007466) reverse transcriptase-like protein [Vicia faba]
5884	GM_109_A1_E10_MR	g2462134	BLASTX	164	1e-10	30	(Y13368) reverse transcriptase [Beta vulgaris]
5885	GM_109_A1_F09_MR	g2160189	BLASTX	270	2e-21	50	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this gene. [Arabidopsis thaliana]
5886	GM_109_A1_G04_MR	g3097320	BLASTN	675	2e-23	80	Glycine max gene for Bd 30K, complete cds
5887	GM_109_A1_H01_MR	g4160362	BLASTN	357	4e-09	63	Saccharomyces cerevisiae complete mitochondrial genome
5888	GM_109_A1_H10_T7	g1431738	BLASTN	672	1e-23	83	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
5889	GM_109_A1_H11_MR	g1890152	BLASTX	207	3e-15	74	(X92510) allene oxide synthase [Arabidopsis thaliana]
5890	GM_109_A2_A01_T7	g3097320	BLASTN	709	5e-25	69	Glycine max gene for Bd 30K, complete cds
5891	GM_109_A2_A02_MR	g1142703	BLASTN	264	7e-14	74	Glycine max satellite STR120-B.1.
5892	GM_109_A2_A02_T7	g505129	BLASTN	362	2e-09	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5893	GM_109_A2_A04_T7	g3377834	BLASTX	207	5e-15	35	(AF075598) No definition line found [Arabidopsis thaliana]
5894	GM_109_A2_A10_MR	g507910	BLASTN	350	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
5895	GM_109_A2_B03_MR	g3435286	BLASTX	148	3e-15	93	(AF082597) cytosolic glyceraldehyde-3-phosphate dehydrogenase [Leavenworthia crassa]
5896	GM_109_A2_B06_T7	g2351065	BLASTN	349	1e-08	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15
5897	GM_109_A2_B10_MR	g3097320	BLASTN	859	7e-32	78	Glycine max gene for Bd 30K, complete cds
5898	GM_109_A2_B12_T7	g3924609	BLASTX	380	6e-33	48	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
5899	GM_109_A2_C01_MR	g2828293	BLASTX	200	6e-14	76	(AL021687) putative protein [Arabidopsis thaliana]
5900	GM_109_A2_C01_T7	g2569938	BLASTX	147	9e-09	35	(Y15193) GAI [Arabidopsis thaliana]
5901	GM_109_A2_C02_T7	g1814401	BLASTX	189	4e-13	69	(U84888) phosphoglucomutase [Mesembryanthemum crystallinum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5902	GM_109_A2_C03_T7	g2443320	BLASTX	201	3e-18	33	(D85597) polyprotein [Oryza australiensis]
5903	GM_109_A2_C07_MR	g1769898	BLASTX	158	5e-16	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5904	GM_109_A2_C09_T7	g3033389	BLASTX	213	6e-20	40	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
5905	GM_109_A2_D04_MR	g469153	BLASTN	355	5e-09	72	P.sativum (Birte) Lox1:Ps:2 gene.
5906	GM_109_A2_D06_MR	g3097320	BLASTN	1339	1e-53	78	Glycine max gene for Bd 30K, complete cds
5907	GM_109_A2_D06_T7	g3645899	BLASTX	341	1e-33	51	(U68408) 5' end not determined experimentally [Zea mays]
5908	GM_109_A2_E01_T7	g3249073	BLASTX	146	9e-09	33	(AC004473) Contains similarity to reverse transcriptase-like protein gb 2244803 from A. thaliana chromosome 4 contig gb Z97336. [Arabidopsis thaliana]
5909	GM_109_A2_E03_T7	g58340	BLASTN	444	3e-13	62	D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & tRNA-Val
5910	GM_109_A2_E06_MR	g507910	BLASTN	383	1e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
5911	GM_109_A2_E07_MR	g3097320	BLASTN	390	1e-10	72	Glycine max gene for Bd 30K, complete cds
5912	GM_109_A2_E07_T7	g22447	BLASTN	367	1e-09	63	Zea mays ZMPMS2 gene for 19 kDa zein protein.
5913	GM_109_A2_E09_T7	g4049647	BLASTN	352	7e-09	60	Melanoplus sanguinipes entomopoxvirus, complete genome
5914	GM_109_A2_E12_T7	g3033393	BLASTX	264	4e-22	71	(AC004238) putative phosphatidylinositol-glycan-class C (PIGC) [Arabidopsis thaliana]
5915	GM_109_A2_F04_MR	g3142328	BLASTN	599	4e-20	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5916	GM_109_A2_F05_MR	g4063760	BLASTX	420	2e-37	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5917	GM_109_A2_F07_T7	g3777527	BLASTX	769	2e-74	94	(AF053008) gag-pol polyprotein [Glycine max]
5918	GM_109_A2_G01_MR	g2146731	BLASTX	161	2e-24	74	FK506-binding protein - Arabidopsis thaliana gi 1354207 (U49453) rof1 [Arabidopsis thaliana]
5919	GM_109_A2_G01_T7	g541817	BLASTX	168	6e-12	72	protein kinase - common ice plant
5920	GM_109_A2_G02_T7	g3777527	BLASTX	199	1e-13	36	(AF053008) gag-pol polyprotein [Glycine max]
5921	GM_109_A2_G08_T7	g99922	BLASTX	581	1e-55	74	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
5922	GM_109_A2_G09_MR	g2129618	BLASTX	157	8e-17	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
5923	GM_109_A2_G12_T7	g3645899	BLASTX	161	9e-10	57	(U68408) 5' end not determined experimentally [Zea mays]
5924	GM_109_A2_H02_T7	g3273387	BLASTN	477	2e-14	63	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
5925	GM_109_A2_H08_MR	g18559	BLASTN	610	1e-20	75	G.max gene for catalase
5926	GM_109_A2_H09_MR	g4063760	BLASTX	362	3e-31	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5927	GM_109_A2_H09_T7	g4063760	BLASTX	218	8e-16	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5928	GM_109_A2_H10_T7	g3645899	BLASTX	396	7e-35	58	(U68408) 5' end not determined experimentally [Zea mays]
5929	GM_109_B1_A09_MR	g3097320	BLASTN	492	3e-15	70	Glycine max gene for Bd 30K, complete cds
5930	GM_109_B1_A12_MR	g3777527	BLASTX	715	1e-68	94	(AF053008) gag-pol polyprotein [Glycine max]
5931	GM_109_B1_B09_MR	g3777527	BLASTX	231	8e-20	42	(AF053008) gag-pol polyprotein [Glycine max]
5932	GM_109_B1_B10_MR	g2522228	BLASTX	392	1e-35	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
5933	GM_109_B1_D08_MR	g2443320	BLASTX	209	9e-15	50	(D85597) polyprotein [Oryza australiensis]
5934	GM_109_B1_D12_MR	g421948	BLASTX	336	9e-30	56	UDP rhamnose--anthocyanidin-3-glucoside rhamnosyltransferase - garden petunia
5935	GM_109_B1_E02_T7	g3122638	BLASTX	101	4e-11	76	PP1/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1 gi 1076381 pir S49820 PRL1 protein - Arabidopsis thaliana gi 577733 (X82824) PRL1 gene product [Arabidopsis thaliana] gi 577735 (X82825) PRL1 gene product [Arabidopsis thaliana] gi 2244947 gnl PID e326958 (Z97339) PRL1 protein - Arabidopsis thaliana [Arabidopsis thaliana]
5936	GM_109_B1_E05_T7	g18559	BLASTN	1067	2e-41	75	G.max gene for catalase
5937	GM_109_B1_E07_MR	g4038056	BLASTX	261	7e-23	43	(AC005897) putative transposon [Arabidopsis thaliana]
5938	GM_109_B1_E09_T7	g3894172	BLASTX	169	1e-11	32	(AC005312) putative cinnamoyl-CoA reductase [Arabidopsis thaliana]
5939	GM_109_B1_E11_T7	g905361	BLASTX	377	2e-33	98	(U22103) gag-protease polyprotein [Glycine max]
5940	GM_109_B1_F01_MR	g3142328	BLASTN	553	5e-18	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5941	GM_109_B1_F04_MR	g507910	BLASTN	356	2e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5942	GM_109_B1_F10_MR	g507910	BLASTN	495	9e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
5943	GM_109_B1_G02_MR	g4102839	BLASTX	294	1e-24	49	(AF016713) LeOPT1 [Lycopersicon esculentum]
5944	GM_109_B1_G02_T7	g2323254	BLASTN	360	3e-09	65	Human Chromosome X, complete sequence [Homo sapiens]
5945	GM_109_B1_G04_T7	g18559	BLASTN	869	2e-32	72	G.max gene for catalase
5946	GM_109_B1_G07_MR	g1769899	BLASTX	167	8e-12	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5947	GM_109_B1_G10_MR	g4063760	BLASTX	514	2e-47	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5948	GM_109_B1_G10_T7	g18559	BLASTN	801	3e-29	72	G.max gene for catalase
5949	GM_109_B1_G11_T7	g2522228	BLASTX	305	2e-26	53	(AB007466) reverse transcriptase-like protein [Vicia faba]
5950	GM_109_B1_H05_MR	g559278	BLASTN	274	1e-11	70	Saccharomyces cerevisiae mitochondrion origin of replication (ori3 and ori4).
5951	GM_109_B1_H10_MR	g585565	BLASTX	165	1e-11	75	RIBOSOME RECYCLING FACTOR HOMOLOG (NUCLEAR LOCATED PROTEIN D2) gi 629661 pir S32716 nuclear protein - carrot gi 297891 (X72384) nuclear located protein [Daucus carota]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5952	GM_109_B1_H10_T7	g3004480	BLASTX	211	2e-16	55	(AJ228333) reverse transcriptase [Pinus elliottii]
5953	GM_109_B2_A01_T7	g2522227	BLASTX	220	2e-17	56	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
5954	GM_109_B2_A08_T7	g2443320	BLASTX	189	1e-12	31	(D85597) polyprotein [Oryza australiensis]
5955	GM_109_B2_B02_T7	g1480927	BLASTN	617	4e-21	75	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
5956	GM_109_B2_B03_T7	g3142328	BLASTN	1323	5e-53	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
5957	GM_109_B2_B04_T7	g2369714	BLASTX	668	7e-65	83	(Z97178) elongation factor 2 [Beta vulgaris]
5958	GM_109_B2_B07_T7	g1769898	BLASTX	287	1e-23	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
5959	GM_109_B2_B12_T7	g4063756	BLASTN	446	4e-13	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
5960	GM_109_B2_C03_T7	g505129	BLASTN	424	3e-12	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
5961	GM_109_B2_C04_T7	g3097320	BLASTN	707	6e-25	74	Glycine max gene for Bd 30K, complete cds
5962	GM_109_B2_C08_T7	g3097320	BLASTN	355	5e-09	67	Glycine max gene for Bd 30K, complete cds
5963	GM_109_B2_C12_T7	g2462935	BLASTX	144	6e-12	43	(Y12321) open reading frame 1 [Brassica oleracea]
5964	GM_109_B2_D01_T7	g3327392	BLASTX	166	2e-18	58	(AC004483) reverse-transcriptase-like protein [Arabidopsis thaliana]
5965	GM_109_B2_D03_T7	g507910	BLASTN	601	1e-20	84	Glycine max BSR-101 satellite SB92 genomic sequence.
5966	GM_109_B2_D04_T7	g3097320	BLASTN	798	4e-29	78	Glycine max gene for Bd 30K, complete cds
5967	GM_109_B2_D10_T7	g535454	BLASTX	215	8e-17	69	(U13940) cysteine proteinase [Alnus glutinosa]
5968	GM_109_B2_E05_T7	g4140691	BLASTX	152	2e-12	50	(AF101972) zeatin O-glucosyltransferase [Phaseolus lunatus]
5969	GM_109_B2_E09_T7	g731675	BLASTX	149	7e-14	67	HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION gi 626631 pir S46811 hypothetical protein YHR074w - yeast (Saccharomyces cerevisiae) gi 500832 (U10556) Yhr074wp [Saccharomyces cerevisiae]
5970	GM_109_B2_E10_T7	g2828293	BLASTX	162	7e-10	72	(AL021687) putative protein [Arabidopsis thaliana]
5971	GM_109_B2_F07_T7	g1272349	BLASTX	278	3e-23	49	(U51740) secreted glycoprotein 3 [Ipomoea trifida]
5972	GM_109_B2_F12_T7	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
5973	GM_109_B2_G02_T7	g19205	BLASTN	541	2e-17	69	L.esculentum enolase gene.
5974	GM_109_B2_G03_T7	g3097320	BLASTN	1042	4e-40	79	Glycine max gene for Bd 30K, complete cds
5975	GM_109_B2_G05_T7	g100484	BLASTX	358	4e-31	51	hypothetical protein - garden snapdragon
5976	GM_109_B2_G06_T7	g3142328	BLASTN	415	9e-12	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
5977	GM_109_B2_G09_T7	g421955	BLASTX	283	4e-24	44	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
5978	GM_109_B2_H08_T7	g2738982	BLASTX	372	2e-33	79	(AF022157) CYP71A10 [Glycine max]
5979	GM_110_A2_A09_T7	g2829870	BLASTX	144	1e-16	60	(AC002396) Hypothetical protein [Arabidopsis thaliana]
5980	GM_110_A2_D01_T7	g3513747	BLASTX	279	4e-22	53	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
5981	GM_110_A2_D04_T7	g4138188	BLASTN	383	4e-11	68	M.fuscata microsatellite DNA, MFGT27 region
5982	GM_110_A2_E05_T7	g507910	BLASTN	350	3e-09	77	Glycine max BSR-101 satellite SB92 genomic sequence.
5983	GM_110_A2_F03_T7	g170603	BLASTN	346	5e-09	71	Broad bean (V.faba) BamHI repetitive element, 990 bp family.
5984	GM_110_A2_F04_T7	g3821288	BLASTN	424	1e-12	65	Pisum sativum repeated element highly similar to the BamHI repeated sequence families of Vicia faba
5985	GM_110_A2_F06_T7	g4126312	BLASTN	370	1e-09	74	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
5986	GM_110_B2_A02_T7	g2995405	BLASTX	265	1e-38	53	(Y12432) polyprotein [Ananas comosus]
5987	GM_110_B2_A03_MR	g1142701	BLASTN	1394	1e-56	88	Glycine max satellite STR120-A.3.
5988	GM_110_B2_A03_T7	g2316024	BLASTX	154	2e-15	56	(U96400) MRP-like ABC transporter [Arabidopsis thaliana]
5989	GM_110_B2_A04_T7	g18559	BLASTN	956	3e-36	77	G.max gene for catalase
5990	GM_110_B2_A05_MR	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
5991	GM_110_B2_A05_T7	g507910	BLASTN	532	2e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
5992	GM_110_B2_A09_T7	g2522228	BLASTX	253	1e-20	45	(AB007466) reverse transcriptase-like protein [Vicia faba]
5993	GM_110_B2_B04_MR	g280492	BLASTX	171	7e-11	42	pol polyprotein homolog - fungus (Cladosporium fulvum) transposon CfT-1 (fragment) gi 2564 (Z11866) Reverse Transcriptase [Cladosporium fulvum]
5994	GM_110_B2_B07_T7	g1346192	BLASTX	189	2e-13	97	GLUTATHIONE REDUCTASE, CHLOROPLAST PRECURSOR (GR) (GRASE) gi 169965 (L11632) glutathione reductase [Glycine max]
5995	GM_110_B2_B11_T7	g3810595	BLASTX	112	5e-09	48	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
5996	GM_110_B2_C04_T7	g3097320	BLASTN	1186	1e-46	83	Glycine max gene for Bd 30K, complete cds
5997	GM_110_B2_C07_T7	g3184508	BLASTN	459	1e-13	65	Homo sapiens chromosome 17, clone HRPC41C23, complete sequence [Homo sapiens]
5998	GM_110_B2_C08_MR	g4063760	BLASTX	193	4e-13	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
5999	GM_110_B2_C09_T7	g3097320	BLASTN	568	1e-18	73	Glycine max gene for Bd 30K, complete cds
6000	GM_110_B2_C11_T7	g2832901	BLASTN	1114	2e-43	78	Cajanus cajan copia-like retrotransposon,Panzee

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6001	GM_110_B2_D04_T7	g629693	BLASTX	233	2e-18	46	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6002	GM_110_B2_D07_MR	g2618683	BLASTN	525	1e-16	67	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]
6003	GM_110_B2_D08_MR	g3142328	BLASTN	1086	3e-42	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6004	GM_110_B2_D09_T7	g2522228	BLASTX	392	1e-35	76	(AB007466) reverse transcriptase-like protein [Vicia faba]
6005	GM_110_B2_D10_MR	g4063760	BLASTX	325	2e-31	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6006	GM_110_B2_E01_T7	g2832657	BLASTX	250	8e-20	52	(AL021710) putative protein [Arabidopsis thaliana]
6007	GM_110_B2_E03_MR	g99755	BLASTX	244	4e-19	49	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
6008	GM_110_B2_E04_MR	g2244802	BLASTX	127	2e-13	57	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
6009	GM_110_B2_E08_T7	g3522943	BLASTX	113	1e-09	69	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]
6010	GM_110_B2_E10_T7	g3142328	BLASTN	1189	6e-47	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6011	GM_110_B2_E11_T7	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6012	GM_110_B2_E12_T7	g1352460	BLASTX	117	2e-16	71	IN2-1 PROTEIN gi 100896 pir S17743 In2-1 protein - maize gi 22347 (X58573) In2-1 gene product [Zea mays]
6013	GM_110_B2_F01_T7	g3645899	BLASTX	224	5e-26	46	(U68408) 5' end not determined experimentally [Zea mays]
6014	GM_110_B2_F04_MR	g1142701	BLASTN	240	9e-21	74	Glycine max satellite STR120-A.3.
6015	GM_110_B2_F08_T7	g905361	BLASTX	203	1e-14	31	(U22103) gag-protease polyprotein [Glycine max]
6016	GM_110_B2_F10_MR	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6017	GM_110_B2_F10_T7	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6018	GM_110_B2_G08_MR	g4063756	BLASTN	404	3e-11	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
6019	GM_110_B2_G09_T7	g1431738	BLASTN	618	4e-21	80	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
6020	GM_110_B2_G10_T7	g3319362	BLASTX	464	3e-42	62	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
6021	GM_110_B2_H01_MR	g3036807	BLASTX	460	8e-43	69	(AL022373) putative protein [Arabidopsis thaliana]
6022	GM_110_B2_H02_MR	g905361	BLASTX	530	6e-56	95	(U22103) gag-protease polyprotein [Glycine max]
6023	GM_110_B2_H08_T7	g2911280	BLASTX	162	5e-34	86	(U73937) PK12 protein kinase [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6024	GM_111_A1_A03_MR	g2996647	BLASTN	631	2e-21	66	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
6025	GM_111_A1_A03_T7	g1769898	BLASTX	303	2e-25	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6026	GM_111_A1_A06_MR	g507910	BLASTN	395	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6027	GM_111_A1_A06_T7	g4063760	BLASTX	202	4e-14	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6028	GM_111_A1_A07_T7	g3142328	BLASTN	441	6e-13	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6029	GM_111_A1_A12_T7	g3142328	BLASTN	1055	7e-41	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6030	GM_111_A1_B01_MR	g905361	BLASTX	817	1e-80	98	(U22103) gag-protease polyprotein [Glycine max]
6031	GM_111_A1_B02_MR	g905361	BLASTX	420	3e-38	98	(U22103) gag-protease polyprotein [Glycine max]
6032	GM_111_A1_B02_T7	g507910	BLASTN	432	6e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6033	GM_111_A1_B07_T7	g1669599	BLASTX	223	3e-26	63	(D88746) AR791 [Arabidopsis thaliana]
6034	GM_111_A1_B08_T7	g2522230	BLASTX	233	9e-19	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
6035	GM_111_A1_B10_T7	g3334661	BLASTX	504	2e-47	72	(Y10490) putative cytochrome P450 [Glycine max]
6036	GM_111_A1_C02_MR	g3738312	BLASTX	183	8e-13	64	(AC005309) hypothetical protein [Arabidopsis thaliana]
6037	GM_111_A1_C02_T7	g3193284	BLASTX	569	2e-54	74	(AF069298) No definition line found [Arabidopsis thaliana]
6038	GM_111_A1_C03_MR	g2443320	BLASTX	167	3e-10	35	(D85597) polyprotein [Oryza australiensis]
6039	GM_111_A1_C03_T7	g4033838	BLASTX	293	1e-24	50	(Y18550) sigma-like factor [Arabidopsis thaliana]
6040	GM_111_A1_C04_MR	g975703	BLASTN	406	2e-11	84	P.sativum GR gene
6041	GM_111_A1_C08_T7	g3021268	BLASTX	92	7e-12	45	(AL022347) putative protein [Arabidopsis thaliana]
6042	GM_111_A1_C09_T7	g2702277	BLASTX	173	2e-11	33	(AC003033) putative cyclin g-associated kinase [Arabidopsis thaliana] gi 2914689 (AC003974) putative cyclin g-associated kinase [Arabidopsis thaliana]
6043	GM_111_A1_C10_MR	g3097320	BLASTN	479	1e-14	68	Glycine max gene for Bd 30K, complete cds
6044	GM_111_A1_C10_T7	g4006831	BLASTX	101	1e-09	33	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
6045	GM_111_A1_C12_MR	g4038056	BLASTX	384	9e-34	51	(AC005897) putative transposon [Arabidopsis thaliana]
6046	GM_111_A1_C12_T7	g4038056	BLASTX	356	9e-31	53	(AC005897) putative transposon [Arabidopsis thaliana]
6047	GM_111_A1_D02_T7	g3510264	BLASTX	379	3e-34	56	(AC005310) hypothetical protein, 5' partial [Arabidopsis thaliana]
6048	GM_111_A1_D03_MR	g2281085	BLASTX	211	2e-16	77	(AC002333) CTR1 protein kinase isolog [Arabidopsis thaliana]
6049	GM_111_A1_D05_MR	g507910	BLASTN	641	2e-22	87	Glycine max BSR-101 satellite SB92 genomic sequence.
6050	GM_111_A1_D05_T7	g3550435	BLASTN	480	1e-14	63	Hordeum vulgare Hotr1 gene
6051	GM_111_A1_D07_MR	g3645899	BLASTX	256	7e-20	47	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6052	GM_111_A1_D10_MR	g3319362	BLASTX	218	4e-17	57	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
6053	GM_111_A1_D11_MR	g2665890	BLASTX	237	2e-18	75	(AF035944) calcium-dependent protein kinase [Fragaria x ananassa]
6054	GM_111_A1_D12_T7	g18768	BLASTN	374	1e-10	72	Soybean Tgm6 transposable element 3' end
6055	GM_111_A1_E03_MR	g1236920	BLASTN	262	7e-10	63	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
6056	GM_111_A1_E04_MR	g507910	BLASTN	387	7e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6057	GM_111_A1_E04_T7	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6058	GM_111_A1_E07_MR	g3746069	BLASTX	128	7e-17	41	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
6059	GM_111_A1_E08_T7	g507910	BLASTN	634	5e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
6060	GM_111_A1_E12_MR	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6061	GM_111_A1_E12_T7	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6062	GM_111_A1_F01_MR	g99755	BLASTX	403	9e-37	51	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
6063	GM_111_A1_F03_MR	g3777527	BLASTX	134	7e-13	28	(AF053008) gag-pol polyprotein [Glycine max]
6064	GM_111_A1_F03_T7	g3097320	BLASTN	476	2e-14	67	Glycine max gene for Bd 30K, complete cds
6065	GM_111_A1_F07_MR	g2213598	BLASTX	191	9e-13	35	(AC000348) T7N9.18 [Arabidopsis thaliana]
6066	GM_111_A1_F09_MR	g1514643	BLASTX	178	2e-11	71	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
6067	GM_111_A1_F10_T7	g3599418	BLASTN	587	1e-19	79	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
6068	GM_111_A1_F11_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6069	GM_111_A1_G03_MR	g2842490	BLASTX	211	3e-16	78	(AL021749) heat-shock protein [Arabidopsis thaliana]
6070	GM_111_A1_G04_MR	g1946265	BLASTX	204	9e-16	82	(Y11414) myb [Oryza sativa]
6071	GM_111_A1_G04_T7	g3063469	BLASTX	179	2e-13	43	(AC003981) F22O13.31 [Arabidopsis thaliana]
6072	GM_111_A1_G06_MR	g18695	BLASTN	582	1e-19	87	Soybean nodulin 22 gene
6073	GM_111_A1_G06_T7	g3790188	BLASTX	228	5e-18	95	(Y14431) NAD-dependent isocitrate dehydrogenase [Nicotiana tabacum]
6074	GM_111_A1_G08_MR	g905361	BLASTX	215	7e-16	34	(U22103) gag-protease polyprotein [Glycine max]
6075	GM_111_A1_G09_MR	g2522228	BLASTX	266	4e-22	73	(AB007466) reverse transcriptase-like protein [Vicia faba]
6076	GM_111_A1_G09_T7	g3687234	BLASTX	191	6e-13	52	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
6077	GM_111_A1_G11_MR	g505129	BLASTN	380	3e-10	71	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6078	GM_111_A1_H01_MR	g3171159	BLASTN	358	4e-09	63	Homo sapiens chromosome 21q22.3 PAC 21L13, complete sequence [Homo sapiens]
6079	GM_111_A1_H02_MR	g18559	BLASTN	442	5e-13	64	G.max gene for catalase
6080	GM_111_A1_H04_MR	g3695395	BLASTX	186	2e-19	55	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
6081	GM_111_A1_H04_T7	g3176788	BLASTN	422	7e-13	63	Homo sapiens allele 8 fragile site locus (FRA10B) minisatellite sequence
6082	GM_111_A1_H07_T7	g2582971	BLASTX	244	4e-28	77	(D83711) TKRP125 [Nicotiana tabacum]
6083	GM_111_A1_H11_T7	g3142328	BLASTN	697	1e-24	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6084	GM_111_A1_H12_MR	g4038056	BLASTX	186	8e-15	52	(AC005897) putative transposon [Arabidopsis thaliana]
6085	GM_111_A1_H12_T7	g2443320	BLASTX	327	2e-27	48	(D85597) polyprotein [Oryza australiensis]
6086	GM_111_A2_A04_T7	g3319366	BLASTX	166	1e-11	69	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
6087	GM_111_A2_A08_MR	g2791896	BLASTX	266	7e-21	57	(Y08997) 146kDa nuclear protein [Xenopus laevis]
6088	GM_111_A2_A11_MR	g3242785	BLASTX	219	2e-26	56	(AF055355) respiratory burst oxidase protein C [Arabidopsis thaliana]
6089	GM_111_A2_B04_MR	g4038056	BLASTX	207	3e-18	34	(AC005897) putative transposon [Arabidopsis thaliana]
6090	GM_111_A2_B04_T7	g3142328	BLASTN	1895	3e-79	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6091	GM_111_A2_B10_MR	g58340	BLASTN	376	4e-10	59	D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & tRNA-Val
6092	GM_111_A2_B11_MR	g905361	BLASTX	266	2e-21	42	(U22103) gag-protease polyprotein [Glycine max]
6093	GM_111_A2_C02_T7	g100484	BLASTX	452	2e-41	54	hypothetical protein - garden snapdragon
6094	GM_111_A2_C03_T7	g4038056	BLASTX	283	6e-23	43	(AC005897) putative transposon [Arabidopsis thaliana]
6095	GM_111_A2_C04_T7	g2708743	BLASTX	187	2e-13	38	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
6096	GM_111_A2_C09_MR	g2129618	BLASTX	311	7e-26	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6097	GM_111_A2_C12_T7	g4156188	BLASTN	385	2e-10	59	Homo sapiens clone DJ0784G16, complete sequence [Homo sapiens]
6098	GM_111_A2_D03_T7	g3687222	BLASTX	197	5e-15	37	(AC005169) hypothetical protein [Arabidopsis thaliana]
6099	GM_111_A2_D04_T7	g3097320	BLASTN	459	9e-14	71	Glycine max gene for Bd 30K, complete cds
6100	GM_111_A2_D07_T7	g3046704	BLASTX	147	8e-09	50	(AL022223) putative protein [Arabidopsis thaliana]
6101	GM_111_A2_D12_MR	g3142328	BLASTN	1590	3e-65	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6102	GM_111_A2_E04_T7	g140292	BLASTX	131	1e-10	42	HYPOTHETICAL 21.5 KD PROTEIN (ORF 184) gi 82208 pir A05197 hypothetical protein 184 - common tobacco chloroplast gi 11843 (Z00044) hypothetical protein [Nicotiana tabacum] gi 225211 prf 1211235AR ORF 184 [Nicotiana tabacum]
6103	GM_111_A2_E07_T7	g3777527	BLASTX	784	5e-76	96	(AF053008) gag-pol polyprotein [Glycine max]
6104	GM_111_A2_E11_T7	g3875706	BLASTX	101	5e-14	50	(Z35598) Phosphoribosylformylglycinamidine synthase; cDNA EST EMBL:D35229 comes from this gene; cDNA EST EMBL:D32558 comes from this gene; cDNA EST EMBL:D35376 comes from this gene; cDNA EST EMBL:D34213 comes from this gene;...
6105	GM_111_A2_F01_T7	g2262107	BLASTX	156	8e-18	96	(AC002343) Ser/Thr protein kinase isolog [Arabidopsis thaliana]
6106	GM_111_A2_F03_T7	g3033400	BLASTX	147	2e-12	31	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]
6107	GM_111_A2_F09_T7	g3142330	BLASTX	149	2e-10	79	(U96295) envelope-like [Glycine max]
6108	GM_111_A2_F11_T7	g2760169	BLASTN	824	3e-30	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFB13, complete sequence [Arabidopsis thaliana]
6109	GM_111_A2_G02_MR	g4063760	BLASTX	153	7e-09	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6110	GM_111_A2_G02_T7	g3777527	BLASTX	736	7e-71	96	(AF053008) gag-pol polyprotein [Glycine max]
6111	GM_111_A2_G04_T7	g2335067	BLASTN	375	7e-10	61	Human BAC clone GS200K05 from 7q21-q22, complete sequence [Homo sapiens]
6112	GM_111_A2_G08_T7	g218269	BLASTX	373	1e-33	86	(D12839) reverse transcriptase [Glycine max]
6113	GM_111_A2_G09_MR	g2558657	BLASTX	195	2e-13	39	(AC002354) No definition line found [Arabidopsis thaliana]
6114	GM_111_A2_G10_MR	g507910	BLASTN	620	2e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
6115	GM_111_A2_G11_MR	g3513745	BLASTX	205	3e-14	33	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
6116	GM_111_A2_H02_T7	g3097320	BLASTN	1934	1e-80	84	Glycine max gene for Bd 30K, complete cds
6117	GM_111_A2_H06_T7	g1945277	BLASTX	140	5e-16	77	(Z94180) branched chain alpha-keto acid dehydrogenase E1-alpha subunit [Lycopersicon esculentum]
6118	GM_111_A2_H12_MR	g3097320	BLASTN	622	4e-21	80	Glycine max gene for Bd 30K, complete cds
6119	GM_111_B1_A02_MR	g3650039	BLASTX	204	1e-14	35	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
6120	GM_111_B1_A02_T7	g3142328	BLASTN	1281	4e-51	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6121	GM_111_B1_A06_MR	g1769899	BLASTX	163	2e-11	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6122	GM_111_B1_A08_MR	g507910	BLASTN	466	2e-14	77	Glycine max BSR-101 satellite SB92 genomic sequence.
6123	GM_111_B1_A09_MR	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
6124	GM_111_B1_A10_T7	g1769898	BLASTX	365	3e-32	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6125	GM_111_B1_A12_T7	g1769898	BLASTX	355	4e-31	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6126	GM_111_B1_B01_T7	g2522228	BLASTX	176	4e-12	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
6127	GM_111_B1_B02_T7	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
6128	GM_111_B1_B03_MR	g1142701	BLASTN	1171	1e-46	81	Glycine max satellite STR120-A.3.
6129	GM_111_B1_B06_MR	g3128172	BLASTX	336	4e-29	48	(AC004521) hypothetical protein [Arabidopsis thaliana]
6130	GM_111_B1_B07_MR	g3777527	BLASTX	736	7e-71	95	(AF053008) gag-pol polyprotein [Glycine max]
6131	GM_111_B1_B12_T7	g4038056	BLASTX	209	5e-15	42	(AC005897) putative transposon [Arabidopsis thaliana]
6132	GM_111_B1_C01_MR	g2245104	BLASTX	427	6e-38	57	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
6133	GM_111_B1_C03_MR	g905361	BLASTX	614	4e-59	95	(U22103) gag-protease polyprotein [Glycine max]
6134	GM_111_B1_C03_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
6135	GM_111_B1_C04_MR	g1666236	BLASTX	224	8e-18	29	(U76261) unknown [Hordeum vulgare]
6136	GM_111_B1_C05_MR	g1431738	BLASTN	412	1e-11	92	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
6137	GM_111_B1_D03_MR	g3142328	BLASTN	1181	1e-46	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6138	GM_111_B1_D04_T7	g3510344	BLASTN	447	4e-13	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJG14, complete sequence [Arabidopsis thaliana]
6139	GM_111_B1_D06_MR	g905361	BLASTX	706	6e-69	93	(U22103) gag-protease polyprotein [Glycine max]
6140	GM_111_B1_D10_MR	g507910	BLASTN	398	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6141	GM_111_B1_D11_MR	g4063760	BLASTX	359	8e-31	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6142	GM_111_B1_E01_MR	g2129618	BLASTX	169	5e-12	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6143	GM_111_B1_E02_MR	g100484	BLASTX	404	3e-36	54	hypothetical protein - garden snapdragon
6144	GM_111_B1_E04_T7	g3930515	BLASTX	126	1e-11	40	(AF059674) putative gag protein [Nicotiana tabacum]
6145	GM_111_B1_E05_T7	g2642157	BLASTX	319	5e-27	91	(AC003000) ankyrin-like protein [Arabidopsis thaliana]
6146	GM_111_B1_E06_T7	g1769897	BLASTX	433	5e-40	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6147	GM_111_B1_E10_MR	g2522228	BLASTX	190	1e-13	78	(AB007466) reverse transcriptase-like protein [Vicia faba]
6148	GM_111_B1_F06_T7	g1769899	BLASTX	247	3e-20	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6149	GM_111_B1_F07_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6150	GM_111_B1_F08_MR	g3242789	BLASTX	251	2e-19	57	(AF055357) respiratory burst oxidase protein D [Arabidopsis thaliana]
6151	GM_111_B1_F12_MR	g3097320	BLASTN	369	1e-09	74	Glycine max gene for Bd 30K, complete cds
6152	GM_111_B1_G01_MR	g99922	BLASTX	660	5e-64	82	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
6153	GM_111_B1_G04_MR	g4063760	BLASTX	571	2e-53	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6154	GM_111_B1_G10_MR	g629693	BLASTX	263	6e-22	48	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6155	GM_111_B1_H04_MR	g507910	BLASTN	362	9e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6156	GM_111_B1_H07_T7	g3482933	BLASTX	475	2e-43	83	(AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana]
6157	GM_111_B1_H09_T7	g3810596	BLASTX	218	6e-16	46	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
6158	GM_111_B1_H11_T7	g3193221	BLASTN	468	4e-14	68	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
6159	GM_111_B1_H12_T7	g4063760	BLASTX	299	2e-24	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6160	GM_111_B2_A02_T7	g3777527	BLASTX	458	3e-41	93	(AF053008) gag-pol polyprotein [Glycine max]
6161	GM_111_B2_A03_T7	g4063760	BLASTX	446	4e-40	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6162	GM_111_B2_A06_MR	g3777527	BLASTX	242	3e-18	38	(AF053008) gag-pol polyprotein [Glycine max]
6163	GM_111_B2_A07_T7	g3510505	BLASTX	193	3e-22	46	(AF030881) pol polyprotein [Fugu rubripes]
6164	GM_111_B2_A08_MR	g2673917	BLASTX	507	3e-46	84	(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]
6165	GM_111_B2_A09_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6166	GM_111_B2_A09_T7	g4063760	BLASTX	357	1e-30	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6167	GM_111_B2_A10_T7	g2244994	BLASTX	652	3e-63	81	(Z97341) similarity to isp4 protein - fission yeast [Arabidopsis thaliana]
6168	GM_111_B2_A11_MR	g3097320	BLASTN	575	5e-19	79	Glycine max gene for Bd 30K, complete cds
6169	GM_111_B2_A11_T7	g2911040	BLASTX	176	2e-11	45	(AL021961) receptor protein kinase - like protein [Arabidopsis thaliana]
6170	GM_111_B2_B01_T7	g2982518	BLASTN	351	7e-09	63	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-07, complete sequence [Plasmodium falciparum]
6171	GM_111_B2_B07_MR	g905361	BLASTX	209	3e-15	36	(U22103) gag-protease polyprotein [Glycine max]
6172	GM_111_B2_B07_T7	g13610	BLASTN	359	2e-09	60	Yeast mitochondrial var1 gene (allele 40.0) a ribosomal protein >gi 343948 gb J01525 YSCMTVAR1 Yeast (S.cerevisiae) mitochondrial var1 gene, 40.0 allele.
6173	GM_111_B2_B09_T7	g2244994	BLASTX	215	8e-16	48	(Z97341) similarity to isp4 protein - fission yeast [Arabidopsis thaliana]
6174	GM_111_B2_B11_MR	g629693	BLASTX	202	5e-15	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6175	GM_111_B2_C01_T7	g2995405	BLASTX	370	3e-32	50	(Y12432) polyprotein [Ananas comosus]
6176	GM_111_B2_C05_MR	g3695294	BLASTN	879	7e-33	92	Glycine max nodule-specific glutamine synthetase gene, complete cds
6177	GM_111_B2_C07_MR	g169984	BLASTN	418	4e-12	67	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.6-L).

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6178	GM_111_B2_C11_T7	g3171875	BLASTN	413	1e-11	65	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.1...
6179	GM_111_B2_D01_T7	g9837	BLASTN	349	9e-09	62	P.falciparum 3.8 gene for putative serine kinase (partial) and GBP130 gene for glycophorin binding protein (partial)
6180	GM_111_B2_D02_MR	g2244802	BLASTX	353	4e-30	53	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
6181	GM_111_B2_D06_MR	g3645899	BLASTX	212	3e-15	36	(U68408) 5' end not determined experimentally [Zea mays]
6182	GM_111_B2_D07_MR	g2995405	BLASTX	453	3e-41	59	(Y12432) polyprotein [Ananas comosus]
6183	GM_111_B2_E03_T7	g531389	BLASTX	351	8e-30	51	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
6184	GM_111_B2_E05_MR	g2708743	BLASTX	192	7e-14	40	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
6185	GM_111_B2_E09_MR	g13774	BLASTN	342	4e-12	62	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
6186	GM_111_B2_E10_T7	g1707007	BLASTX	180	5e-12	36	(U78721) hypothetical protein [Arabidopsis thaliana]
6187	GM_111_B2_F01_T7	g3097320	BLASTN	448	3e-13	72	Glycine max gene for Bd 30K, complete cds
6188	GM_111_B2_F12_MR	g3142328	BLASTN	823	3e-30	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6189	GM_111_B2_G05_T7	g1149595	BLASTX	180	7e-13	79	(Z49860) 1-acyl-sn-glycerol-3-phosphate acyltransferase [Brassica napus]
6190	GM_111_B2_G10_MR	g4063760	BLASTX	424	9e-38	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6191	GM_111_B2_H02_MR	g4160362	BLASTN	313	2e-11	68	Saccharomyces cerevisiae complete mitochondrial genome
6192	GM_111_B2_H06_T7	g3142328	BLASTN	1131	3e-44	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6193	GM_112_A1_A03_MR	g1944341	BLASTN	350	8e-09	71	Soybean DNA for cysteine proteinase inhibitor, complete cds
6194	GM_112_A1_A03_T7	g2316016	BLASTX	200	9e-14	51	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
6195	GM_112_A1_A04_MR	g2129473	BLASTX	174	1e-12	39	arabinogalactan-like protein - loblolly pine gi 607774 (U09556) arabinogalactan-like protein [Pinus taeda]
6196	GM_112_A1_A05_MR	g2244803	BLASTX	226	4e-18	46	(Z97336) reverse transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6197	GM_112_A1_A06_T7	g130405	BLASTX	183	4e-12	37	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 17.6) gi 74642 pir GNFF17 retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) transposon 17.6 gi 1335613 gnl PID e1849 (X01472) ORF 2, pot. reverse transcriptase [Drosophila melanogaster] gi 224319 prf 1101404B ORF 2 [Drosophila melanogaster]
6198	GM_112_A1_A09_T7	g3777527	BLASTX	651	8e-62	94	(AF053008) gag-pol polyprotein [Glycine max]
6199	GM_112_A1_A10_MR	g2292907	BLASTX	235	1e-17	35	(Y10099) P-glycoprotein homologue [Hordeum vulgare]
6200	GM_112_A1_A11_T7	g3142328	BLASTN	600	4e-20	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6201	GM_112_A1_B06_MR	g4102181	BLASTN	350	9e-09	66	Mus musculus phosphoenolpyruvate carboxykinase (PEPCK) gene, complete cds
6202	GM_112_A1_B11_T7	g2462936	BLASTX	316	1e-27	53	(Y12321) open reading frame 2 [Brassica oleracea]
6203	GM_112_A1_B12_T7	g18683	BLASTN	640	4e-22	72	G.max N-20t gene
6204	GM_112_A1_C04_MR	g18559	BLASTN	398	5e-11	62	G.max gene for catalase
6205	GM_112_A1_C12_MR	g571330	BLASTX	184	2e-12	56	(U11034) ent-kaurene synthetase A [Arabidopsis thaliana]
6206	GM_112_A1_D01_T7	g2129618	BLASTX	230	3e-17	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6207	GM_112_A1_D02_MR	g4063770	BLASTX	280	3e-30	51	(AB004906) transposase [Ipomoea purpurea]
6208	GM_112_A1_D02_T7	g170029	BLASTN	371	9e-10	78	Glycine max cv. Dare nodulin 26 gene fragment.
6209	GM_112_A1_D03_T7	g2642157	BLASTX	212	2e-15	39	(AC003000) ankyrin-like protein [Arabidopsis thaliana]
6210	GM_112_A1_E01_T7	g507910	BLASTN	663	2e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
6211	GM_112_A1_E02_MR	g1769899	BLASTX	246	3e-20	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6212	GM_112_A1_E05_T7	g3201680	BLASTX	197	6e-31	59	(AF060941) extra-large G-protein [Arabidopsis thaliana]
6213	GM_112_A1_E10_T7	g2995405	BLASTX	305	2e-27	57	(Y12432) polyprotein [Ananas comosus]
6214	GM_112_A1_F04_MR	g3097320	BLASTN	647	3e-22	77	Glycine max gene for Bd 30K, complete cds
6215	GM_112_A1_F06_MR	g1524103	BLASTN	405	1e-12	61	Human DNA sequence from cosmid U223G7, between markers DXS6791 and DXS8038 on chromosome X
6216	GM_112_A1_G01_T7	g2522228	BLASTX	485	2e-45	63	(AB007466) reverse transcriptase-like protein [Vicia faba]
6217	GM_112_A1_G03_T7	g3142328	BLASTN	865	3e-32	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6218	GM_112_A1_G05_MR	g4063770	BLASTX	160	8e-10	43	(AB004906) transposase [Ipomoea purpurea]
6219	GM_112_A1_G10_T7	g1769898	BLASTX	484	2e-45	69	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6220	GM_112_A1_G12_T7	g1346389	BLASTX	83	7e-09	75	KNOTTED-LIKE HOMEOBOX PROTEIN 5 >gi 1045046 (X92394) KNAT5 homeobox protein [Arabidopsis thaliana]
6221	GM_112_A1_H03_T7	g4063760	BLASTX	283	2e-25	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6222	GM_112_A1_H11_T7	g3695395	BLASTX	181	3e-12	41	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
6223	GM_112_B1_A01_MR	g2388577	BLASTX	212	3e-15	39	(AC000098) Similar to Arabidopsis putative ion-channel PID:g2262157 (gb AC002329). [Arabidopsis thaliana]
6224	GM_112_B1_A02_MR	g3746069	BLASTX	204	3e-17	40	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
6225	GM_112_B1_A05_MR	g1488267	BLASTX	142	3e-13	70	(U57412) low affinity calcium antiporter CAX2 [Arabidopsis thaliana]
6226	GM_112_B1_A11_T7	g4038056	BLASTX	304	4e-25	47	(AC005897) putative transposon [Arabidopsis thaliana]
6227	GM_112_B1_A12_T7	g3599418	BLASTN	351	7e-09	86	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
6228	GM_112_B1_B01_T7	g2252856	BLASTX	122	2e-11	53	(AF013294) No definition line found [Arabidopsis thaliana]
6229	GM_112_B1_B02_MR	g18559	BLASTN	560	2e-18	70	G.max gene for catalase
6230	GM_112_B1_B02_T7	g2522230	BLASTX	297	1e-25	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
6231	GM_112_B1_B04_MR	g3097320	BLASTN	425	3e-12	70	Glycine max gene for Bd 30K, complete cds
6232	GM_112_B1_B05_MR	g905361	BLASTX	351	1e-30	79	(U22103) gag-protease polyprotein [Glycine max]
6233	GM_112_B1_B05_T7	g507910	BLASTN	398	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6234	GM_112_B1_B08_MR	g3097320	BLASTN	467	4e-14	71	Glycine max gene for Bd 30K, complete cds
6235	GM_112_B1_B10_T7	g905361	BLASTX	192	2e-13	35	(U22103) gag-protease polyprotein [Glycine max]
6236	GM_112_B1_C01_T7	g3176784	BLASTN	383	5e-11	65	Homo sapiens allele 7 fragile site locus (FRA10B) minisatellite sequence
6237	GM_112_B1_C03_MR	g3810596	BLASTX	331	5e-28	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
6238	GM_112_B1_C05_MR	g1431738	BLASTN	684	4e-24	83	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
6239	GM_112_B1_C06_MR	g629693	BLASTX	360	7e-38	54	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6240	GM_112_B1_C11_MR	g3142303	BLASTX	452	1e-40	62	(AC002411) Strong similarity to MRP-like ABC transporter gb U92650 from A. thaliana and canalicular multi-drug resistance protein gb L49379 from Rattus norvegicus. [Arabidopsis thaliana]
6241	GM_112_B1_C11_T7	g170067	BLASTN	367	1e-09	66	Soybean (G.max) proline-rich cell wall protein (SbPRP3) gene, complete cds.
6242	GM_112_B1_D02_MR	g1142703	BLASTN	277	2e-15	75	Glycine max satellite STR120-B.1.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6243	GM_112_B1_D03_T7	g507910	BLASTN	350	3e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
6244	GM_112_B1_D06_MR	g905361	BLASTX	241	1e-18	39	(U22103) gag-protease polyprotein [Glycine max]
6245	GM_112_B1_D06_T7	g2522230	BLASTX	245	5e-20	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
6246	GM_112_B1_D08_MR	g3985952	BLASTN	404	3e-11	77	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]
6247	GM_112_B1_D08_T7	g4038056	BLASTX	235	8e-18	38	(AC005897) putative transposon [Arabidopsis thaliana]
6248	GM_112_B1_E01_T7	g1335862	BLASTX	355	3e-30	71	(U42608) clathrin heavy chain [Glycine max]
6249	GM_112_B1_E02_MR	g4063760	BLASTX	251	3e-19	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6250	GM_112_B1_E05_T7	g3738294	BLASTX	315	2e-26	63	(AC005309) hypothetical protein [Arabidopsis thaliana]
6251	GM_112_B1_E07_MR	g1666236	BLASTX	169	1e-11	29	(U76261) unknown [Hordeum vulgare]
6252	GM_112_B1_E12_MR	g3810595	BLASTX	329	1e-29	52	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
6253	GM_112_B1_E12_T7	g2245109	BLASTX	202	6e-15	68	(Z97343) carboxyl-terminal proteinase homolog [Arabidopsis thaliana]
6254	GM_112_B1_F02_MR	g1480927	BLASTN	624	2e-21	85	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
6255	GM_112_B1_F02_T7	g3334667	BLASTX	295	7e-25	43	(Y10493) putative cytochrome P450 [Glycine max]
6256	GM_112_B1_F04_MR	g4138290	BLASTX	122	1e-14	82	(AJ005841) thioredoxin M [Oryza sativa]
6257	GM_112_B1_F05_MR	g3142328	BLASTN	1273	9e-51	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6258	GM_112_B1_F05_T7	g3510343	BLASTN	802	3e-29	78	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJC20, complete sequence [Arabidopsis thaliana]
6259	GM_112_B1_F06_T7	g2522230	BLASTX	200	3e-15	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
6260	GM_112_B1_F11_MR	g99719	BLASTX	157	1e-17	50	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Landsberg) (fragment) gi 16384 (X53976) orf 2 [Arabidopsis thaliana]
6261	GM_112_B1_F11_T7	g2979574	BLASTN	424	4e-12	66	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence [Homo sapiens]
6262	GM_112_B1_G01_MR	g3738208	BLASTX	178	6e-20	55	(AL031853) strong similarity to human Rev interacting protein Rip-1 [Schizosaccharomyces pombe]
6263	GM_112_B1_G03_T7	g3097320	BLASTN	576	5e-19	74	Glycine max gene for Bd 30K, complete cds
6264	GM_112_B1_G04_MR	g3513747	BLASTX	163	9e-10	45	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6265	GM_112_B1_G09_T7	g1703200	BLASTX	278	2e-32	88	PROTEIN KINASE AFC2 gi 601789 (U16177) protein kinase [Arabidopsis thaliana] gi 642130 gnl PID d1008809 (D45353) protein kinase [Arabidopsis thaliana]
6266	GM_112_B1_H05_MR	g2245104	BLASTX	218	8e-19	37	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
6267	GM_112_B1_H06_T7	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
6268	GM_112_B1_H07_MR	g3779030	BLASTX	201	2e-15	36	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
6269	GM_112_B1_H09_MR	g507910	BLASTN	393	4e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6270	GM_112_B1_H10_T7	g3335357	BLASTX	308	4e-26	48	(AC003028) putative diphenol oxidase [Arabidopsis thaliana]
6271	GM_113_A1_A09_T7	g3645899	BLASTX	290	2e-23	54	(U68408) 5' end not determined experimentally [Zea mays]
6272	GM_113_A1_A10_T7	g2462826	BLASTX	198	1e-13	51	(AF000657) unknown protein [Arabidopsis thaliana]
6273	GM_113_A1_B10_T7	g629693	BLASTX	148	4e-09	41	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6274	GM_113_A1_C01_MR	g3777527	BLASTX	211	6e-15	72	(AF053008) gag-pol polyprotein [Glycine max]
6275	GM_113_A1_C02_MR	g629693	BLASTX	90	6e-10	63	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6276	GM_113_A1_C04_MR	g507910	BLASTN	534	2e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
6277	GM_113_A1_C05_T7	g505129	BLASTN	353	5e-09	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
6278	GM_113_A1_C12_T7	g135444	BLASTX	282	5e-24	86	TUBULIN BETA-1 CHAIN gi 16122 (X54852) beta-tubulin [Avena sativa]
6279	GM_113_A1_D06_T7	g100484	BLASTX	252	9e-20	43	hypothetical protein - garden snapdragon
6280	GM_113_A1_D12_MR	g1167523	BLASTX	297	4e-24	52	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
6281	GM_113_A1_E10_MR	g3142379	BLASTX	208	2e-15	68	(AF053008) envelope-like [Glycine max]
6282	GM_113_A1_E11_T7	g100484	BLASTX	352	1e-30	57	hypothetical protein - garden snapdragon
6283	GM_113_A1_F06_T7	g99922	BLASTX	348	4e-41	66	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
6284	GM_113_A1_F09_MR	g2244859	BLASTX	166	1e-10	40	(Z97337) hypothetical protein [Arabidopsis thaliana]
6285	GM_113_A1_F10_T7	g2264312	BLASTN	413	1e-11	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]
6286	GM_113_A1_G09_T7	g18559	BLASTN	527	7e-17	71	G.max gene for catalase
6287	GM_113_A1_H02_T7	g1658457	BLASTX	329	6e-29	70	(U75248) reverse transcriptase [Gossypium barbadense]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6288	GM_113_A1_H09_MR	g1465818	BLASTX	91	8e-10	94	(U64855) coded for by C. elegans cDNA CEESS16F; coded for by C. elegans cDNA yk76b10.3; coded for by C. elegans cDNA yk14d4.3; coded for by C. elegans cDNA CEESS16F; coded for by C. elegans cDNA yk49a11.5; coded for by C. elegans cDNA yk48c6...
6289	GM_113_A1_H10_T7	g2462936	BLASTX	160	5e-11	56	(Y12321) open reading frame 2 [Brassica oleracea]
6290	GM_113_A1_H12_T7	g3777527	BLASTX	533	3e-49	90	(AF053008) gag-pol polyprotein [Glycine max]
6291	GM_113_B1_A04_MR	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6292	GM_113_B1_A04_T7	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6293	GM_113_B1_A05_T7	g18559	BLASTN	991	6e-38	74	G.max gene for catalase
6294	GM_113_B1_A09_MR	g1000971	BLASTN	472	3e-14	65	Hansenula wingei mitochondrial DNA, complete sequence
6295	GM_113_B1_A10_T7	g2522226	BLASTN	544	1e-17	65	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
6296	GM_113_B1_B03_T7	g2462058	BLASTX	209	8e-20	60	(Y13389) reverse transcriptase [Antirrhinum majus]
6297	GM_113_B1_B08_MR	g1480927	BLASTN	493	2e-15	78	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
6298	GM_113_B1_B11_MR	g100484	BLASTX	378	2e-33	53	hypothetical protein - garden snapdragon
6299	GM_113_B1_B12_T7	g4156188	BLASTN	357	4e-09	64	Homo sapiens clone DJ0784G16, complete sequence [Homo sapiens]
6300	GM_113_B1_C01_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6301	GM_113_B1_C03_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6302	GM_113_B1_C03_T7	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6303	GM_113_B1_C05_T7	g507910	BLASTN	593	3e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
6304	GM_113_B1_C07_MR	g1170878	BLASTX	188	4e-13	80	MALATE SYNTHASE, GLYOXYSOMAL (MS) gi 170026 (L01629) malate synthase [Glycine max]
6305	GM_113_B1_C09_T7	g507910	BLASTN	378	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6306	GM_113_B1_D01_T7	g1142702	BLASTN	249	2e-12	71	Glycine max satellite STR120-A.4.
6307	GM_113_B1_D03_T7	g3777527	BLASTX	187	2e-12	36	(AF053008) gag-pol polyprotein [Glycine max]
6308	GM_113_B1_D04_MR	g3097320	BLASTN	476	2e-14	68	Glycine max gene for Bd 30K, complete cds
6309	GM_113_B1_E02_T7	g505129	BLASTN	423	4e-12	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
6310	GM_113_B1_E04_MR	g2642431	BLASTX	187	3e-13	52	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
6311	GM_113_B1_E04_T7	g1710587	BLASTX	121	4e-12	58	60S ACIDIC RIBOSOMAL PROTEIN P0 gi 1196897 (L46848) acidic ribosomal protein P0 [Glycine max]
6312	GM_113_B1_F01_MR	g3395938	BLASTX	134	4e-13	65	(AF076924) polypyrimidine tract-binding protein homolog [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6313	GM_113_B1_F02_T7	g3097320	BLASTN	431	2e-12	73	Glycine max gene for Bd 30K, complete cds
6314	GM_113_B1_F03_T7	g4115363	BLASTX	237	6e-18	45	(AC005957) putative disease resistance protein [Arabidopsis thaliana]
6315	GM_113_B1_F06_T7	g4063760	BLASTX	422	1e-37	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6316	GM_113_B1_G04_MR	g1769556	BLASTX	160	1e-10	62	(U81158) Forsythia x intermedia (+)-pinoresinol/(+)-lariciresinol reductase (PLR) protein, complete sequence [Forsythia x intermedia]
6317	GM_113_B1_G07_T7	g3142328	BLASTN	1065	3e-41	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6318	GM_113_B1_G08_T7	g313723	BLASTN	353	2e-15	74	P.sativum hemC mRNA for hydroxymethylbilane synthase
6319	GM_113_B1_G11_T7	g507910	BLASTN	347	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6320	GM_113_B1_H08_MR	g1840106	BLASTN	415	2e-12	68	Human fragile site locus (FRA16B) minisatellite repeat
6321	GM_113_B1_H08_T7	g2462058	BLASTX	332	3e-29	52	(Y13389) reverse transcriptase [Antirrhinum majus]
6322	GM_113_B1_H09_MR	g1769898	BLASTX	235	4e-18	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6323	GM_113_B1_H10_T7	g226407	BLASTX	204	3e-14	39	retrotransposon del1-46 [Lilium henryi]
6324	GM_113_B2_A01_MR	g100484	BLASTX	405	3e-36	53	hypothetical protein - garden snapdragon
6325	GM_113_B2_A01_T7	g3097320	BLASTN	465	5e-14	69	Glycine max gene for Bd 30K, complete cds
6326	GM_113_B2_A03_T7	g629693	BLASTX	150	3e-09	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6327	GM_113_B2_A06_T7	g3097320	BLASTN	645	4e-22	79	Glycine max gene for Bd 30K, complete cds
6328	GM_113_B2_A07_T7	g18559	BLASTN	851	2e-31	72	G.max gene for catalase
6329	GM_113_B2_A12_MR	g507910	BLASTN	519	8e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
6330	GM_113_B2_B02_T7	g342952	BLASTN	331	7e-09	59	paramecium species 1,168 mt dna dimer: replication init. region.
6331	GM_113_B2_B03_MR	g3746069	BLASTX	220	1e-17	40	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
6332	GM_113_B2_B08_MR	g507910	BLASTN	384	9e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6333	GM_113_B2_B09_T7	g100484	BLASTX	241	1e-18	52	hypothetical protein - garden snapdragon
6334	GM_113_B2_B11_T7	g4063760	BLASTX	243	2e-18	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6335	GM_113_B2_C03_MR	g2979597	BLASTN	438	9e-13	66	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
6336	GM_113_B2_C07_MR	g454847	BLASTN	948	5e-36	74	Glycine max ribosomal protein S11 gene, complete cds
6337	GM_113_B2_C10_MR	g3650039	BLASTX	171	4e-11	35	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
6338	GM_113_B2_D01_MR	g2462936	BLASTX	288	2e-30	45	(Y12321) open reading frame 2 [Brassica oleracea]
6339	GM_113_B2_D09_MR	g3142379	BLASTX	266	6e-22	59	(AF053008) envelope-like [Glycine max]
6340	GM_113_B2_D11_MR	g2462134	BLASTX	333	4e-29	48	(Y13368) reverse transcriptase [Beta vulgaris]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6341	GM_113_B2_E02_MR	g4092471	BLASTN	492	3e-15	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
6342	GM_113_B2_E03_MR	g3319362	BLASTX	188	4e-25	59	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
6343	GM_113_B2_F01_MR	g4063760	BLASTX	267	5e-21	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6344	GM_113_B2_F05_T7	g2495365	BLASTX	173	3e-11	49	HEAT SHOCK PROTEIN 81-2 (HSP81-2) gi 445127 prf 1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]
6345	GM_113_B2_F06_T7	g3449315	BLASTN	481	1e-14	73	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K23L20, complete sequence [Arabidopsis thaliana]
6346	GM_113_B2_F07_MR	g1666236	BLASTX	238	2e-19	33	(U76261) unknown [Hordeum vulgare]
6347	GM_113_B2_F09_MR	g2832611	BLASTN	391	1e-10	66	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)
6348	GM_113_B2_F10_MR	g2129648	BLASTX	369	3e-33	72	MYB-related protein 33,3K - Arabidopsis thaliana gi 1263095 gnl PID e197888 (Z54136) MYB-related protein [Arabidopsis thaliana]
6349	GM_113_B2_G07_T7	g18559	BLASTN	769	8e-28	72	G.max gene for catalase
6350	GM_113_B2_G08_MR	g1769897	BLASTX	257	1e-20	37	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6351	GM_113_B2_G09_MR	g1769898	BLASTX	201	4e-28	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6352	GM_113_B2_G11_MR	g3645899	BLASTX	114	5e-19	56	(U68408) 5' end not determined experimentally [Zea mays]
6353	GM_113_B2_H02_MR	g2522228	BLASTX	277	2e-23	48	(AB007466) reverse transcriptase-like protein [Vicia faba]
6354	GM_113_B2_H03_MR	g2443320	BLASTX	383	3e-33	48	(D85597) polyprotein [Oryza australiensis]
6355	GM_113_B2_H04_T7	g2398853	BLASTX	176	9e-12	58	(AB004822) plastid RNA polymerase sigma-subunit [Arabidopsis thaliana]
6356	GM_113_B2_H06_MR	g2129618	BLASTX	233	2e-17	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6357	GM_113_B2_H08_MR	g2801423	BLASTN	358	4e-09	64	Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence [Homo sapiens]
6358	GM_113_B2_H11_MR	g2465923	BLASTX	189	8e-13	52	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]
6359	GM_113_B2_H12_MR	g2522227	BLASTX	278	1e-23	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
6360	GM_114_A1_A03_MR	g2213582	BLASTX	177	2e-24	45	(AC000348) T7N9.2 [Arabidopsis thaliana]
6361	GM_114_A1_A04_MR	g3176965	BLASTX	121	7e-15	82	(AF067967) pyrroline-5-carboxylate synthetase [Mesembryanthemum crystallinum]
6362	GM_114_A1_A11_MR	g2995405	BLASTX	367	6e-32	59	(Y12432) polyprotein [Ananas comosus]
6363	GM_114_A1_A12_T7	g3097320	BLASTN	438	9e-13	74	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6364	GM_114_A1_B03_MR	g3930515	BLASTX	117	6e-14	47	(AF059674) putative gag protein [Nicotiana tabacum]
6365	GM_114_A1_B03_T7	g3645899	BLASTX	226	6e-24	51	(U68408) 5' end not determined experimentally [Zea mays]
6366	GM_114_A1_B04_T7	g2129618	BLASTX	211	4e-15	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6367	GM_114_A1_B05_T7	g505129	BLASTN	397	5e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
6368	GM_114_A1_B09_T7	g3264544	BLASTN	378	5e-10	65	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
6369	GM_114_A1_C02_MR	g4006831	BLASTX	174	3e-15	34	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
6370	GM_114_A1_C03_MR	g2244802	BLASTX	219	2e-28	43	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
6371	GM_114_A1_C03_T7	g2522228	BLASTX	453	4e-42	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
6372	GM_114_A1_C07_MR	g4160362	BLASTN	421	6e-12	62	Saccharomyces cerevisiae complete mitochondrial genome
6373	GM_114_A1_C08_MR	g507910	BLASTN	462	3e-14	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6374	GM_114_A1_C09_T7	g2655926	BLASTX	94	6e-11	60	(Y09057) sf21 [Helianthus annuus]
6375	GM_114_A1_C11_T7	g507910	BLASTN	529	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
6376	GM_114_A1_D10_MR	g508826	BLASTN	359	3e-09	63	Drosophila melanogaster Oregon-R mitochondrial A+T region.
6377	GM_114_A1_E01_T7	g507910	BLASTN	368	5e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6378	GM_114_A1_E03_T7	g3097320	BLASTN	1190	7e-47	80	Glycine max gene for Bd 30K, complete cds
6379	GM_114_A1_E04_MR	g2579858	BLASTN	392	1e-11	62	Homo sapiens genomic DNA, 21q region, clone: S39BG29
6380	GM_114_A1_E04_T7	g2213602	BLASTX	205	8e-15	56	(AC000348) T7N9.22 [Arabidopsis thaliana]
6381	GM_114_A1_E05_MR	g4063760	BLASTX	315	4e-26	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6382	GM_114_A1_E07_MR	g4050011	BLASTN	719	2e-25	66	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
6383	GM_114_A1_E09_T7	g2462936	BLASTX	201	4e-29	49	(Y12321) open reading frame 2 [Brassica oleracea]
6384	GM_114_A1_F01_MR	g4049647	BLASTN	351	8e-09	62	Melanoplus sanguinipes entomopoxvirus, complete genome
6385	GM_114_A1_F03_MR	g507910	BLASTN	445	2e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6386	GM_114_A1_F03_T7	g507910	BLASTN	396	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6387	GM_114_A1_F04_MR	g2191194	BLASTX	190	3e-14	56	(AF007271) contains weak to the SAPB protein (TR:E236624) [Arabidopsis thaliana]
6388	GM_114_A1_F07_MR	g100484	BLASTX	310	5e-26	46	hypothetical protein - garden snapdragon
6389	GM_114_A1_G05_MR	g478148	BLASTX	379	3e-34	83	reverse transcriptase (copia-like retrotransposon) - soybean (fragment) >gi 169949 (M94493) reverse transcriptase [Glycine max]
6390	GM_114_A1_G07_T7	g2462058	BLASTX	285	2e-24	55	(Y13389) reverse transcriptase [Antirrhinum majus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6391	GM_114_A1_G09_MR	g421954	BLASTX	191	3e-13	44	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
6392	GM_114_A1_G11_MR	g18559	BLASTN	823	3e-30	74	G.max gene for catalase
6393	GM_114_A1_G12_MR	g2914700	BLASTX	289	7e-46	84	(AC003974) tRNA-processing protein SEN3-like [Arabidopsis thaliana]
6394	GM_114_A1_H01_MR	g18559	BLASTN	1009	1e-38	75	G.max gene for catalase
6395	GM_114_A1_H07_MR	g3377848	BLASTX	200	1e-14	44	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
6396	GM_114_A1_H10_MR	g478148	BLASTX	416	3e-38	87	reverse transcriptase (copia-like retrotransposon) - soybean (fragment) >gi 169949 (M94493) reverse transcriptase [Glycine max]
6397	GM_114_A1_H12_T7	g547683	BLASTX	135	5e-15	64	HEAT SHOCK COGNATE PROTEIN 80 gi 170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] gi 445601 prf 1909348A heat shock protein hsp80 [Lycopersicon esculentum]
6398	GM_114_B1_A01_T7	g2995405	BLASTX	191	1e-24	56	(Y12432) polyprotein [Ananas comosus]
6399	GM_114_B1_A04_T7	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6400	GM_114_B1_A05_T7	g505129	BLASTN	371	1e-12	71	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
6401	GM_114_B1_A08_T7	g1666236	BLASTX	196	1e-14	34	(U76261) unknown [Hordeum vulgare]
6402	GM_114_B1_A12_MR	g4063760	BLASTX	478	1e-43	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6403	GM_114_B1_B01_T7	g1769898	BLASTX	310	3e-26	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6404	GM_114_B1_B02_T7	g136636	BLASTX	189	4e-14	88	UBIQUITIN-CONJUGATING ENZYME E2-17 KD 1 (UBIQUITIN-PROTEIN LIGASE 1) (UBIQUITIN CARRIER PROTEIN 1) gi 1076424 pir S43781 ubiquitin-conjugating enzyme UBC1 - Arabidopsis thaliana gi 442594 pdb 1AAK Ubiquitin Conjugating Enzyme (E.C.6.3.2.19) gi 2981894 pdb 2AAK Ubiquitin Conjugating Enzyme From Arabidopsis Thaliana Ubiquitin Conjugation, Ligase Mol_id: 1; Molecule: Ubiquitin Conjugating Enzyme; Chain: Null; Synonym: Ubc1; Ec: 6.3.2.19; Engineered: Yes gi 166924 (M62721) ubiquitin carrier protein [Arabidopsis thaliana] gi 431260 (L19351) ubiquitin conjugating enzyme [Arabidopsis thaliana]
6405	GM_114_B1_B10_T7	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6406	GM_114_B1_C03_MR	g3097320	BLASTN	724	9e-26	75	Glycine max gene for Bd 30K, complete cds
6407	GM_114_B1_C04_MR	g18559	BLASTN	982	2e-37	73	G.max gene for catalase
6408	GM_114_B1_C05_T7	g2995405	BLASTX	293	5e-24	44	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6409	GM_114_B1_C11_MR	g507910	BLASTN	374	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6410	GM_114_B1_D10_T7	g4038056	BLASTX	392	1e-34	54	(AC005897) putative transposon [Arabidopsis thaliana]
6411	GM_114_B1_D12_T7	g387902	BLASTX	145	1e-12	51	(L23524) ORF [Hordeum vulgare]
6412	GM_114_B1_E01_MR	g13619	BLASTN	489	4e-16	66	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
6413	GM_114_B1_E02_MR	g629693	BLASTX	154	1e-09	48	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6414	GM_114_B1_E03_MR	g2443320	BLASTX	492	6e-45	63	(D85597) polyprotein [Oryza australiensis]
6415	GM_114_B1_E04_MR	g4006831	BLASTX	245	1e-18	34	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
6416	GM_114_B1_E09_T7	g4038056	BLASTX	335	2e-28	48	(AC005897) putative transposon [Arabidopsis thaliana]
6417	GM_114_B1_E10_MR	g3777527	BLASTX	713	2e-68	95	(AF053008) gag-pol polyprotein [Glycine max]
6418	GM_114_B1_F01_T7	g2623307	BLASTX	151	8e-09	65	(AC002409) putative ubiquitin protease [Arabidopsis thaliana]
6419	GM_114_B1_F07_MR	g4063760	BLASTX	467	2e-42	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6420	GM_114_B1_F08_MR	g4063760	BLASTX	556	7e-52	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6421	GM_114_B1_F08_T7	g2244915	BLASTX	260	2e-20	48	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
6422	GM_114_B1_F10_MR	g507910	BLASTN	567	5e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
6423	GM_114_B1_G01_T7	g1769898	BLASTX	247	1e-25	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6424	GM_114_B1_G03_MR	g3892061	BLASTX	130	3e-09	34	(AC002330) putative reverse transcriptase [Arabidopsis thaliana]
6425	GM_114_B1_G12_MR	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
6426	GM_116_B2_A05_T7	g100484	BLASTX	245	5e-19	53	hypothetical protein - garden snapdragon
6427	GM_116_B2_B02_MR	g2864621	BLASTX	129	2e-16	52	hypothetical protein [Arabidopsis thaliana]
6428	GM_116_B2_B12_T7	g130582	BLASTX	293	7e-28	56	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
6429	GM_116_B2_C02_T7	g3845197	BLASTN	363	2e-09	66	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
6430	GM_116_B2_C04_T7	g2828293	BLASTX	220	4e-16	72	(AL021687) putative protein [Arabidopsis thaliana]
6431	GM_116_B2_C08_T7	g3142328	BLASTN	573	6e-19	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6432	GM_116_B2_D04_T7	g4115920	BLASTX	321	4e-27	44	(AF118222) similar to the subtilase family of serine proteases (Pfam: PF00082, score; 45.8, E=1.1e-11, n=2) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6433	GM_116_B2_D08_T7	g14293	BLASTN	342	3e-09	63	Yeast R0.54 mutant mitochondrial DNA lacking ori1 sequence recombination junction with tRNA-Pro and 15S rRNA genes
6434	GM_116_B2_D10_MR	g2384672	BLASTN	363	1e-09	73	Arabidopsis thaliana putative potassium transporter AtKT3p (AtKT3) mRNA, partial cds.
6435	GM_116_B2_E01_T7	g2462134	BLASTX	167	7e-11	29	(Y13368) reverse transcriptase [Beta vulgaris]
6436	GM_116_B2_E02_MR	g3142328	BLASTN	1011	7e-39	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6437	GM_116_B2_E03_T7	g2764526	BLASTN	429	2e-12	62	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
6438	GM_116_B2_E05_T7	g3777527	BLASTX	420	3e-58	93	(AF053008) gag-pol polyprotein [Glycine max]
6439	GM_116_B2_E06_MR	g1326016	BLASTX	154	5e-09	41	TY3-2 orfB
6440	GM_116_B2_E08_MR	g1086625	BLASTX	106	2e-12	48	(U41012) Similar to aminoacylase-1. [Caenorhabditis elegans]
6441	GM_116_B2_E08_T7	g2121303	BLASTN	447	4e-13	67	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
6442	GM_116_B2_E11_MR	g18559	BLASTN	961	2e-36	78	G.max gene for catalase
6443	GM_116_B2_E11_T7	g1769897	BLASTX	170	4e-11	33	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6444	GM_116_B2_F02_MR	g3282170	BLASTN	730	6e-26	71	Arabidopsis thaliana chromosome 1 BAC F8K4 sequence, complete sequence [Arabidopsis thaliana]
6445	GM_116_B2_F05_MR	g527618	BLASTN	370	2e-21	84	Glycine max 3-methylcrotonyl-CoA carboxylase mRNA, biotin-carrier domain, partial cds.
6446	GM_116_B2_F07_T7	g13583	BLASTN	286	2e-09	68	Yeast mitochondrial ori(o) repeat unit of petite mutant 5 (petite strain s-10/7/2)
6447	GM_116_B2_G01_MR	g2369714	BLASTX	467	4e-47	70	(Z97178) elongation factor 2 [Beta vulgaris]
6448	GM_116_B2_G04_T7	g3273111	BLASTN	382	3e-10	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-09, complete sequence [Plasmodium falciparum]
6449	GM_116_B2_H03_MR	g1184075	BLASTX	209	7e-15	48	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
6450	GM_116_B2_H03_T7	g2429543	BLASTX	150	4e-14	54	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]
6451	GM_116_B2_H09_T7	g18559	BLASTN	1055	8e-41	78	G.max gene for catalase
6452	GM_116_B2_H12_T7	g3320104	BLASTX	179	5e-12	77	(AJ007366) calcium-dependent protein kinase [Zea mays]
6453	GM_117_B1_A01_T7	g1944188	BLASTN	568	4e-19	74	Soybean DNA for nodulin 35, partial cds
6454	GM_117_B1_A07_MR	g4092471	BLASTN	482	1e-14	66	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6455	GM_117_B1_B02_MR	g1402878	BLASTX	370	2e-33	65	(X98130) unknown [Arabidopsis thaliana]
6456	GM_117_B1_B04_T7	g3319362	BLASTX	275	5e-22	47	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
6457	GM_117_B1_B08_T7	g4063770	BLASTX	222	2e-16	39	(AB004906) transposase [Ipomoea purpurea]
6458	GM_117_B1_B09_MR	g1666236	BLASTX	194	2e-14	28	(U76261) unknown [Hordeum vulgare]
6459	GM_117_B1_B09_T7	g2995405	BLASTX	196	1e-13	38	(Y12432) polyprotein [Ananas comosus]
6460	GM_117_B1_C02_T7	g100484	BLASTX	228	1e-30	55	hypothetical protein - garden snapdragon
6461	GM_117_B1_C03_T7	g507910	BLASTN	657	4e-23	84	Glycine max BSR-101 satellite SB92 genomic sequence.
6462	GM_117_B1_C05_T7	g4063760	BLASTX	261	2e-20	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6463	GM_117_B1_C06_MR	g507910	BLASTN	623	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
6464	GM_117_B1_C06_T7	g4063760	BLASTX	280	2e-22	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6465	GM_117_B1_C07_T7	g226407	BLASTX	518	1e-47	64	retrotransposon del1-46 [Lilium henryi]
6466	GM_117_B1_C09_MR	g4063760	BLASTX	459	2e-41	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6467	GM_117_B1_C09_T7	g905361	BLASTX	176	1e-11	30	(U22103) gag-protease polyprotein [Glycine max]
6468	GM_117_B1_D01_MR	g507910	BLASTN	429	9e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
6469	GM_117_B1_D01_T7	g507910	BLASTN	390	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6470	GM_117_B1_D03_MR	g4063760	BLASTX	295	5e-24	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6471	GM_117_B1_D03_T7	g507910	BLASTN	678	5e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
6472	GM_117_B1_D09_MR	g1619300	BLASTX	119	9e-09	40	(X95269) LRR protein [Lycopersicon esculentum]
6473	GM_117_B1_D11_T7	g3695294	BLASTN	447	3e-13	78	Glycine max nodule-specific glutamine synthetase gene, complete cds
6474	GM_117_B1_E02_T7	g3319351	BLASTX	338	2e-28	47	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
6475	GM_117_B1_E04_T7	g629693	BLASTX	372	1e-33	51	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6476	GM_117_B1_E10_MR	g507910	BLASTN	388	6e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6477	GM_117_B1_E10_T7	g507910	BLASTN	407	9e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6478	GM_117_B1_E12_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
6479	GM_117_B1_E12_T7	g507910	BLASTN	376	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6480	GM_117_B1_F01_MR	g4115365	BLASTX	173	6e-11	32	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
6481	GM_117_B1_F01_T7	g3810596	BLASTX	322	4e-28	53	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
6482	GM_117_B1_F02_T7	g1352316	BLASTX	150	5e-10	76	DR1 PROTEIN HOMOLOG gi 633026 gnl PID d1007866 (D38110) Dr1 [Arabidopsis thaliana]
6483	GM_117_B1_F08_T7	g3142379	BLASTX	175	6e-12	64	(AF053008) envelope-like [Glycine max]
6484	GM_117_B1_F11_MR	g4063760	BLASTX	388	3e-35	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6485	GM_117_B1_G01_MR	g2288886	BLASTN	397	4e-11	80	Arabidopsis thaliana mRNA for mevalonate diphosphate decarboxylase.
6486	GM_117_B1_G05_T7	g421953	BLASTX	105	3e-10	40	hypothetical protein 2 - potato transposon Tst1 gi 21432 (X52387) ORF2 [Solanum tuberosum]
6487	GM_117_B1_G10_MR	g18695	BLASTN	347	9e-09	67	Soybean nodulin 22 gene
6488	GM_117_B1_H04_T7	g4140712	BLASTX	154	2e-10	38	(AF110183) putative integrase [Oryza sativa]
6489	GM_117_B1_H07_T7	g18559	BLASTN	896	1e-33	70	G.max gene for catalase
6490	GM_117_B1_H08_MR	g4115365	BLASTX	202	1e-23	41	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
6491	GM_117_B1_H09_MR	g507910	BLASTN	346	5e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
6492	GM_117_B1_H09_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6493	GM_117_B2_A02_MR	g3219937	BLASTX	159	2e-10	40	HYPOTHETICAL 35.1 KD PROTEIN C57A10.07 IN CHROMOSOME I gi 2058374 gnl PID e313998 (Z94864) unknown [Schizosaccharomyces pombe]
6494	GM_117_B2_A08_T7	g3979928	BLASTN	372	9e-10	64	Caenorhabditis elegans cosmid Y18D10A, complete sequence [Caenorhabditis elegans]
6495	GM_117_B2_A12_MR	g3738114	BLASTN	365	2e-09	63	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
6496	GM_117_B2_B03_MR	g99755	BLASTX	356	2e-31	55	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
6497	GM_117_B2_B08_MR	g2244881	BLASTX	164	1e-15	40	(Z97338) PDR5-like ABC transporter [Arabidopsis thaliana]
6498	GM_117_B2_C02_MR	g3426334	BLASTN	348	1e-08	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
6499	GM_117_B2_C04_T7	g3142328	BLASTN	461	7e-14	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6500	GM_117_B2_C05_T7	g1142701	BLASTN	1292	5e-52	84	Glycine max satellite STR120-A.3.
6501	GM_117_B2_D01_MR	g100484	BLASTX	348	4e-30	59	hypothetical protein - garden snapdragon
6502	GM_117_B2_D03_MR	g1666236	BLASTX	164	6e-11	34	(U76261) unknown [Hordeum vulgare]
6503	GM_117_B2_D05_T7	g3810596	BLASTX	247	5e-19	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
6504	GM_117_B2_D06_MR	g507910	BLASTN	396	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6505	GM_117_B2_D07_T7	g3645899	BLASTX	316	3e-26	49	(U68408) 5' end not determined experimentally [Zea mays]
6506	GM_117_B2_D09_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6507	GM_117_B2_D10_T7	g507910	BLASTN	573	3e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
6508	GM_117_B2_E01_MR	g3097320	BLASTN	487	5e-15	72	Glycine max gene for Bd 30K, complete cds
6509	GM_117_B2_E02_T7	g4063760	BLASTX	231	4e-17	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6510	GM_117_B2_E04_T7	g4063760	BLASTX	189	3e-24	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6511	GM_117_B2_E11_T7	g130582	BLASTX	160	1e-09	35	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
6512	GM_117_B2_F01_T7	g3695395	BLASTX	128	1e-15	55	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
6513	GM_117_B2_F02_T7	g3953466	BLASTX	164	3e-10	58	(AC002328) F20N2.11 [Arabidopsis thaliana]
6514	GM_117_B2_F03_T7	g2443320	BLASTX	234	2e-17	47	(D85597) polyprotein [Oryza australiensis]
6515	GM_117_B2_F05_T7	g507910	BLASTN	545	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
6516	GM_117_B2_F07_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
6517	GM_117_B2_F08_T7	g3777527	BLASTX	469	5e-43	96	(AF053008) gag-pol polyprotein [Glycine max]
6518	GM_117_B2_F09_MR	g4063770	BLASTX	166	2e-10	43	(AB004906) transposase [Ipomoea purpurea]
6519	GM_117_B2_F10_MR	g18559	BLASTN	787	1e-28	76	G.max gene for catalase
6520	GM_117_B2_F11_T7	g4063760	BLASTX	319	2e-26	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6521	GM_117_B2_F12_MR	g507910	BLASTN	433	6e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6522	GM_117_B2_G02_MR	g3033375	BLASTX	329	2e-31	49	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]
6523	GM_117_B2_G02_T7	g3688209	BLASTX	157	9e-10	68	(AJ010093) MAP3K beta 1 protein kinase [Brassica napus]
6524	GM_117_B2_G03_MR	g3785991	BLASTX	242	5e-19	65	(AC005560) putative MAP kinase [Arabidopsis thaliana]
6525	GM_117_B2_G06_MR	g1769898	BLASTX	332	1e-28	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6526	GM_117_B2_G11_MR	g421955	BLASTX	350	3e-31	57	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
6527	GM_117_B2_G11_T7	g4063760	BLASTX	254	1e-19	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6528	GM_117_B2_G12_MR	g3548808	BLASTX	556	5e-53	81	(AC005313) unknown protein [Arabidopsis thaliana]
6529	GM_117_B2_H01_MR	g18559	BLASTN	629	2e-21	73	G.max gene for catalase
6530	GM_117_B2_H01_T7	g3142328	BLASTN	722	1e-25	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6531	GM_117_B2_H04_T7	g3738114	BLASTN	355	5e-09	64	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
6532	GM_117_B2_H06_T7	g4063760	BLASTX	259	4e-20	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6533	GM_117_B2_H07_MR	g3108025	BLASTN	407	2e-11	71	Arabidopsis thaliana chromosome 1 BAC T13D8, complete sequence [Arabidopsis thaliana]
6534	GM_117_B2_H08_MR	g3142328	BLASTN	1014	5e-39	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6535	GM_117_B2_H11_T7	g3341443	BLASTX	156	2e-10	90	(AJ223074) acid phosphatase [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6536	GM_118_A1_A03_MR	g3142328	BLASTN	998	3e-38	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6537	GM_118_A1_A04_T7	g3810596	BLASTX	291	9e-24	47	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
6538	GM_118_A1_A08_MR	g2444178	BLASTX	181	9e-12	70	(U94784) unconventional myosin [Helianthus annuus]
6539	GM_118_A1_A08_T7	g1514643	BLASTX	210	8e-15	75	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
6540	GM_118_A1_A09_T7	g2982521	BLASTN	378	5e-10	61	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-14, complete sequence [Plasmodium falciparum]
6541	GM_118_A1_B02_T7	g3142328	BLASTN	1576	1e-64	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6542	GM_118_A1_B09_T7	g1169198	BLASTX	151	9e-10	77	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR gi 479738 pir S35270 hypothetical protein - Arabidopsis thaliana gi 166926 (L11367) [Arabidopsis thaliana unidentified mRNA sequence, complete cds.], gene product [Arabidopsis thaliana]
6543	GM_118_A1_B12_T7	g2828293	BLASTX	213	2e-15	70	(AL021687) putative protein [Arabidopsis thaliana]
6544	GM_118_A1_C07_T7	g3046855	BLASTN	379	4e-10	65	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]
6545	GM_118_A1_C09_T7	g507910	BLASTN	595	3e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
6546	GM_118_A1_C10_MR	g505129	BLASTN	359	3e-09	71	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
6547	GM_118_A1_D02_T7	g99922	BLASTX	630	7e-61	76	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
6548	GM_118_A1_D06_T7	g100484	BLASTX	375	5e-33	60	hypothetical protein - garden snapdragon
6549	GM_118_A1_D07_MR	g1666236	BLASTX	180	9e-13	30	(U76261) unknown [Hordeum vulgare]
6550	GM_118_A1_D07_T7	g99922	BLASTX	232	1e-18	60	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
6551	GM_118_A1_D09_MR	g3097320	BLASTN	884	5e-33	76	Glycine max gene for Bd 30K, complete cds
6552	GM_118_A1_E03_MR	g905361	BLASTX	239	2e-18	41	(U22103) gag-protease polyprotein [Glycine max]
6553	GM_118_A1_E08_T7	g2598587	BLASTX	123	4e-16	92	(Y15366) cycloartenol synthase [Medicago truncatula]
6554	GM_118_A1_E09_T7	g218269	BLASTX	190	3e-14	71	(D12839) reverse transcriptase [Glycine max]
6555	GM_118_A1_E12_T7	g629693	BLASTX	343	2e-30	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6556	GM_118_A1_F11_MR	g507910	BLASTN	375	2e-10	78	Glycine max BSR-101 satellite SB92 genomic sequence.
6557	GM_118_A1_F11_T7	g507910	BLASTN	568	5e-19	79	Glycine max BSR-101 satellite SB92 genomic sequence.
6558	GM_118_A1_G04_MR	g2924523	BLASTX	221	4e-18	36	(AL022023) putative protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6559	GM_118_A1_G08_T7	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6560	GM_118_A1_G09_T7	g4063760	BLASTX	424	9e-38	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6561	GM_118_A1_G11_T7	g4063760	BLASTX	314	5e-26	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6562	GM_118_A1_G12_MR	g507910	BLASTN	425	1e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
6563	GM_118_A1_H12_T7	g99726	BLASTX	111	3e-13	56	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976) orf 3 [Arabidopsis thaliana]
6564	GM_118_A2_A02_MR	g3142328	BLASTN	723	9e-26	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6565	GM_118_A2_A05_T7	g950319	BLASTX	252	1e-19	37	(M11240) unknown protein [Drosophila melanogaster]
6566	GM_118_A2_B01_MR	g507910	BLASTN	537	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
6567	GM_118_A2_B03_T7	g3097320	BLASTN	466	5e-14	70	Glycine max gene for Bd 30K, complete cds
6568	GM_118_A2_B07_T7	g1346790	BLASTX	115	3e-09	68	PATHOGENESIS-RELATED HOMEODOMAIN PROTEIN (PRHA) gi 507220 (L21991) homeodomain protein [Arabidopsis thaliana] gi 2501810 (U48864) PRHA [Arabidopsis thaliana]
6569	GM_118_A2_B09_MR	g3645899	BLASTX	323	4e-27	48	(U68408) 5' end not determined experimentally [Zea mays]
6570	GM_118_A2_B09_T7	g4063760	BLASTX	258	5e-20	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6571	GM_118_A2_B10_MR	g507910	BLASTN	511	2e-16	82	Glycine max BSR-101 satellite SB92 genomic sequence.
6572	GM_118_A2_B10_T7	g2522230	BLASTX	230	2e-18	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
6573	GM_118_A2_B11_T7	g2244802	BLASTX	98	8e-11	26	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
6574	GM_118_A2_C01_MR	g3142328	BLASTN	1498	5e-61	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6575	GM_118_A2_C02_MR	g4063760	BLASTX	195	2e-13	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6576	GM_118_A2_C07_MR	g3513747	BLASTX	141	6e-19	62	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
6577	GM_118_A2_C08_T7	g3097320	BLASTN	461	8e-14	69	Glycine max gene for Bd 30K, complete cds
6578	GM_118_A2_C09_MR	g3142328	BLASTN	747	7e-51	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6579	GM_118_A2_C10_T7	g3046848	BLASTN	485	7e-15	65	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18C1, complete sequence.
6580	GM_118_A2_D01_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6581	GM_118_A2_D03_MR	g2316016	BLASTX	349	1e-29	64	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6582	GM_118_A2_D04_T7	g130582	BLASTX	208	1e-14	34	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
6583	GM_118_A2_D09_T7	g4063760	BLASTX	138	1e-10	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6584	GM_118_A2_E01_T7	g3097320	BLASTN	494	2e-15	82	Glycine max gene for Bd 30K, complete cds
6585	GM_118_A2_E03_T7	g226407	BLASTX	182	8e-12	32	retrotransposon del1-46 [Lilium henryi]
6586	GM_118_A2_E04_T7	g1785699	BLASTX	133	4e-12	36	(Y08501) orf145a [Arabidopsis thaliana]
6587	GM_118_A2_E09_MR	g4063760	BLASTX	346	2e-29	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6588	GM_118_A2_F04_T7	g3097320	BLASTN	826	2e-30	73	Glycine max gene for Bd 30K, complete cds
6589	GM_118_A2_F08_MR	g18559	BLASTN	488	4e-15	64	G.max gene for catalase
6590	GM_118_A2_G01_MR	g3176798	BLASTN	422	7e-13	62	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite, 5' sequence
6591	GM_118_A2_G02_MR	g2388580	BLASTX	180	2e-15	82	(AC000098) Similar to Sequence 10 from patent 5477002 (gb 1253956). [Arabidopsis thaliana]
6592	GM_118_A2_G03_MR	g507910	BLASTN	586	7e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
6593	GM_118_A2_G07_MR	g4063760	BLASTX	137	7e-17	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6594	GM_118_A2_G10_MR	g226407	BLASTX	185	4e-12	36	retrotransposon del1-46 [Lilium henryi]
6595	GM_118_A2_H03_T7	g3075394	BLASTX	287	8e-24	38	(AC004484) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana] gi 3559809 gnl PID e1319149 (AJ010713) fiddlehead protein [Arabidopsis thaliana]
6596	GM_118_B1_A06_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6597	GM_118_B1_A06_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6598	GM_118_B1_A08_MR	g1890143	BLASTN	371	8e-10	65	A.aegypti DNA, copia-like transposable element ZebedeeII
6599	GM_118_B1_A09_MR	g2654440	BLASTX	188	5e-14	45	(U70076) Lemir [Lycopersicon esculentum]
6600	GM_118_B1_A09_T7	g2655313	BLASTN	261	5e-10	69	Bactrocera umbrosa strain Vanuatu mitochondrial D-loop region, complete sequence
6601	GM_118_B1_B02_MR	g4092470	BLASTN	393	1e-10	64	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
6602	GM_118_B1_B06_MR	g18559	BLASTN	606	2e-20	80	G.max gene for catalase
6603	GM_118_B1_B07_T7	g3157949	BLASTX	177	5e-12	43	(AC002131) Similar to glucan endo-1,3-beta-D-glucosidase precursor gb Z28697 from Nicotiana tabacum. ESTs gb Z18185 and gb AA605362 come from this gene. [Arabidopsis thaliana]
6604	GM_118_B1_B11_MR	g2462936	BLASTX	290	7e-25	38	(Y12321) open reading frame 2 [Brassica oleracea]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6605	GM_118_B1_C01_T7	g3097320	BLASTN	465	5e-14	72	Glycine max gene for Bd 30K, complete cds
6606	GM_118_B1_C09_T7	g3142328	BLASTN	455	1e-13	69	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6607	GM_118_B1_C11_MR	g1769898	BLASTX	265	2e-21	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6608	GM_118_B1_C12_MR	g507910	BLASTN	371	4e-10	68	Glycine max BSR-101 satellite SB92 genomic sequence.
6609	GM_118_B1_D01_T7	g2182289	BLASTN	351	8e-09	66	Arabidopsis thaliana chromosome I BAC F11P17 genomic sequence, complete sequence [Arabidopsis thaliana]
6610	GM_118_B1_D02_MR	g1402883	BLASTX	130	2e-10	40	(X98130) unknown [Arabidopsis thaliana] gi 1495263 gnl PID e242837 (X97487) orf09 [Arabidopsis thaliana]
6611	GM_118_B1_D03_T7	g2462134	BLASTX	209	2e-15	41	(Y13368) reverse transcriptase [Beta vulgaris]
6612	GM_118_B1_D09_MR	g3421384	BLASTX	243	2e-19	63	(AF081067) IAA-Ala hydrolase; IAA-amino acid hydrolase [Arabidopsis thaliana]
6613	GM_118_B1_D09_T7	g3337396	BLASTN	380	4e-10	66	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence [Homo sapiens]
6614	GM_118_B1_D12_MR	g2564048	BLASTN	386	2e-10	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]
6615	GM_118_B1_E03_MR	g340796	BLASTN	384	3e-11	62	Figure 6. DNA sequence of three 3' apoB VNTR alleles.
6616	GM_118_B1_E04_T7	g387902	BLASTX	163	1e-25	53	(L23524) ORF [Hordeum vulgare]
6617	GM_118_B1_E09_T7	g4038352	BLASTX	163	1e-16	37	(AF098951) breast cancer resistance protein [Homo sapiens]
6618	GM_118_B1_F05_T7	g4150930	BLASTN	425	4e-12	65	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
6619	GM_118_B1_F08_MR	g507910	BLASTN	395	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6620	GM_118_B1_F09_MR	g507910	BLASTN	578	2e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
6621	GM_118_B1_G04_T7	g507910	BLASTN	416	3e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
6622	GM_118_B1_H02_MR	g3777527	BLASTX	283	3e-29	58	(AF053008) gag-pol polyprotein [Glycine max]
6623	GM_118_B1_H04_MR	g507910	BLASTN	366	6e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6624	GM_118_B1_H04_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
6625	GM_118_B1_H06_T7	g2522226	BLASTN	444	4e-13	63	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
6626	GM_118_B1_H09_T7	g130582	BLASTX	240	4e-18	46	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
6627	GM_118_B2_A04_MR	g2522228	BLASTX	211	6e-16	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
6628	GM_118_B2_A05_MR	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6629	GM_118_B2_A08_T7	g2340108	BLASTX	161	7e-10	51	(U65948) starch branching enzyme IIa [Zea mays]
6630	GM_118_B2_A11_MR	g2995405	BLASTX	236	6e-18	47	(Y12432) polyprotein [Ananas comosus]
6631	GM_118_B2_C07_T7	g2970554	BLASTN	403	3e-11	66	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
6632	GM_118_B2_C12_MR	g4063760	BLASTX	243	2e-18	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6633	GM_118_B2_D04_MR	g3142328	BLASTN	380	3e-10	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6634	GM_118_B2_D05_T7	g2995405	BLASTX	280	1e-22	64	(Y12432) polyprotein [Ananas comosus]
6635	GM_118_B2_D06_T7	g4063760	BLASTX	329	1e-27	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6636	GM_118_B2_E08_T7	g1705678	BLASTX	317	1e-26	91	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP) gi 862480 (U20213) valosin-containing protein [Glycine max]
6637	GM_118_B2_E10_MR	g18768	BLASTN	407	5e-12	76	Soybean Tgm6 transposable element 3' end
6638	GM_118_B2_E12_MR	g2995405	BLASTX	325	2e-27	60	(Y12432) polyprotein [Ananas comosus]
6639	GM_118_B2_G12_T7	g507910	BLASTN	386	8e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6640	GM_118_B2_H02_T7	g132086	BLASTX	290	7e-25	100	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1 PRECURSOR gi 68053 pir RKSYS ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor SRS1 - soybean gi 18742 (V00458) rubpcase [Glycine max]
6641	GM_118_B2_H03_T7	g1142699	BLASTN	226	1e-09	70	Glycine max satellite STR120-A.1.
6642	GM_119_B2_A05_MR	g2827514	BLASTX	193	1e-13	75	(AL021633) predicted protein [Arabidopsis thaliana]
6643	GM_119_B2_A06_MR	g1143381	BLASTX	175	3e-12	42	(Z49063) polygalacturonase inhibitor [Actinidia deliciosa]
6644	GM_119_B2_A11_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6645	GM_119_B2_B11_MR	g2443320	BLASTX	268	5e-21	54	(D85597) polyprotein [Oryza australiensis]
6646	GM_119_B2_B12_MR	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
6647	GM_119_B2_C01_MR	g507910	BLASTN	611	5e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
6648	GM_119_B2_C04_MR	g507910	BLASTN	611	5e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
6649	GM_119_B2_D02_MR	g18559	BLASTN	981	2e-37	76	G.max gene for catalase
6650	GM_119_B2_D05_MR	g18559	BLASTN	987	1e-37	77	G.max gene for catalase
6651	GM_119_B2_D08_MR	g2130082	BLASTX	373	2e-32	53	protein kinase Xa21 (EC 2.7.1.-) - rice gi 1122443 (U37133) receptor kinase-like protein [Oryza sativa] gi 2586085 (U72723) receptor kinase-like protein [Oryza longistaminata] gi 1586408 prf 2203451A receptor kinase-like protein [Oryza sativa]
6652	GM_119_B2_D09_MR	g3097320	BLASTN	664	5e-23	75	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6653	GM_119_B2_D10_MR	g130582	BLASTX	319	2e-26	52	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
6654	GM_119_B2_D12_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
6655	GM_119_B2_E01_MR	g3283026	BLASTX	226	5e-17	34	putative transposase [Arabidopsis thaliana]
6656	GM_119_B2_E03_MR	g3645899	BLASTX	436	3e-39	62	(U68408) 5' end not determined experimentally [Zea mays]
6657	GM_119_B2_E08_MR	g4063760	BLASTX	256	7e-20	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6658	GM_119_B2_F01_MR	g507910	BLASTN	397	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6659	GM_119_B2_F03_MR	g3281870	BLASTX	184	9e-12	38	(AL031004) putative protein [Arabidopsis thaliana]
6660	GM_120_A1_A07_T7	g130582	BLASTX	400	4e-35	62	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
6661	GM_120_A1_A08_MR	g3786414	BLASTN	374	7e-10	71	Caenorhabditis elegans cosmid H28G03
6662	GM_120_A1_A09_T7	g507910	BLASTN	603	1e-20	85	Glycine max BSR-101 satellite SB92 genomic sequence.
6663	GM_120_A1_A10_MR	g2522228	BLASTX	560	2e-53	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
6664	GM_120_A1_A10_T7	g3377836	BLASTX	84	6e-09	32	(AF075598) contains similarity to reverse transcriptases [Arabidopsis thaliana]
6665	GM_120_A1_A11_MR	g3985957	BLASTN	365	2e-09	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]
6666	GM_120_A1_A11_T7	g4063760	BLASTX	371	4e-32	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6667	GM_120_A1_A12_T7	g1167523	BLASTX	365	2e-31	49	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
6668	GM_120_A1_B04_T7	g13619	BLASTN	334	1e-08	58	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
6669	GM_120_A1_B05_T7	g3378134	BLASTX	240	8e-19	40	(AF071503) brahma associated protein 60 kDa [Drosophila melanogaster]
6670	GM_120_A1_B06_MR	g3135969	BLASTN	358	4e-09	64	Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family prot...
6671	GM_120_A1_B08_MR	g4063760	BLASTX	396	9e-35	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6672	GM_120_A1_B09_T7	g2443320	BLASTX	373	4e-33	52	(D85597) polyprotein [Oryza australiensis]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6673	GM_120_A1_B12_T7	g4063760	BLASTX	403	2e-35	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6674	GM_120_A1_C02_MR	g4063760	BLASTX	353	3e-30	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6675	GM_120_A1_C03_MR	g4050011	BLASTN	488	5e-15	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
6676	GM_120_A1_C04_MR	g4063760	BLASTX	275	7e-22	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6677	GM_120_A1_C05_MR	g2924653	BLASTN	327	7e-09	85	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDA7, complete sequence [Arabidopsis thaliana]
6678	GM_120_A1_C06_MR	g4160362	BLASTN	351	8e-09	61	Saccharomyces cerevisiae complete mitochondrial genome
6679	GM_120_A1_C11_MR	g3930515	BLASTX	122	4e-12	38	(AF059674) putative gag protein [Nicotiana tabacum]
6680	GM_120_A1_D03_MR	g2522227	BLASTX	226	4e-18	38	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
6681	GM_120_A1_D05_MR	g1666236	BLASTX	164	6e-11	26	(U76261) unknown [Hordeum vulgare]
6682	GM_120_A1_D07_MR	g4050011	BLASTN	474	2e-14	64	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
6683	GM_120_A1_D08_MR	g3033389	BLASTX	198	8e-14	41	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
6684	GM_120_A1_D11_MR	g3695395	BLASTX	152	4e-09	52	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
6685	GM_120_A1_D11_T7	g4063760	BLASTX	389	5e-34	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6686	GM_120_A1_D12_MR	g4063760	BLASTX	191	5e-16	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6687	GM_120_A1_E07_MR	g507910	BLASTN	387	7e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6688	GM_120_A1_E07_T7	g507910	BLASTN	401	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6689	GM_120_A1_E09_T7	g3738114	BLASTN	374	7e-10	61	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
6690	GM_120_A1_F03_T7	g4050011	BLASTN	560	3e-18	66	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
6691	GM_120_A1_F04_MR	g547683	BLASTX	660	4e-64	94	HEAT SHOCK COGNATE PROTEIN 80 gi 170456 (M96549) heat shock cognate protein 80 [Solanum lycopersicum] gi 445601 prf 1909348A heat shock protein hsp80 [Lycopersicon esculentum]
6692	GM_120_A1_F06_MR	g18559	BLASTN	875	1e-32	75	G.max gene for catalase
6693	GM_120_A1_F08_T7	g100484	BLASTX	379	2e-33	54	hypothetical protein - garden snapdragon
6694	GM_120_A1_F09_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6695	GM_120_A1_F09_T7	g507910	BLASTN	342	7e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6696	GM_120_A1_G01_T7	g1769898	BLASTX	316	7e-27	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6697	GM_120_A1_G03_T7	g3097320	BLASTN	619	5e-21	78	Glycine max gene for Bd 30K, complete cds
6698	GM_120_A1_G04_T7	g18559	BLASTN	1147	5e-45	76	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6699	GM_120_A1_G05_MR	g226407	BLASTX	161	7e-15	44	retrotransposon del1-46 [Lilium henryi]
6700	GM_120_A1_G09_MR	g2832304	BLASTX	299	9e-26	46	(AF044489) receptor-like protein kinase [Oryza sativa]
6701	GM_120_A1_G10_T7	g1419129	BLASTX	171	3e-12	72	(Z75517) reverse transcriptase [Oryza sativa]
6702	GM_120_A1_G12_MR	g3645899	BLASTX	208	1e-16	48	(U68408) 5' end not determined experimentally [Zea mays]
6703	GM_120_A1_H01_T7	g2522228	BLASTX	460	8e-43	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
6704	GM_120_A1_H07_T7	g4063760	BLASTX	208	1e-14	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6705	GM_120_A1_H10_MR	g3810596	BLASTX	182	4e-12	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
6706	GM_120_A2_A02_MR	g507910	BLASTN	556	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
6707	GM_120_A2_A05_MR	g417073	BLASTX	607	8e-57	90	GLUTAMATE SYNTHASE (NADH) PRECURSOR (NADH-GOGAT) gi 484529 pir JQ1977 glutamate synthase (NADH) (EC 1.4.1.14) - alfalfa gi 166412 (L01660) NADH-glutamate synthase [Medicago sativa]
6708	GM_120_A2_B03_MR	g4115382	BLASTX	164	4e-11	35	(AC005967) hypothetical protein [Arabidopsis thaliana]
6709	GM_120_A2_B08_MR	g3426334	BLASTN	530	6e-17	63	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
6710	GM_120_A2_B12_MR	g3237327	BLASTX	356	7e-32	60	(AF030260) CYP94A1 [Vicia sativa]
6711	GM_120_A2_C07_MR	g18559	BLASTN	767	9e-28	72	G.max gene for catalase
6712	GM_120_A2_D12_MR	g1769897	BLASTX	237	2e-18	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6713	GM_120_A2_E03_MR	g18559	BLASTN	361	3e-09	65	G.max gene for catalase
6714	GM_120_A2_E05_MR	g3645899	BLASTX	372	2e-32	58	(U68408) 5' end not determined experimentally [Zea mays]
6715	GM_120_A2_E09_MR	g3810595	BLASTX	303	9e-25	46	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
6716	GM_120_A2_F04_MR	g3777527	BLASTX	691	3e-67	95	(AF053008) gag-pol polyprotein [Glycine max]
6717	GM_120_A2_G06_MR	g4092471	BLASTN	513	4e-16	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
6718	GM_120_A2_G08_MR	g4050011	BLASTN	535	4e-17	64	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
6719	GM_120_A2_G12_MR	g3047085	BLASTX	186	3e-13	55	(AF058914) No definition line found [Arabidopsis thaliana]
6720	GM_120_A2_H07_MR	g3930515	BLASTX	108	2e-11	47	(AF059674) putative gag protein [Nicotiana tabacum]
6721	GM_120_B2_A11_T7	g1142703	BLASTN	286	3e-16	76	Glycine max satellite STR120-B.1.
6722	GM_120_B2_C11_T7	g2244749	BLASTX	216	3e-16	76	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
6723	GM_120_B2_D02_T7	g4063760	BLASTX	251	3e-19	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6724	GM_120_B2_D12_T7	g3377855	BLASTX	305	2e-26	71	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
6725	GM_120_B2_E04_T7	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
6726	GM_120_B2_F12_T7	g3283435	BLASTX	155	5e-16	61	(AF069495) cytochrome P450 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6727	GM_120_B2_G08_T7	g18559	BLASTN	408	2e-11	72	G.max gene for catalase
6728	GM_120_B2_H04_T7	g531389	BLASTX	214	3e-15	54	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
6729	GM_121_A1_A06_MR	g4140712	BLASTX	160	4e-11	64	(AF110183) putative integrase [Oryza sativa]
6730	GM_121_A1_A06_T7	g3097320	BLASTN	464	6e-14	68	Glycine max gene for Bd 30K, complete cds
6731	GM_121_A1_A09_MR	g4063760	BLASTX	145	2e-16	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6732	GM_121_A1_A10_MR	g3777527	BLASTX	204	3e-14	86	(AF053008) gag-pol polyprotein [Glycine max]
6733	GM_121_A1_B03_T7	g2522227	BLASTX	218	3e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
6734	GM_121_A1_B09_T7	g3176791	BLASTN	342	3e-09	62	Homo sapiens allele 11 fragile site locus (FRA10B) minisatellite, 5' sequence
6735	GM_121_A1_C02_T7	g1769897	BLASTX	198	3e-14	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6736	GM_121_A1_C03_MR	g3128168	BLASTX	156	7e-10	61	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]
6737	GM_121_A1_C08_MR	g2995405	BLASTX	192	6e-21	47	(Y12432) polyprotein [Ananas comosus]
6738	GM_121_A1_D02_T7	g507910	BLASTN	491	1e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
6739	GM_121_A1_D07_T7	g4063760	BLASTX	311	1e-25	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6740	GM_121_A1_D08_MR	g18559	BLASTN	705	6e-25	71	G.max gene for catalase
6741	GM_121_A1_E06_MR	g3319362	BLASTX	199	7e-14	51	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
6742	GM_121_A1_F02_T7	g1666236	BLASTX	202	3e-15	31	(U76261) unknown [Hordeum vulgare]
6743	GM_121_A1_F12_T7	g3097320	BLASTN	474	2e-14	69	Glycine max gene for Bd 30K, complete cds
6744	GM_121_A1_G01_T7	g3763850	BLASTN	395	7e-11	77	Glycine max GmENOD93 gene for early nodulin, complete cds
6745	GM_121_A1_G05_MR	g507910	BLASTN	468	1e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6746	GM_121_A1_G05_T7	g4063760	BLASTX	196	2e-13	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6747	GM_121_A1_G10_MR	g3142379	BLASTX	199	1e-14	77	(AF053008) envelope-like [Glycine max]
6748	GM_121_A1_H07_MR	g2407790	BLASTX	131	2e-13	50	(AF019910) grr1 [Glycine max]
6749	GM_121_A2_A01_T7	g1769897	BLASTX	101	2e-14	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6750	GM_121_A2_A05_MR	g531389	BLASTX	180	1e-11	34	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
6751	GM_121_A2_A08_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6752	GM_121_A2_A11_T7	g2494111	BLASTX	170	1e-10	80	(AC002376) Contains similarity to Glycine protein kinase 6 (gb M67449). [Arabidopsis thaliana]
6753	GM_121_A2_B01_MR	g2443320	BLASTX	315	5e-26	56	(D85597) polyprotein [Oryza australiensis]
6754	GM_121_A2_B02_T7	g18559	BLASTN	622	4e-21	71	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6755	GM_121_A2_B04_MR	g4063760	BLASTX	202	4e-14	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6756	GM_121_A2_B07_T7	g1769898	BLASTX	336	5e-29	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6757	GM_121_A2_B10_T7	g1769899	BLASTX	167	8e-12	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6758	GM_121_A2_C01_MR	g4165194	BLASTX	228	7e-17	41	(AJ009736) Pol protein [Drosophila melanogaster]
6759	GM_121_A2_C02_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6760	GM_121_A2_C02_T7	g507910	BLASTN	410	6e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6761	GM_121_A2_C03_MR	g2129618	BLASTX	208	7e-15	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6762	GM_121_A2_C05_MR	g538067	BLASTX	166	4e-10	34	(M77661) putative pol polyprotein [Magnaporthe grisea]
6763	GM_121_A2_C07_T7	g18559	BLASTN	523	1e-16	67	G.max gene for catalase
6764	GM_121_A2_C10_T7	g4063756	BLASTN	532	5e-17	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
6765	GM_121_A2_C11_MR	g3142328	BLASTN	581	3e-19	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6766	GM_121_A2_D04_MR	g3142328	BLASTN	833	9e-31	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6767	GM_121_A2_D05_T7	g508826	BLASTN	405	3e-11	64	Drosophila melanogaster Oregon-R mitochondrial A+T region.
6768	GM_121_A2_D10_T7	g2130150	BLASTX	358	5e-34	62	hypothetical protein 137 - maize chloroplast gi 902263 gnl PID e225682 (X86563) ORF137 [Zea mays] gi 902308 gnl PID e225686 (X86563) ORF137 [Zea mays]
6769	GM_121_A2_D12_T7	g18559	BLASTN	446	5e-26	65	G.max gene for catalase
6770	GM_121_A2_E02_T7	g2443320	BLASTX	395	1e-34	52	(D85597) polyprotein [Oryza australiensis]
6771	GM_121_A2_E05_T7	g2244802	BLASTX	292	2e-23	47	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
6772	GM_121_A2_E08_MR	g3695395	BLASTX	194	1e-13	45	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
6773	GM_121_A2_E11_MR	g4063760	BLASTX	253	2e-19	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6774	GM_121_A2_E12_MR	g531389	BLASTX	161	2e-18	51	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
6775	GM_121_A2_F06_T7	g4063760	BLASTX	489	1e-44	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6776	GM_121_A2_G04_MR	g3142328	BLASTN	604	2e-20	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6777	GM_121_A2_G10_MR	g4105800	BLASTX	109	4e-10	47	(AF049931) PGP301 [Petunia x hybrida]
6778	GM_121_A2_G11_T7	g469153	BLASTN	381	3e-10	68	P.sativum (Birte) Lox1:Ps:2 gene.
6779	GM_121_A2_H01_MR	g3097320	BLASTN	503	1e-15	63	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6780	GM_121_A2_H09_T7	g2129618	BLASTX	201	4e-14	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6781	GM_121_B2_B06_MR	g507910	BLASTN	485	3e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
6782	GM_121_B2_C09_MR	g2980777	BLASTX	189	7e-15	54	(AL022198) putative protein [Arabidopsis thaliana]
6783	GM_121_B2_D03_MR	g2995405	BLASTX	272	9e-26	57	(Y12432) polyprotein [Ananas comosus]
6784	GM_121_B2_D07_MR	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6785	GM_121_B2_E05_MR	g507910	BLASTN	620	2e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
6786	GM_121_B2_E09_MR	g99922	BLASTX	265	3e-22	60	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
6787	GM_121_B2_F12_MR	g3777527	BLASTX	358	1e-30	89	(AF053008) gag-pol polyprotein [Glycine max]
6788	GM_121_B2_G02_MR	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
6789	GM_121_B2_G03_MR	g905361	BLASTX	419	3e-38	93	(U22103) gag-protease polyprotein [Glycine max]
6790	GM_121_B2_G09_MR	g3395421	BLASTN	491	4e-15	68	Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, complete sequence [Arabidopsis thaliana]
6791	GM_121_B2_H02_MR	g3142328	BLASTN	1323	5e-53	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6792	GM_121_B2_H05_MR	g408791	BLASTN	356	3e-09	83	Glycine soja chloroplast omega-3 fatty acid desaturase (Fadd) mRNA, complete cds.
6793	GM_121_B2_H07_MR	g2997694	BLASTX	139	6e-11	35	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
6794	GM_121_B2_H08_MR	g507910	BLASTN	350	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6795	GM_122_A1_A03_MR	g100484	BLASTX	96	5e-12	39	hypothetical protein - garden snapdragon
6796	GM_122_A1_A05_T7	g507910	BLASTN	527	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
6797	GM_122_A1_B05_T7	g4038056	BLASTX	244	9e-19	48	(AC005897) putative transposon [Arabidopsis thaliana]
6798	GM_122_A1_C03_MR	g507910	BLASTN	428	1e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
6799	GM_122_A1_C03_T7	g3142379	BLASTX	349	1e-42	77	(AF053008) envelope-like [Glycine max]
6800	GM_122_A1_C04_MR	g3127892	BLASTX	240	1e-19	74	(AJ006025) acyl-coA synthetase [Cicer arietinum]
6801	GM_122_A1_C07_MR	g3176791	BLASTN	376	9e-11	65	Homo sapiens allele 11 fragile site locus (FRA10B) minisatellite, 5' sequence
6802	GM_122_A1_D03_T7	g507910	BLASTN	510	2e-16	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6803	GM_122_A1_E04_MR	g3777527	BLASTX	196	2e-13	40	(AF053008) gag-pol polyprotein [Glycine max]
6804	GM_122_A1_E07_T7	g3645899	BLASTX	141	2e-11	61	(U68408) 5' end not determined experimentally [Zea mays]
6805	GM_122_A1_F01_MR	g3142379	BLASTX	208	1e-15	54	(AF053008) envelope-like [Glycine max]
6806	GM_122_A1_F03_T7	g3142328	BLASTN	875	1e-32	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6807	GM_122_A1_G03_MR	g2429543	BLASTX	200	6e-19	41	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]
6808	GM_122_A1_G04_T7	g2129618	BLASTX	148	3e-10	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6809	GM_122_A1_H01_T7	g3142328	BLASTN	605	2e-20	69	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6810	GM_122_A2_A02_MR	g3142328	BLASTN	463	6e-14	68	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6811	GM_122_A2_A03_MR	g3243214	BLASTN	359	3e-09	64	Arabidopsis thaliana BAC T19B17 from chromsome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]
6812	GM_122_A2_A03_T7	g4063760	BLASTX	199	9e-14	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6813	GM_122_A2_A04_MR	g336279	BLASTN	413	1e-11	69	Apis mellifera ligustica complete mitochondrial genome
6814	GM_122_A2_A08_T7	g507910	BLASTN	478	5e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
6815	GM_122_A2_A09_T7	g2462748	BLASTX	187	3e-13	84	(AC002292) putative Clathrin Coat Assembly protein [Arabidopsis thaliana]
6816	GM_122_A2_B04_MR	g99729	BLASTX	273	5e-23	45	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
6817	GM_122_A2_B12_MR	g507910	BLASTN	654	6e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
6818	GM_122_A2_C02_MR	g507910	BLASTN	449	1e-13	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6819	GM_122_A2_C02_T7	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
6820	GM_122_A2_C04_T7	g507910	BLASTN	557	1e-18	82	Glycine max BSR-101 satellite SB92 genomic sequence.
6821	GM_122_A2_C07_MR	g3097320	BLASTN	471	3e-14	68	Glycine max gene for Bd 30K, complete cds
6822	GM_122_A2_C08_MR	g1217971	BLASTN	368	1e-09	66	P.tetraurelia gamma1-51D immobilisation antigen gene, 3' coding and non-coding region
6823	GM_122_A2_C09_MR	g3930515	BLASTX	149	5e-09	33	(AF059674) putative gag protein [Nicotiana tabacum]
6824	GM_122_A2_C12_MR	g507910	BLASTN	665	2e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
6825	GM_122_A2_C12_T7	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
6826	GM_122_A2_D03_MR	g2815519	BLASTN	380	4e-10	67	Arabidopsis thaliana BAC T5J8 from chromosome IV, top arm, complete sequence [Arabidopsis thaliana]
6827	GM_122_A2_D07_T7	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6828	GM_122_A2_D10_MR	g3367517	BLASTX	233	5e-18	51	(AC004392) Similar to F4I1.26 putative beta-glucosidase gi 3128187 from A. thaliana BAC gb AC004521. ESTs gb N97083, gb F19868 and gb F15482 come from this gene. [Arabidopsis thaliana]

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6829	GM_122_A2_E01_T7	g18559	BLASTN	487	5e-15	76	G.max gene for catalase
6830	GM_122_A2_E05_T7	g4063760	BLASTX	153	7e-09	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6831	GM_122_A2_E08_MR	g3287695	BLASTX	227	6e-17	52	(AC003979) Similar to hypothetical protein C34B7.2 gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis thaliana]
6832	GM_122_A2_E09_T7	g1769897	BLASTX	288	6e-24	72	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6833	GM_122_A2_F01_T7	g2160694	BLASTX	375	8e-34	97	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
6834	GM_122_A2_F02_MR	g3142328	BLASTN	523	9e-34	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6835	GM_122_A2_F04_MR	g3777527	BLASTX	246	1e-18	43	(AF053008) gag-pol polyprotein [Glycine max]
6836	GM_122_A2_F08_MR	g4063760	BLASTX	178	2e-11	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6837	GM_122_A2_F08_T7	g507910	BLASTN	517	9e-17	84	Glycine max BSR-101 satellite SB92 genomic sequence.
6838	GM_122_A2_F09_MR	g1142614	BLASTX	223	1e-17	88	(U17250) ubiquitin conjugating enzyme, E2 [Brassica oleracea]
6839	GM_122_A2_F10_T7	g1813979	BLASTX	126	5e-12	74	(Y10860) hypothetical protein [Musa acuminata]
6840	GM_122_A2_F11_MR	g3402749	BLASTX	145	1e-09	47	(AL031187) putative protein [Arabidopsis thaliana]
6841	GM_122_A2_F12_MR	g3645899	BLASTX	237	1e-23	54	(U68408) 5' end not determined experimentally [Zea mays]
6842	GM_122_A2_G03_MR	g3421038	BLASTN	421	6e-12	64	Human DNA sequence from clone 35C21 on chromosome 1q23-24. Contains STSs, complete sequence [Homo sapiens]
6843	GM_122_A2_G05_MR	g4115365	BLASTX	169	2e-10	32	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
6844	GM_122_A2_G05_T7	g3777527	BLASTX	408	7e-36	94	(AF053008) gag-pol polyprotein [Glycine max]
6845	GM_122_A2_G10_T7	g4063760	BLASTX	188	3e-13	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6846	GM_122_A2_G11_MR	g2522228	BLASTX	280	9e-24	79	(AB007466) reverse transcriptase-like protein [Vicia faba]
6847	GM_122_A2_H03_T7	g3687234	BLASTX	166	3e-10	49	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
6848	GM_122_A2_H06_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6849	GM_122_A2_H06_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6850	GM_122_A2_H07_MR	g1769899	BLASTX	262	7e-22	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6851	GM_122_A2_H11_MR	g4063756	BLASTN	464	6e-14	72	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
6852	GM_122_B2_A01_T7	g4063760	BLASTX	417	5e-37	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6853	GM_122_B2_A04_MR	g1769898	BLASTX	419	3e-38	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6854	GM_122_B2_A05_T7	g4006867	BLASTX	363	2e-31	63	(Z99707) putative protein [Arabidopsis thaliana]
6855	GM_122_B2_B03_MR	g343595	BLASTN	343	7e-09	62	T.brucei kinetoplast cytochrome c oxidase III (COIII) gene, complete cds.
6856	GM_122_B2_B05_T7	g3777527	BLASTX	651	8e-62	96	(AF053008) gag-pol polyprotein [Glycine max]
6857	GM_122_B2_B09_MR	g4063760	BLASTX	488	1e-44	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6858	GM_122_B2_C04_MR	g4063760	BLASTX	411	2e-36	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6859	GM_122_B2_C04_T7	g4063760	BLASTX	478	2e-43	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6860	GM_122_B2_C08_MR	g4063760	BLASTX	257	6e-20	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6861	GM_122_B2_C08_T7	g507910	BLASTN	497	7e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
6862	GM_122_B2_C09_MR	g3869068	BLASTN	360	2e-16	71	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDC16, complete sequence [Arabidopsis thaliana]
6863	GM_122_B2_C12_MR	g2865424	BLASTX	221	5e-16	53	(AF039371) polyprotein [Arabidopsis thaliana]
6864	GM_122_B2_D01_MR	g2443320	BLASTX	105	1e-11	42	(D85597) polyprotein [Oryza australiensis]
6865	GM_122_B2_D01_T7	g18559	BLASTN	354	4e-12	72	G.max gene for catalase
6866	GM_122_B2_D06_MR	g226407	BLASTX	303	9e-25	44	retrotransposon del1-46 [Lilium henryi]
6867	GM_122_B2_D06_T7	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6868	GM_122_B2_D10_MR	g343344	BLASTN	464	4e-18	81	Soybean chloroplast 16S rRNA (3' end), 18S rRNA (5' end), Ile-tRNA, and Ala-tRNA genes.
6869	GM_122_B2_E06_MR	g629693	BLASTX	277	1e-32	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
6870	GM_122_B2_E08_T7	g507910	BLASTN	565	6e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
6871	GM_122_B2_E10_MR	g3097320	BLASTN	374	7e-10	71	Glycine max gene for Bd 30K, complete cds
6872	GM_122_B2_E12_T7	g1022917	BLASTN	371	2e-10	63	Trypanosoma cruzi kinetoplast minicircle ATPase subunit 6 mRNA, complete cds.
6873	GM_122_B2_F01_MR	g507910	BLASTN	433	6e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
6874	GM_122_B2_F03_MR	g4106408	BLASTN	733	6e-27	68	Oryza sativa subsp. indica dispersed centromeric repeat family RCS1
6875	GM_122_B2_F04_T7	g3645899	BLASTX	318	2e-26	49	(U68408) 5' end not determined experimentally [Zea mays]
6876	GM_122_B2_F05_MR	g507910	BLASTN	358	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6877	GM_122_B2_F05_T7	g507910	BLASTN	365	7e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
6878	GM_122_B2_F09_T7	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
6879	GM_122_B2_F10_MR	g3777527	BLASTX	324	4e-28	67	(AF053008) gag-pol polyprotein [Glycine max]
6880	GM_122_B2_G01_T7	g2443320	BLASTX	225	2e-29	54	(D85597) polyprotein [Oryza australiensis]
6881	GM_122_B2_G08_MR	g1361985	BLASTX	172	5e-11	33	disease resistance protein RPM1 - Arabidopsis thaliana gi 963017 (X87851) disease resistance gene; pid:e183919 [Arabidopsis thaliana]
6882	GM_122_B2_G09_T7	g3142379	BLASTX	343	2e-30	69	(AF053008) envelope-like [Glycine max]
6883	GM_122_B2_G11_MR	g3645899	BLASTX	191	6e-13	38	(U68408) 5' end not determined experimentally [Zea mays]
6884	GM_122_B2_H02_T7	g3810584	BLASTN	442	6e-13	61	Arabidopsis thaliana chromosome II BAC T6B13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6885	GM_122_B2_H03_T7	g2129618	BLASTX	223	2e-16	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6886	GM_122_B2_H06_MR	g3142328	BLASTN	1160	1e-45	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6887	GM_122_B2_H08_T7	g984307	BLASTN	1251	9e-55	90	Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precurso...
6888	GM_123_A1_A03_MR	g1843462	BLASTX	204	3e-15	37	(L10211) isoliquiritigenin 2'-O-methyltransferase [Medicago sativa]
6889	GM_123_A1_A05_T7	g2129618	BLASTX	220	4e-16	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6890	GM_123_A1_B05_T7	g3097320	BLASTN	554	5e-18	74	Glycine max gene for Bd 30K, complete cds
6891	GM_123_A1_B10_T7	g3319362	BLASTX	268	3e-21	49	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
6892	GM_123_A1_C02_MR	g3193290	BLASTX	197	1e-23	47	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabido...
6893	GM_123_A1_C04_T7	g4063760	BLASTX	354	3e-30	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6894	GM_123_A1_C05_MR	g3859610	BLASTN	398	6e-11	66	Arabidopsis thaliana BAC T9E19
6895	GM_123_A1_C06_T7	g100484	BLASTX	356	6e-31	60	hypothetical protein - garden snapdragon
6896	GM_123_A1_C09_T7	g3097320	BLASTN	631	1e-21	75	Glycine max gene for Bd 30K, complete cds
6897	GM_123_A1_D03_MR	g133917	BLASTX	271	8e-23	92	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 gi 70856 pir R3NT2 ribosomal protein S2 - common tobacco chloroplast gi 11814 (Z00044) ribosomal protein S2 [Nicotiana tabacum] gi 225274 prf 1211235J ribosomal protein S2 [Nicotiana tabacum]
6898	GM_123_A1_D03_T7	g12212	BLASTN	1099	2e-48	93	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
6899	GM_123_A1_D04_MR	g461736	BLASTX	128	4e-22	89	MITOCHONDRIAL CHAPERONIN HSP60-2 PRECURSOR gi 478786 pir S29316 chaperonin 60 - cucurbit gi 12546 gnl PID e1188586 (X70868) chaperonin 60 [Cucurbita sp.]
6900	GM_123_A1_D06_T7	g2618688	BLASTX	161	6e-11	96	(AC002510) putative esterase D [Arabidopsis thaliana]
6901	GM_123_A1_D07_MR	g3930515	BLASTX	106	5e-09	37	(AF059674) putative gag protein [Nicotiana tabacum]
6902	GM_123_A1_D09_T7	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
6903	GM_123_A1_D10_T7	g3461813	BLASTX	111	9e-12	64	(AC004138) putative sucrose/H+ symporter [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6904	GM_123_A1_E04_MR	g507910	BLASTN	377	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
6905	GM_123_A1_E04_T7	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
6906	GM_123_A1_E07_T7	g3859610	BLASTN	580	4e-19	65	Arabidopsis thaliana BAC T9E19
6907	GM_123_A1_E09_MR	g4115365	BLASTX	158	2e-09	32	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
6908	GM_123_A1_E10_MR	g2995405	BLASTX	309	6e-34	61	(Y12432) polyprotein [Ananas comosus]
6909	GM_123_A1_E11_MR	g507910	BLASTN	378	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
6910	GM_123_A1_F10_MR	g4063760	BLASTX	252	2e-19	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6911	GM_123_A1_G01_T7	g1171978	BLASTX	461	6e-43	81	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) gi 304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] gi 2911051 gnl PID e1253339 (AL021961) poly(A)-binding protein [Arabidopsis thaliana]
6912	GM_123_A1_G02_MR	g99726	BLASTX	122	1e-16	31	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976) orf 3 [Arabidopsis thaliana]
6913	GM_123_A1_G04_T7	g2864621	BLASTX	152	2e-09	46	hypothetical protein [Arabidopsis thaliana]
6914	GM_123_A1_G11_MR	g4115365	BLASTX	318	2e-26	55	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
6915	GM_123_A1_H03_T7	g4063756	BLASTN	456	1e-13	69	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
6916	GM_123_A1_H04_MR	g1769898	BLASTX	482	3e-45	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6917	GM_123_A1_H05_T7	g4063760	BLASTX	159	2e-09	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6918	GM_123_A1_H08_MR	g2522230	BLASTX	233	9e-19	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
6919	GM_123_A1_H08_T7	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
6920	GM_123_A1_H10_MR	g3142328	BLASTN	419	6e-12	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6921	GM_123_A1_H11_MR	g99922	BLASTX	168	2e-11	35	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
6922	GM_123_A1_H12_MR	g507910	BLASTN	591	4e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
6923	GM_123_A2_A04_MR	g2129618	BLASTX	190	6e-13	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6924	GM_123_A2_A12_T7	g3142328	BLASTN	410	1e-11	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6925	GM_123_A2_B08_T7	g1666236	BLASTX	157	3e-10	32	(U76261) unknown [Hordeum vulgare]
6926	GM_123_A2_B09_MR	g170080	BLASTN	487	5e-15	70	Soybean seed lectin gene transposable element tgm1.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6927	GM_123_A2_B12_T7	g2121303	BLASTN	457	1e-13	65	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
6928	GM_123_A2_C04_MR	g3695395	BLASTX	204	1e-14	39	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
6929	GM_123_A2_C04_T7	g1769896	BLASTN	486	5e-15	66	A.thaliana lectin receptor kinase gene
6930	GM_123_A2_D04_MR	g4063760	BLASTX	189	9e-13	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6931	GM_123_A2_D10_T7	g507910	BLASTN	339	1e-08	68	Glycine max BSR-101 satellite SB92 genomic sequence.
6932	GM_123_A2_E03_MR	g3650039	BLASTX	224	8e-17	34	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
6933	GM_123_A2_E04_MR	g2522228	BLASTX	170	2e-11	65	(AB007466) reverse transcriptase-like protein [Vicia faba]
6934	GM_123_A2_E07_T7	g18559	BLASTN	649	2e-22	72	G.max gene for catalase
6935	GM_123_A2_F01_MR	g3142328	BLASTN	681	7e-24	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6936	GM_123_A2_F02_MR	g2997694	BLASTX	206	6e-26	45	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
6937	GM_123_A2_F05_T7	g4063760	BLASTX	124	5e-11	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6938	GM_123_A2_F09_T7	g2129618	BLASTX	208	7e-15	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
6939	GM_123_A2_F10_MR	g4038056	BLASTX	115	5e-13	47	(AC005897) putative transposon [Arabidopsis thaliana]
6940	GM_123_A2_G01_T7	g3650039	BLASTX	215	8e-16	57	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
6941	GM_123_A2_G09_MR	g507910	BLASTN	621	2e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
6942	GM_123_A2_H01_MR	g18768	BLASTN	428	5e-13	67	Soybean Tgm6 transposable element 3' end
6943	GM_123_A2_H04_T7	g1684913	BLASTX	188	1e-12	40	(U77888) receptor-like protein kinase [Ipomoea nil]
6944	GM_123_A2_H07_T7	g2443320	BLASTX	271	2e-21	43	(D85597) polyprotein [Oryza australiensis]
6945	GM_123_A2_H08_MR	g4092470	BLASTN	379	4e-10	62	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
6946	GM_123_A2_H08_T7	g3097320	BLASTN	360	3e-09	63	Glycine max gene for Bd 30K, complete cds
6947	GM_123_A2_H10_MR	g4140712	BLASTX	235	5e-19	49	(AF110183) putative integrase [Oryza sativa]
6948	GM_123_A2_H11_MR	g100484	BLASTX	248	2e-19	51	hypothetical protein - garden snapdragon
6949	GM_123_B1_A02_T7	g4063760	BLASTX	169	1e-10	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6950	GM_123_B1_A08_MR	g507910	BLASTN	615	4e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
6951	GM_123_B1_A12_MR	g3097320	BLASTN	433	1e-12	76	Glycine max gene for Bd 30K, complete cds
6952	GM_123_B1_B03_MR	g4063760	BLASTX	247	7e-19	75	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6953	GM_123_B1_B03_T7	g4063760	BLASTX	161	1e-09	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6954	GM_123_B1_B11_MR	g3142328	BLASTN	832	1e-30	98	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
6955	GM_123_B1_B11_T7	g2244747	BLASTN	349	1e-08	71	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 0
6956	GM_123_B1_C06_MR	g2642431	BLASTX	189	1e-12	58	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
6957	GM_123_B1_E02_T7	g478148	BLASTX	337	7e-30	91	reverse transcriptase (copia-like retrotransposon) - soybean (fragment) >gi 169949 (M94493) reverse transcriptase [Glycine max]
6958	GM_123_B1_E04_T7	g507910	BLASTN	355	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
6959	GM_123_B1_E06_MR	g507910	BLASTN	482	4e-15	80	Glycine max BSR-101 satellite SB92 genomic sequence.
6960	GM_123_B1_E10_MR	g4063760	BLASTX	230	5e-17	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6961	GM_123_B1_F10_T7	g3097320	BLASTN	447	3e-13	73	Glycine max gene for Bd 30K, complete cds
6962	GM_123_B1_G01_T7	g4092470	BLASTN	440	8e-13	73	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
6963	GM_123_B1_G06_T7	g905361	BLASTX	352	9e-31	94	(U22103) gag-protease polyprotein [Glycine max]
6964	GM_123_B1_G07_T7	g217993	BLASTX	149	6e-10	55	(D12849) reverse transcriptase [Pinus thunbergiana]
6965	GM_123_B1_G12_T7	g507910	BLASTN	443	2e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
6966	GM_123_B1_H03_T7	g3142379	BLASTX	210	1e-15	59	(AF053008) envelope-like [Glycine max]
6967	GM_123_B1_H08_T7	g4063760	BLASTX	234	2e-17	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6968	GM_123_B1_H11_T7	g1769899	BLASTX	212	1e-16	69	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6969	GM_123_B2_A03_T7	g2769655	BLASTN	379	4e-10	64	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
6970	GM_123_B2_A04_T7	g3091216	BLASTX	362	2e-32	57	(AF060192) putative resistance protein [Glycine max]
6971	GM_123_B2_A08_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6972	GM_123_B2_B01_T7	g3176799	BLASTN	353	1e-09	62	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite sequence
6973	GM_123_B2_B03_T7	g170029	BLASTN	407	2e-11	81	Glycine max cv. Dare nodulin 26 gene fragment.
6974	GM_123_B2_B06_T7	g1769898	BLASTX	145	9e-13	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
6975	GM_123_B2_B07_T7	g2522227	BLASTX	223	9e-18	56	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
6976	GM_123_B2_B12_T7	g1171591	BLASTN	356	5e-09	60	P.falciparum complete gene map of plastid-like DNA (IR-B)
6977	GM_123_B2_C01_T7	g3097320	BLASTN	1110	3e-43	80	Glycine max gene for Bd 30K, complete cds
6978	GM_123_B2_C05_T7	g4063760	BLASTX	451	1e-40	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
6979	GM_123_B2_C09_T7	g3097320	BLASTN	430	2e-12	72	Glycine max gene for Bd 30K, complete cds
6980	GM_123_B2_D01_T7	g170029	BLASTN	1714	1e-70	97	Glycine max cv. Dare nodulin 26 gene fragment.
6981	GM_123_B2_D06_T7	g2827715	BLASTX	331	6e-28	78	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
6982	GM_123_B2_D10_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
6983	GM_123_B2_E04_T7	g4063760	BLASTX	170	1e-10	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6984	GM_123_B2_E09_T7	g4115370	BLASTN	393	1e-10	66	Arabidopsis thaliana chromosome II BAC F27D4 genomic sequence, complete sequence [Arabidopsis thaliana]
6985	GM_123_B2_F01_MR	g1658457	BLASTX	155	2e-12	64	(U75248) reverse transcriptase [Gossypium barbadense]
6986	GM_123_B2_F05_T7	g4038056	BLASTX	189	8e-13	42	(AC005897) putative transposon [Arabidopsis thaliana]
6987	GM_123_B2_F08_T7	g3171875	BLASTN	432	2e-12	63	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.1...
6988	GM_123_B2_G02_T7	g170029	BLASTN	434	1e-12	84	Glycine max cv. Dare nodulin 26 gene fragment.
6989	GM_123_B2_G06_T7	g2244877	BLASTX	227	3e-18	52	(Z97338) hypothetical protein [Arabidopsis thaliana]
6990	GM_123_B2_H03_T7	g3513747	BLASTX	364	4e-31	47	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
6991	GM_123_B2_H09_T7	g507910	BLASTN	571	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
6992	GM_124_A1_A04_T7	g2522228	BLASTX	154	1e-09	29	(AB007466) reverse transcriptase-like protein [Vicia faba]
6993	GM_124_A1_A05_MR	g3319351	BLASTX	278	4e-22	37	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
6994	GM_124_A1_A07_MR	g4063760	BLASTX	157	3e-09	36	(AC005561) putative POL3 protein [Arabidopsis thaliana]
6995	GM_124_A1_A08_T7	g2522230	BLASTX	218	3e-17	36	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
6996	GM_124_A1_A11_T7	g1055224	BLASTX	151	4e-10	43	(U20977) cellular nucleic acid binding protein [Xenopus laevis]
6997	GM_124_A1_B01_MR	g3258568	BLASTX	199	4e-14	45	(U89959) Unknown protein [Arabidopsis thaliana]
6998	GM_124_A1_B01_T7	g509768	BLASTN	438	6e-13	68	Glycine max seed-specific low molecular weight sulfur-rich protein.
6999	GM_124_A1_B03_MR	g2982452	BLASTX	564	5e-53	72	(AL022223) receptor protein kinase - like protein [Arabidopsis thaliana]
7000	GM_124_A1_B05_MR	g3599418	BLASTN	375	6e-10	70	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7001	GM_124_A1_B06_MR	g505129	BLASTN	386	2e-10	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
7002	GM_124_A1_B06_T7	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7003	GM_124_A1_B07_MR	g343755	BLASTN	339	6e-09	60	yeast (s.cerevisiae) mitochondrial atpase proteolipid (subunit 9) gene, 5' end.
7004	GM_124_A1_B11_T7	g2522228	BLASTX	386	5e-35	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
7005	GM_124_A1_C03_T7	g4019231	BLASTN	487	6e-15	64	Ateline herpesvirus 3 complete genome
7006	GM_124_A1_C06_T7	g2764526	BLASTN	629	2e-21	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
7007	GM_124_A1_C07_MR	g13596	BLASTN	332	7e-09	66	Yeast mit DNA for promoter upstream of tRNA-Leu gene 3 *Source:
7008	GM_124_A1_C09_T7	g507910	BLASTN	369	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7009	GM_124_A1_C11_MR	g2315737	BLASTN	368	1e-09	63	Caenorhabditis elegans cosmid R12A1
7010	GM_124_A1_C11_T7	g505129	BLASTN	291	2e-09	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
7011	GM_124_A1_C12_T7	g507910	BLASTN	702	4e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
7012	GM_124_A1_D01_T7	g2764732	BLASTX	209	2e-15	81	(AJ002490) ndhB [Arabidopsis thaliana]
7013	GM_124_A1_D02_MR	g4063760	BLASTX	332	6e-28	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7014	GM_124_A1_D02_T7	g4063760	BLASTX	292	1e-23	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7015	GM_124_A1_D04_MR	g18559	BLASTN	375	6e-10	68	G.max gene for catalase
7016	GM_124_A1_D06_MR	g2367675	BLASTX	274	8e-22	43	(AF017040) Pol [Dictyostelium discoideum]
7017	GM_124_A1_D07_MR	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7018	GM_124_A1_D08_T7	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
7019	GM_124_A1_E04_T7	g396249	BLASTN	282	6e-09	72	S.douglasii mitochondrial ATP subunit 9 gene, complete CDS
7020	GM_124_A1_E05_T7	g4063760	BLASTX	524	2e-48	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7021	GM_124_A1_E08_T7	g115471	BLASTX	180	9e-13	89	CARBONIC ANHYDRASE, CHLOROPLAST PRECURSOR (CARBONATE DEHYDRATASE) gi 100078 pir S10200 carbonate dehydratase (EC 4.2.1.1) precursor - garden pea gi 20673 (X52558) precursor peptide (AA -104 to 224) [Pisum sativum]
7022	GM_124_A1_E09_MR	g507910	BLASTN	498	7e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
7023	GM_124_A1_E09_T7	g507910	BLASTN	556	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
7024	GM_124_A1_E11_T7	g3914002	BLASTX	187	8e-14	54	MITOCHONDRIAL LON PROTEASE HOMOLOG 1 PRECURSOR >gi 2935279 (AF033862) Lon protease [Arabidopsis thaliana]
7025	GM_124_A1_F02_MR	g1653718	BLASTX	127	5e-10	38	(D90916) hypothetical protein [Synechocystis sp.]
7026	GM_124_A1_F02_T7	g3132696	BLASTX	266	6e-23	94	(AF061962) SAR DNA-binding protein-1 [Pisum sativum]
7027	GM_124_A1_F03_MR	g505129	BLASTN	375	5e-10	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7028	GM_124_A1_F04_MR	g2130082	BLASTX	155	9e-22	60	protein kinase Xa21 (EC 2.7.1.-) - rice gi 1122443 (U37133) receptor kinase-like protein [Oryza sativa] gi 2586085 (U72723) receptor kinase-like protein [Oryza longistaminata] gi 1586408 prf 2203451A receptor kinase-like protein [Oryza sativa]
7029	GM_124_A1_F08_MR	g3273127	BLASTN	349	9e-09	65	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-54, complete sequence [Plasmodium falciparum]
7030	GM_124_A1_F08_T7	g905361	BLASTX	252	7e-20	41	(U22103) gag-protease polyprotein [Glycine max]
7031	GM_124_A1_F09_MR	g3142328	BLASTN	1903	1e-79	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7032	GM_124_A1_F11_MR	g126151	BLASTX	625	2e-60	96	LECTIN PRECURSOR (AGGLUTININ) (SBA) gi 282898 pir S27365 lectin precursor - soybean gi 170006 (K00821) lectin prepeptide [Glycine max]
7033	GM_124_A1_G01_MR	g441205	BLASTN	372	8e-10	72	Soybean lox1gm4 gene encoding lipxygenase L-4
7034	GM_124_A1_G03_MR	g4092471	BLASTN	446	4e-13	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
7035	GM_124_A1_G04_MR	g2443320	BLASTX	341	8e-29	47	(D85597) polyprotein [Oryza australiensis]
7036	GM_124_A1_G05_T7	g3319362	BLASTX	430	1e-38	57	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
7037	GM_124_A1_G08_MR	g905361	BLASTX	424	9e-39	95	(U22103) gag-protease polyprotein [Glycine max]
7038	GM_124_A1_G10_MR	g389029	BLASTN	346	6e-09	57	Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence.
7039	GM_124_A1_G12_MR	g2801676	BLASTN	439	1e-13	65	Glycine max telomere-associated sequence STAS5
7040	GM_124_A1_G12_T7	g3985931	BLASTN	495	2e-15	67	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]
7041	GM_124_A1_H04_MR	g3033393	BLASTX	231	1e-22	67	(AC004238) putative phosphatidylinositol-glycan-class C (PIGC) [Arabidopsis thaliana]
7042	GM_124_A1_H05_T7	g18559	BLASTN	553	5e-18	70	G.max gene for catalase
7043	GM_124_A1_H06_MR	g4063760	BLASTX	287	4e-23	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7044	GM_124_A1_H07_MR	g507910	BLASTN	389	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7045	GM_124_A1_H08_T7	g2827514	BLASTX	197	4e-22	75	(AL021633) predicted protein [Arabidopsis thaliana]
7046	GM_124_B1_A05_MR	g2443320	BLASTX	238	7e-18	44	(D85597) polyprotein [Oryza australiensis]
7047	GM_124_B1_A06_T7	g421955	BLASTX	250	2e-20	60	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
7048	GM_124_B1_A07_MR	g2104945	BLASTN	747	8e-27	68	Glycine max copia-like retrotransposon Tgmr, complete sequence
7049	GM_124_B1_A09_MR	g4156149	BLASTN	358	4e-09	64	Homo sapiens clone GS114I09, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7050	GM_124_B1_B02_T7	g4063756	BLASTN	354	6e-09	66	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
7051	GM_124_B1_B05_MR	g1769898	BLASTX	436	2e-40	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7052	GM_124_B1_B06_MR	g3063473	BLASTX	152	6e-09	64	(AC003981) F22O13.35 [Arabidopsis thaliana]
7053	GM_124_B1_B07_MR	g3097320	BLASTN	406	2e-11	72	Glycine max gene for Bd 30K, complete cds
7054	GM_124_B1_B08_T7	g2104945	BLASTN	457	1e-13	75	Glycine max copia-like retrotransposon Tgmr, complete sequence
7055	GM_124_B1_B12_MR	g3269291	BLASTX	166	2e-10	46	(AL030978) putative receptor protein kinase [Arabidopsis thaliana]
7056	GM_124_B1_C02_MR	g2443320	BLASTX	287	4e-23	46	(D85597) polyprotein [Oryza australiensis]
7057	GM_124_B1_C03_MR	g3777527	BLASTX	683	3e-65	92	(AF053008) gag-pol polyprotein [Glycine max]
7058	GM_124_B1_C05_MR	g2995405	BLASTX	298	1e-24	51	(Y12432) polyprotein [Ananas comosus]
7059	GM_124_B1_C05_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7060	GM_124_B1_C07_MR	g2642431	BLASTX	321	1e-26	47	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
7061	GM_124_B1_C09_T7	g3891586	BLASTX	201	2e-15	49	Chain B, Complex Porcine Pancreatic TrypsinSOYBEAN TRYPSIN Inhibitor, Orthorhombic Crystal Form
7062	GM_124_B1_C12_T7	g4038056	BLASTX	190	6e-13	50	(AC005897) putative transposon [Arabidopsis thaliana]
7063	GM_124_B1_D05_MR	g4063760	BLASTX	233	2e-17	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7064	GM_124_B1_D05_T7	g4063760	BLASTX	190	7e-13	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7065	GM_124_B1_D09_MR	g2443320	BLASTX	181	8e-12	31	(D85597) polyprotein [Oryza australiensis]
7066	GM_124_B1_D09_T7	g1711306	BLASTX	105	5e-12	63	(Y09746) heat shock protein 70 [Hydra oligactis]
7067	GM_124_B1_D10_MR	g507910	BLASTN	361	1e-09	76	Glycine max BSR-101 satellite SB92 genomic sequence.
7068	GM_124_B1_D10_T7	g2245608	BLASTX	112	1e-09	61	(AF006007) heat shock cognate 70 kDa protein [Danio rerio]
7069	GM_124_B1_D12_MR	g2795792	BLASTN	350	9e-09	64	Homo sapiens DNA from chromosome 19, cosmid F20191, complete sequence [Homo sapiens]
7070	GM_124_B1_E08_MR	g1769898	BLASTX	107	3e-11	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7071	GM_124_B1_E09_MR	g1480927	BLASTN	464	4e-14	89	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
7072	GM_124_B1_F01_MR	g99922	BLASTX	536	6e-51	72	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
7073	GM_124_B1_F04_MR	g498931	BLASTX	317	1e-27	50	(Z12825) ORF167; homologous to reverse transcriptases from retroviral-like transposons TNT 1-94 from tobacco and COPIA from Drosophila [Beta vulgaris]
7074	GM_124_B1_F05_T7	g2564046	BLASTN	498	2e-15	72	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]
7075	GM_124_B1_G04_MR	g2995405	BLASTX	307	2e-25	42	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7076	GM_124_B1_G06_MR	g3746568	BLASTX	106	1e-11	83	(AF061638) branched-chain alpha-keto acid decarboxylase E1 beta subunit [Arabidopsis thaliana]
7077	GM_124_B1_G07_T7	g3319351	BLASTX	264	1e-20	70	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
7078	GM_124_B1_G11_MR	g2995405	BLASTX	295	3e-24	44	(Y12432) polyprotein [Ananas comosus]
7079	GM_124_B1_G12_MR	g2129618	BLASTX	218	6e-16	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7080	GM_124_B1_H06_T7	g100484	BLASTX	186	1e-12	45	hypothetical protein - garden snapdragon
7081	GM_125_B1_A05_MR	g12137	BLASTN	425	3e-12	66	Pea chloroplast DNA (4.7 kb) 5' to ATP-synthase a subunit gene
7082	GM_125_B1_A07_MR	g2522227	BLASTX	181	4e-13	47	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
7083	GM_125_B1_B03_MR	g3309619	BLASTX	165	3e-10	31	(AF074916) NBS/LRR disease resistance protein [Arabidopsis thaliana]
7084	GM_125_B1_B12_MR	g507910	BLASTN	391	5e-11	82	Glycine max BSR-101 satellite SB92 genomic sequence.
7085	GM_125_B1_C10_MR	g2995405	BLASTX	385	6e-34	62	(Y12432) polyprotein [Ananas comosus]
7086	GM_125_B1_D03_T7	g4150930	BLASTN	441	7e-13	63	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
7087	GM_125_B1_D04_T7	g4140712	BLASTX	210	2e-16	48	(AF110183) putative integrase [Oryza sativa]
7088	GM_125_B1_D07_MR	g3450889	BLASTX	411	1e-37	64	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
7089	GM_125_B1_E01_MR	g4063760	BLASTX	302	9e-25	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7090	GM_125_B1_E02_MR	g3426334	BLASTN	443	5e-13	63	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
7091	GM_125_B1_E10_MR	g3097320	BLASTN	839	6e-31	78	Glycine max gene for Bd 30K, complete cds
7092	GM_125_B1_H04_MR	g2982444	BLASTX	166	2e-10	36	(AL022224) CLV1 receptor kinase like protein [Arabidopsis thaliana]
7093	GM_125_B1_H08_T7	g1402881	BLASTX	204	2e-14	50	(X98130) non-ltr retrotransposon reverse transcriptase-like protein [Arabidopsis thaliana]
7094	GM_125_B2_F01_T7	g1171591	BLASTN	413	1e-11	64	P.falciparum complete gene map of plastid-like DNA (IR-B)
7095	GM_126_A1_A01_T7	g905361	BLASTX	207	5e-15	41	(U22103) gag-protease polyprotein [Glycine max]
7096	GM_126_A1_A03_MR	g1167523	BLASTX	372	4e-32	53	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
7097	GM_126_A1_A04_MR	g3377834	BLASTX	204	1e-14	35	(AF075598) No definition line found [Arabidopsis thaliana]
7098	GM_126_A1_B05_MR	g343917	BLASTN	362	3e-10	62	yeast (s.cerevisiae) mitochondrial rep1 region & repetitive unit.
7099	GM_126_A1_B05_T7	g3142328	BLASTN	1501	4e-61	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7100	GM_126_A1_B09_MR	g3777527	BLASTX	556	1e-51	98	(AF053008) gag-pol polyprotein [Glycine max]
7101	GM_126_A1_B09_T7	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7102	GM_126_A1_B11_MR	g2894612	BLASTX	153	9e-11	56	(AL021889) putative protein [Arabidopsis thaliana]
7103	GM_126_A1_B12_T7	g3702731	BLASTN	393	1e-10	78	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]
7104	GM_126_A1_C10_MR	g1418331	BLASTX	280	6e-23	53	(X95909) receptor like protein kinase [Arabidopsis thaliana]
7105	GM_126_A1_D02_T7	g2443320	BLASTX	371	5e-32	60	(D85597) polyprotein [Oryza australiensis]
7106	GM_126_A1_D03_MR	g18768	BLASTN	411	3e-12	76	Soybean Tgm6 transposable element 3' end
7107	GM_126_A1_D03_T7	g3860247	BLASTX	153	4e-18	90	(AC005824) unknown protein [Arabidopsis thaliana]
7108	GM_126_A1_D06_T7	g4063760	BLASTX	201	5e-14	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7109	GM_126_A1_D10_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7110	GM_126_A1_D10_T7	g507910	BLASTN	386	8e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7111	GM_126_A1_D12_MR	g343950	BLASTN	270	7e-10	66	S.cerevisiae mitochondrion Tyr-tRNA gene.
7112	GM_126_A1_E02_T7	g3142328	BLASTN	1151	3e-45	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7113	GM_126_A1_E05_MR	g1769897	BLASTX	169	5e-11	37	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7114	GM_126_A1_E09_T7	g2213599	BLASTX	189	1e-12	44	(AC000348) T7N9.19 [Arabidopsis thaliana]
7115	GM_126_A1_F03_T7	g2655098	BLASTX	205	7e-15	35	(AF023472) peptide transporter [Hordeum vulgare]
7116	GM_126_A1_F05_T7	g3056591	BLASTX	177	1e-11	52	(AC004255) T1F9.12 [Arabidopsis thaliana]
7117	GM_126_A1_F06_T7	g1769897	BLASTX	172	2e-11	37	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7118	GM_126_A1_F09_T7	g4092471	BLASTN	531	6e-17	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
7119	GM_126_A1_F10_MR	g3599418	BLASTN	358	3e-09	73	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7120	GM_126_A1_F10_T7	g3097320	BLASTN	569	1e-18	82	Glycine max gene for Bd 30K, complete cds
7121	GM_126_A1_G04_MR	g4063760	BLASTX	131	4e-17	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7122	GM_126_A1_G08_MR	g4092471	BLASTN	423	4e-12	71	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
7123	GM_126_A1_G09_MR	g629693	BLASTX	354	1e-31	58	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
7124	GM_126_A1_G11_T7	g4063760	BLASTX	284	7e-23	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7125	GM_126_A1_G12_MR	g2864621	BLASTX	185	6e-13	41	hypothetical protein [Arabidopsis thaliana]
7126	GM_126_A1_G12_T7	g2462134	BLASTX	162	2e-10	37	(Y13368) reverse transcriptase [Beta vulgaris]
7127	GM_126_A1_H02_T7	g1142699	BLASTN	271	4e-14	68	Glycine max satellite STR120-A.1.
7128	GM_126_A1_H04_T7	g100484	BLASTX	348	4e-30	61	hypothetical protein - garden snapdragon
7129	GM_126_A1_H05_MR	g1755162	BLASTX	286	2e-24	63	(U75192) germin-like protein [Arabidopsis thaliana]
7130	GM_126_A2_A05_T7	g4063760	BLASTX	254	1e-19	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7131	GM_126_A2_A07_T7	g3334667	BLASTX	149	5e-09	84	(Y10493) putative cytochrome P450 [Glycine max]
7132	GM_126_A2_A10_T7	g1620908	BLASTN	470	3e-15	82	Carrot mRNA for DcARF1, complete cds
7133	GM_126_A2_B07_T7	g905361	BLASTX	161	4e-10	40	(U22103) gag-protease polyprotein [Glycine max]
7134	GM_126_A2_B10_T7	g3142328	BLASTN	781	2e-28	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7135	GM_126_A2_D12_T7	g2244859	BLASTX	110	1e-10	54	(Z97337) hypothetical protein [Arabidopsis thaliana]
7136	GM_126_A2_E02_T7	g4063760	BLASTX	278	4e-23	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7137	GM_126_A2_E06_T7	g4063760	BLASTX	482	6e-44	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7138	GM_126_A2_E09_T7	g3599418	BLASTN	741	1e-26	81	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7139	GM_126_A2_E11_T7	g2980806	BLASTX	215	7e-16	61	(AL022197) putative protein [Arabidopsis thaliana]
7140	GM_126_A2_E12_MR	g3176777	BLASTN	420	5e-13	66	Homo sapiens allele 4 fragile site locus (FRA10B) minisatellite, 3' sequence
7141	GM_126_A2_F01_T7	g2104945	BLASTN	393	9e-11	66	Glycine max copia-like retrotransposon Tgmr, complete sequence
7142	GM_126_A2_F06_T7	g2104945	BLASTN	429	2e-12	68	Glycine max copia-like retrotransposon Tgmr, complete sequence
7143	GM_126_A2_F09_T7	g4063760	BLASTX	309	2e-25	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7144	GM_126_A2_F10_T7	g3142328	BLASTN	535	3e-17	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7145	GM_126_A2_F11_T7	g18559	BLASTN	520	1e-16	69	G.max gene for catalase
7146	GM_126_A2_G06_T7	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
7147	GM_126_A2_G07_T7	g3142328	BLASTN	652	1e-22	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7148	GM_126_A2_H05_T7	g507910	BLASTN	355	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7149	GM_126_A2_H06_T7	g3860247	BLASTX	148	2e-16	93	(AC005824) unknown protein [Arabidopsis thaliana]
7150	GM_126_A2_H11_T7	g3935164	BLASTX	171	3e-11	46	(AC004557) F17L21.7 [Arabidopsis thaliana]
7151	GM_126_B1_A05_T7	g507910	BLASTN	415	4e-12	80	Glycine max BSR-101 satellite SB92 genomic sequence.
7152	GM_126_B1_B03_T7	g3645899	BLASTX	158	2e-09	57	(U68408) 5' end not determined experimentally [Zea mays]
7153	GM_126_B1_C05_T7	g1769898	BLASTX	211	2e-15	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7154	GM_126_B1_D03_T7	g114532	BLASTX	245	2e-19	86	ATP SYNTHASE ALPHA CHAIN gi 67824 pir PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast gi 11769 (V00162) alpha subunit of ATPase [Nicotiana tabacum] gi 11811 (Z00044) ATPase alpha subunit [Nicotiana tabacum] gi 225270 prf 1211235E ATPase alpha [Nicotiana tabacum]
7155	GM_126_B1_D08_T7	g3033399	BLASTX	159	7e-10	52	(AC004238) hypothetical protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7156	GM_126_B1_E04_T7	g507910	BLASTN	422	2e-12	85	Glycine max BSR-101 satellite SB92 genomic sequence.
7157	GM_126_B1_E12_T7	g99922	BLASTX	144	1e-08	54	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
7158	GM_126_B1_G01_T7	g507910	BLASTN	426	1e-12	79	Glycine max BSR-101 satellite SB92 genomic sequence.
7159	GM_126_B1_G06_T7	g1769898	BLASTX	236	4e-18	78	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7160	GM_127_A1_A01_MR	g2459426	BLASTX	152	3e-09	43	(AC002332) putative splicing factor U2AF large chain [Arabidopsis thaliana]
7161	GM_127_A1_A02_MR	g4063760	BLASTX	228	7e-17	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7162	GM_127_A1_B02_MR	g507910	BLASTN	438	4e-13	78	Glycine max BSR-101 satellite SB92 genomic sequence.
7163	GM_127_A1_B07_MR	g507910	BLASTN	546	5e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
7164	GM_127_A1_B10_MR	g3845204	BLASTN	385	2e-10	64	Plasmodium falciparum chromosome 2, section 37 of 73 of the complete sequence
7165	GM_127_A1_C01_MR	g3033389	BLASTX	156	3e-09	30	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
7166	GM_127_A1_C02_MR	g4063760	BLASTX	213	3e-15	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7167	GM_127_A1_C04_MR	g100484	BLASTX	290	8e-24	44	hypothetical protein - garden snapdragon
7168	GM_127_A1_C06_MR	g3645899	BLASTX	277	4e-22	50	(U68408) 5' end not determined experimentally [Zea mays]
7169	GM_127_A1_C10_MR	g100484	BLASTX	319	6e-27	58	hypothetical protein - garden snapdragon
7170	GM_127_A1_C12_MR	g3915037	BLASTX	322	6e-41	79	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi 2570067 gnl PID e1154401 (AJ001071) second sucrose synthase [Pisum sativum]
7171	GM_127_A1_D02_MR	g3777527	BLASTX	738	4e-71	95	(AF053008) gag-pol polyprotein [Glycine max]
7172	GM_127_A1_E01_MR	g296873	BLASTN	280	3e-10	64	W.mrakii mitochondrial DNA
7173	GM_127_A1_E02_MR	g3668069	BLASTX	218	5e-17	93	(U28007) Pto kinase interactor 1 [Lycopersicon esculentum]
7174	GM_127_A1_E04_MR	g2245003	BLASTX	161	3e-10	34	(Z97341) similarity to a membrane-associated salt-inducible protein - Nicotiana tabacum [Arabidopsis thaliana]
7175	GM_127_A1_E05_MR	g4050011	BLASTN	434	1e-12	60	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
7176	GM_127_A1_E10_MR	g2828280	BLASTX	168	2e-10	82	(AL021687) putative protein [Arabidopsis thaliana] gi 2832633 gnl PID e1249651 (AL021711) putative protein [Arabidopsis thaliana]
7177	GM_127_A1_F04_MR	g3645899	BLASTX	287	3e-31	63	(U68408) 5' end not determined experimentally [Zea mays]
7178	GM_127_A1_F09_MR	g3426334	BLASTN	391	1e-10	65	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
7179	GM_127_A1_G04_MR	g507910	BLASTN	491	1e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
7180	GM_127_A1_G09_MR	g507910	BLASTN	342	7e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7181	GM_127_A1_G12_MR	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7182	GM_127_A1_H06_MR	g13533	BLASTN	251	1e-08	68	Yeast mitochondrial tRNA genes (several, map positions 3.5 to 8.6) encoding tRNAs for Lys, Arg, Gly, Asp, Ser, Arg, and Ala.
7183	GM_127_A1_H08_MR	g3645899	BLASTX	184	1e-19	46	(U68408) 5' end not determined experimentally [Zea mays]
7184	GM_127_A1_H09_MR	g2827718	BLASTX	254	1e-19	42	(AL021684) retrotransposon - like protein [Arabidopsis thaliana]
7185	GM_127_A2_A01_MR	g2501353	BLASTX	219	7e-24	91	TRANSKETOLASE, CHLOROPLAST (TK) gi 1084440 pir S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) gi 664901 (Z46646) transketolase [Craterostigma plantagineum]
7186	GM_127_A2_A01_T7	g4063770	BLASTX	226	6e-17	39	(AB004906) transposase [Ipomoea purpurea]
7187	GM_127_A2_A04_MR	g4160362	BLASTN	349	1e-08	59	Saccharomyces cerevisiae complete mitochondrial genome
7188	GM_127_A2_A05_T7	g3047127	BLASTX	236	3e-18	79	(AF058919) No definition line found [Arabidopsis thaliana]
7189	GM_127_A2_A06_MR	g507910	BLASTN	503	4e-16	81	Glycine max BSR-101 satellite SB92 genomic sequence.
7190	GM_127_A2_A08_MR	g2443320	BLASTX	177	2e-11	34	(D85597) polyprotein [Oryza australiensis]
7191	GM_127_A2_A09_MR	g2764526	BLASTN	410	1e-17	67	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
7192	GM_127_A2_B01_MR	g4102600	BLASTX	127	8e-16	68	(AF013467) ARF6 [Arabidopsis thaliana]
7193	GM_127_A2_B04_MR	g3777527	BLASTX	704	2e-67	95	(AF053008) gag-pol polyprotein [Glycine max]
7194	GM_127_A2_B06_MR	g1666236	BLASTX	144	9e-09	32	(U76261) unknown [Hordeum vulgare]
7195	GM_127_A2_B11_T7	g3402690	BLASTX	174	6e-12	52	(AC004697) hypothetical protein, 3' partial [Arabidopsis thaliana]
7196	GM_127_A2_B12_MR	g3777527	BLASTX	387	1e-33	94	(AF053008) gag-pol polyprotein [Glycine max]
7197	GM_127_A2_B12_T7	g1785736	BLASTX	139	8e-09	55	(Y08502) orf119 [Arabidopsis thaliana]
7198	GM_127_A2_C02_T7	g3668080	BLASTX	217	1e-16	84	(AC004667) unknown protein [Arabidopsis thaliana]
7199	GM_127_A2_C03_T7	g2688822	BLASTX	204	9e-16	93	(U93272) pyrophosphate-dependent phosphofructo-1-kinase [Prunus armeniaca]
7200	GM_127_A2_C04_MR	g3193302	BLASTX	167	7e-11	38	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 166.20) and to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 139.32) [Arabidopsis thaliana]
7201	GM_127_A2_C04_T7	g4006833	BLASTX	289	3e-23	41	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
7202	GM_127_A2_C05_T7	g4063760	BLASTX	205	2e-14	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7203	GM_127_A2_C07_MR	g1769897	BLASTX	188	7e-16	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7204	GM_127_A2_C07_T7	g3142328	BLASTN	581	3e-19	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7205	GM_127_A2_C12_T7	g2651305	BLASTX	157	5e-10	50	(AC002336) hypothetical protein [Arabidopsis thaliana]
7206	GM_127_A2_D02_MR	g2213586	BLASTX	232	8e-18	42	(AC000348) T7N9.6 [Arabidopsis thaliana]
7207	GM_127_A2_D02_T7	g421955	BLASTX	184	5e-13	56	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7208	GM_127_A2_D03_MR	g3142330	BLASTX	718	3e-70	94	(U96295) envelope-like [Glycine max]
7209	GM_127_A2_D04_T7	g421955	BLASTX	392	1e-35	54	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
7210	GM_127_A2_D07_MR	g1769899	BLASTX	224	4e-28	81	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7211	GM_127_A2_D08_MR	g3142379	BLASTX	443	5e-41	75	(AF053008) envelope-like [Glycine max]
7212	GM_127_A2_D10_MR	g1666236	BLASTX	196	1e-14	31	(U76261) unknown [Hordeum vulgare]
7213	GM_127_A2_E02_T7	g3777527	BLASTX	729	4e-70	95	(AF053008) gag-pol polyprotein [Glycine max]
7214	GM_127_A2_E08_T7	g905361	BLASTX	176	1e-11	30	(U22103) gag-protease polyprotein [Glycine max]
7215	GM_127_A2_E09_T7	g3243214	BLASTN	455	2e-13	65	Arabidopsis thaliana BAC T19B17 from chromsome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]
7216	GM_127_A2_E12_MR	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7217	GM_127_A2_E12_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7218	GM_127_A2_F05_T7	g4063760	BLASTX	296	4e-24	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7219	GM_127_A2_F06_T7	g4063760	BLASTX	272	1e-21	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7220	GM_127_A2_F07_T7	g2443320	BLASTX	287	4e-23	45	(D85597) polyprotein [Oryza australiensis]
7221	GM_127_A2_F09_MR	g857398	BLASTN	542	8e-21	81	Soybean mRNA for mitotic cyclin b1-type, complete cds
7222	GM_127_A2_F11_MR	g320569	BLASTX	153	3e-10	44	transposon TNT1 - Arabidopsis thaliana (fragment)
7223	GM_127_A2_F11_T7	g4038056	BLASTX	151	8e-09	30	(AC005897) putative transposon [Arabidopsis thaliana]
7224	GM_127_A2_F12_T7	g4063770	BLASTX	179	7e-12	36	(AB004906) transposase [Ipomoea purpurea]
7225	GM_127_A2_G02_MR	g505129	BLASTN	365	1e-09	71	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
7226	GM_127_A2_G11_MR	g1769899	BLASTX	165	1e-11	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7227	GM_127_A2_G12_MR	g3777527	BLASTX	582	2e-54	94	(AF053008) gag-pol polyprotein [Glycine max]
7228	GM_127_A2_H09_T7	g18559	BLASTN	667	1e-32	73	G.max gene for catalase
7229	GM_127_B1_A02_T7	g4063760	BLASTX	341	7e-29	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7230	GM_127_B1_A04_MR	g3582342	BLASTX	266	8e-22	41	(AC005496) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]
7231	GM_127_B1_A09_MR	g905361	BLASTX	155	1e-18	38	(U22103) gag-protease polyprotein [Glycine max]
7232	GM_127_B1_A10_MR	g2995405	BLASTX	597	4e-57	60	(Y12432) polyprotein [Ananas comosus]
7233	GM_127_B1_B01_MR	g2443320	BLASTX	386	1e-33	55	(D85597) polyprotein [Oryza australiensis]
7234	GM_127_B1_B04_T7	g3249111	BLASTX	162	2e-10	52	(AC003114) T12M4.7 [Arabidopsis thaliana]
7235	GM_127_B1_B08_MR	g1370171	BLASTN	619	4e-22	77	L.japonicus mRNA for small GTP-binding protein, RAB1X.
7236	GM_127_B1_C01_MR	g2464913	BLASTX	251	5e-20	43	(Z99708) myo-inositol transport protein homolog [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7237	GM_127_B1_C02_MR	g1066856	BLASTN	313	2e-12	75	Glycine max acetyl coenzyme A carboxylase (ACCase-B) gene, 5' end of cds.
7238	GM_127_B1_C10_MR	g2735017	BLASTX	311	5e-27	64	(U82481) KI domain interacting kinase 1 [Zea mays]
7239	GM_127_B1_C12_MR	g4063760	BLASTX	209	7e-15	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7240	GM_127_B1_D08_MR	g1171642	BLASTX	198	7e-26	71	PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK gi 481206 pir S38326 protein kinase - Arabidopsis thaliana gi 166809 (L07248) protein kinase [Arabidopsis thaliana]
7241	GM_127_B1_D10_MR	g3540195	BLASTX	165	4e-10	63	(AC004260) Unknown protein [Arabidopsis thaliana]
7242	GM_127_B1_D10_T7	g4063760	BLASTX	481	1e-51	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7243	GM_127_B1_E02_MR	g2708743	BLASTX	270	3e-21	38	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
7244	GM_127_B1_E03_T7	g1000971	BLASTN	382	3e-10	65	Hansenula wingei mitochondrial DNA, complete sequence
7245	GM_127_B1_E05_MR	g3142328	BLASTN	1866	7e-78	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7246	GM_127_B1_E05_T7	g559273	BLASTN	368	1e-09	60	Saccharomyces cerevisiae mitochondrion oxi3 gene, aapI gene, oli2 gene, ORF4, replication of origin (ori7 and ori2), and ORF5.
7247	GM_127_B1_E06_MR	g509768	BLASTN	450	2e-13	69	Glycine max seed-specific low molecular weight sulfur-rich protein.
7248	GM_127_B1_E07_MR	g4115365	BLASTX	139	3e-09	26	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
7249	GM_127_B1_E08_MR	g3915037	BLASTX	292	5e-30	80	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi 2570067 gnl PID e1154401 (AJ001071) second sucrose synthase [Pisum sativum]
7250	GM_127_B1_E09_MR	g3097320	BLASTN	478	1e-14	69	Glycine max gene for Bd 30K, complete cds
7251	GM_127_B1_E11_T7	g2708743	BLASTX	180	1e-11	36	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
7252	GM_127_B1_E12_T7	g2316016	BLASTX	320	2e-26	62	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
7253	GM_127_B1_F02_MR	g130582	BLASTX	214	2e-15	34	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
7254	GM_127_B1_F05_MR	g1778822	BLASTN	492	3e-16	77	Glycine max early light-induced protein (ELIP) mRNA, complete cds
7255	GM_127_B1_F06_MR	g4063756	BLASTN	609	2e-20	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
7256	GM_127_B1_F08_T7	g905361	BLASTX	410	3e-37	90	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7257	GM_127_B1_F10_T7	g2979597	BLASTN	384	3e-10	61	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
7258	GM_127_B1_G04_T7	g18695	BLASTN	389	1e-10	74	Soybean nodulin 22 gene
7259	GM_127_B1_G05_MR	g2828182	BLASTN	548	7e-19	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]
7260	GM_127_B1_G06_MR	g3777527	BLASTX	756	5e-73	94	(AF053008) gag-pol polyprotein [Glycine max]
7261	GM_127_B1_H04_MR	g2129618	BLASTX	151	4e-12	30	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7262	GM_127_B1_H07_MR	g18559	BLASTN	484	7e-15	68	G.max gene for catalase
7263	GM_127_B1_H09_T7	g2864625	BLASTX	180	6e-12	68	(AL021811) putative protein [Arabidopsis thaliana]
7264	GM_127_B1_H12_T7	g3513745	BLASTX	217	2e-15	36	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
7265	GM_127_B2_A04_MR	g3873182	BLASTN	433	2e-12	64	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
7266	GM_127_B2_A06_T7	g2253579	BLASTX	103	5e-10	64	(U78721) hypothetical protein [Arabidopsis thaliana]
7267	GM_127_B2_B01_MR	g3142328	BLASTN	392	1e-10	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7268	GM_127_B2_B02_MR	g905361	BLASTX	137	1e-14	68	(U22103) gag-protease polyprotein [Glycine max]
7269	GM_127_B2_B10_MR	g3281850	BLASTX	135	3e-09	83	(AL031004) monogalactosyldiacylglycerol synthase - like protein [Arabidopsis thaliana]
7270	GM_127_B2_C01_T7	g4160362	BLASTN	449	1e-14	60	Saccharomyces cerevisiae complete mitochondrial genome
7271	GM_127_B2_C04_MR	g836954	BLASTX	292	6e-24	72	(U20948) receptor protein kinase [Ipomoea trifida]
7272	GM_127_B2_C06_T7	g1204057	BLASTN	417	8e-12	60	Caenorhabditis elegans cosmid C04B4, complete sequence [Caenorhabditis elegans]
7273	GM_127_B2_C07_MR	g99755	BLASTX	331	2e-33	54	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
7274	GM_127_B2_C11_T7	g2995405	BLASTX	200	5e-14	41	(Y12432) polyprotein [Ananas comosus]
7275	GM_127_B2_D03_T7	g3695387	BLASTX	212	7e-18	59	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
7276	GM_127_B2_D07_T7	g3097320	BLASTN	993	6e-38	78	Glycine max gene for Bd 30K, complete cds
7277	GM_127_B2_D10_T7	g3282159	BLASTN	374	7e-10	58	Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7278	GM_127_B2_D12_MR	g1170781	BLASTX	214	6e-30	80	LACTOYLGLUTATHIONE LYASE (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) gi 629615 pir S47177 lactoylglutathione lyase (EC 4.4.1.5) - soybean gi 505585 (X68819) lactoylglutathione lyase [Glycine max]
7279	GM_127_B2_E01_T7	g3193320	BLASTX	156	5e-16	54	(AF069299) contains similarity to the subtilase family of serine proteases (Pfam: subtilase.hmm, score: 47.57); strong similarity to Cucumis melo (muskmelon) cucumisin (GB:D32206) [Arabidopsis thaliana]
7280	GM_127_B2_E06_T7	g3193320	BLASTX	149	4e-13	52	(AF069299) contains similarity to the subtilase family of serine proteases (Pfam: subtilase.hmm, score: 47.57); strong similarity to Cucumis melo (muskmelon) cucumisin (GB:D32206) [Arabidopsis thaliana]
7281	GM_127_B2_E09_MR	g3845321	BLASTN	377	5e-10	63	Plasmodium falciparum chromosome 2, section 66 of 73 of the complete sequence
7282	GM_127_B2_E10_T7	g1666236	BLASTX	256	3e-21	34	(U76261) unknown [Hordeum vulgare]
7283	GM_127_B2_E12_T7	g2191174	BLASTX	173	6e-26	64	(AF007270) similar to the peptidase family S16 [Arabidopsis thaliana]
7284	GM_127_B2_F06_MR	g282873	BLASTX	171	1e-11	60	transforming protein (myb) homolog - Arabidopsis thaliana gi 217859 gnl PID d1002205 (D10936) ATMYB1 protein [Arabidopsis thaliana]
7285	GM_127_B2_F12_T7	g2244803	BLASTX	229	2e-18	42	(Z97336) reverse transcriptase-like protein [Arabidopsis thaliana]
7286	GM_127_B2_G03_T7	g507910	BLASTN	371	4e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7287	GM_127_B2_G12_T7	g4063756	BLASTN	614	1e-20	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
7288	GM_127_B2_H03_MR	g507910	BLASTN	394	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7289	GM_127_B2_H04_MR	g505129	BLASTN	427	2e-12	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
7290	GM_127_B2_H10_T7	g18559	BLASTN	1119	1e-43	74	G.max gene for catalase
7291	GM_128_A2_A04_T7	g1171591	BLASTN	380	4e-10	63	P.falciparum complete gene map of plastid-like DNA (IR-B)
7292	GM_128_A2_A06_T7	g4063760	BLASTX	157	2e-10	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7293	GM_128_A2_A10_MR	g629693	BLASTX	161	2e-10	33	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
7294	GM_128_A2_A11_MR	g3821044	BLASTN	374	7e-10	66	Human DNA sequence from clone 878O8 on chromosome Xq21.1-21.33. Contains an EST, STSs, a GSS and genomic marker DXS472, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7295	GM_128_A2_A11_T7	g2196878	BLASTX	104	7e-09	52	(Y08292) NADH glutamate dehydrogenase [Nicotiana plumbaginifolia]
7296	GM_128_A2_B01_MR	g4063760	BLASTX	485	3e-44	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7297	GM_128_A2_B01_T7	g2196878	BLASTX	295	1e-27	77	(Y08292) NADH glutamate dehydrogenase [Nicotiana plumbaginifolia]
7298	GM_128_A2_B02_T7	g3810595	BLASTX	284	9e-23	41	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
7299	GM_128_A2_B04_T7	g2245029	BLASTX	155	4e-09	52	(Z97341) limonene cyclase homolog [Arabidopsis thaliana]
7300	GM_128_A2_B10_T7	g1170644	BLASTX	166	1e-10	35	RING CANAL PROTEIN (KELCH PROTEIN) gi 577276 (L08483) ring canal protein [Drosophila melanogaster]
7301	GM_128_A2_C02_MR	g3599418	BLASTN	391	1e-10	76	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7302	GM_128_A2_C04_MR	g3738114	BLASTN	367	1e-09	62	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
7303	GM_128_A2_C07_T7	g1769898	BLASTX	341	1e-29	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7304	GM_128_A2_C09_MR	g3810596	BLASTX	221	3e-16	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
7305	GM_128_A2_D07_MR	g4115365	BLASTX	255	1e-19	41	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
7306	GM_128_A2_D07_T7	g1769897	BLASTX	225	4e-17	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7307	GM_128_A2_D11_MR	g629693	BLASTX	165	6e-11	32	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
7308	GM_128_A2_E01_MR	g18559	BLASTN	699	1e-24	73	G.max gene for catalase
7309	GM_128_A2_E02_T7	g2522228	BLASTX	398	3e-36	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
7310	GM_128_A2_E04_MR	g3142379	BLASTX	338	6e-30	72	(AF053008) envelope-like [Glycine max]
7311	GM_128_A2_E06_MR	g2129618	BLASTX	204	2e-14	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7312	GM_128_A2_E10_MR	g18559	BLASTN	465	5e-14	69	G.max gene for catalase
7313	GM_128_A2_E12_MR	g3142328	BLASTN	518	2e-16	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7314	GM_128_A2_F04_MR	g2129618	BLASTX	154	6e-19	47	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7315	GM_128_A2_F08_MR	g2832901	BLASTN	286	9e-12	65	Cajanus cajan copia-like retrotransposon,Panzee
7316	GM_128_A2_G03_MR	g4092471	BLASTN	499	2e-15	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
7317	GM_128_A2_G05_T7	g905361	BLASTX	149	9e-09	83	(U22103) gag-protease polyprotein [Glycine max]
7318	GM_128_A2_G06_MR	g507910	BLASTN	353	2e-09	75	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7319	GM_128_A2_G07_T7	g4106406	BLASTN	428	4e-13	64	Sorghum bicolor centromere specific element pHind22, complete sequence
7320	GM_128_A2_G08_T7	g1769897	BLASTX	322	8e-28	67	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7321	GM_128_A2_H01_T7	g3786009	BLASTX	164	1e-22	58	(AC005499) unknown protein [Arabidopsis thaliana]
7322	GM_128_A2_H06_MR	g507910	BLASTN	592	4e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
7323	GM_128_A2_H06_T7	g507910	BLASTN	395	3e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7324	GM_128_A2_H08_MR	g507910	BLASTN	693	1e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
7325	GM_128_B1_A05_MR	g4063760	BLASTX	585	5e-55	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7326	GM_128_B1_A07_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
7327	GM_128_B1_A08_T7	g2462058	BLASTX	232	1e-18	58	(Y13389) reverse transcriptase [Antirrhinum majus]
7328	GM_128_B1_B02_MR	g4159703	BLASTN	373	8e-10	66	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K5F14, complete sequence [Arabidopsis thaliana]
7329	GM_128_B1_B08_T7	g2522228	BLASTX	135	4e-11	83	(AB007466) reverse transcriptase-like protein [Vicia faba]
7330	GM_128_B1_B09_MR	g4063756	BLASTN	533	5e-17	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
7331	GM_128_B1_B10_MR	g3645899	BLASTX	221	3e-16	38	(U68408) 5' end not determined experimentally [Zea mays]
7332	GM_128_B1_B12_MR	g1769898	BLASTX	327	2e-38	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7333	GM_128_B1_C08_MR	g18559	BLASTN	521	1e-16	74	G.max gene for catalase
7334	GM_128_B1_D02_MR	g3193221	BLASTN	1126	5e-44	94	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
7335	GM_128_B1_D03_MR	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7336	GM_128_B1_D03_T7	g3777527	BLASTX	621	3e-59	93	(AF053008) gag-pol polyprotein [Glycine max]
7337	GM_128_B1_D09_T7	g2832611	BLASTN	362	3e-09	63	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)
7338	GM_128_B1_E06_T7	g3688328	BLASTX	262	7e-22	50	(AJ228325) reverse transcriptase [Ginkgo biloba]
7339	GM_128_B1_E09_MR	g18559	BLASTN	512	4e-16	70	G.max gene for catalase
7340	GM_128_B1_E09_T7	g1666236	BLASTX	165	4e-11	31	(U76261) unknown [Hordeum vulgare]
7341	GM_128_B1_F03_MR	g507910	BLASTN	374	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7342	GM_128_B1_F03_T7	g507910	BLASTN	356	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7343	GM_128_B1_F05_MR	g4063756	BLASTN	441	7e-13	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
7344	GM_128_B1_F05_T7	g507910	BLASTN	527	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
7345	GM_128_B1_F09_T7	g1167523	BLASTX	135	2e-09	40	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
7346	GM_128_B1_F12_T7	g3695294	BLASTN	371	9e-10	69	Glycine max nodule-specific glutamine synthetase gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7347	GM_128_B1_G07_MR	g505129	BLASTN	360	3e-09	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
7348	GM_128_B1_G10_MR	g507910	BLASTN	521	6e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
7349	GM_128_B1_H02_MR	g4063760	BLASTX	464	5e-42	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7350	GM_128_B1_H03_MR	g1350783	BLASTX	301	9e-25	54	RECEPTOR-LIKE PROTEIN KINASE 5 PRECURSOR gi 282883 pir S27756 receptor-like protein kinase precursor - Arabidopsis thaliana gi 166850 (M84660) receptor-like protein kinase [Arabidopsis thaliana] gi 2842492 gnl PID e1250067 (AL021749) receptor-like protein kinase 5 precursor (RLK5) [Arabidopsis thaliana]
7351	GM_128_B1_H08_T7	g3201680	BLASTX	211	1e-25	86	(AF060941) extra-large G-protein [Arabidopsis thaliana]
7352	GM_128_B1_H09_MR	g4115534	BLASTX	276	1e-25	49	(AB012114) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]
7353	GM_128_B1_H09_T7	g3241916	BLASTN	403	4e-11	65	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]
7354	GM_128_B2_A01_T7	g100484	BLASTX	316	1e-26	56	hypothetical protein - garden snapdragon
7355	GM_128_B2_A07_T7	g4063760	BLASTX	270	2e-21	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7356	GM_128_B2_A08_MR	g3777527	BLASTX	291	2e-23	46	(AF053008) gag-pol polyprotein [Glycine max]
7357	GM_128_B2_A08_T7	g3550435	BLASTN	555	4e-18	64	Hordeum vulgare Hotr1 gene
7358	GM_128_B2_A12_MR	g2495590	BLASTX	154	1e-09	71	HYPOTHETICAL 51.8 KD PROTEIN IN PHOH-CSGG INTERGENIC REGION gi 1787262 (AE000204) o452; This 452 aa ORF is 31 pct identical (20 gaps) to 179 residues of an approx. 248 aa protein YHUH_STRGR SW: P24222 [Escherichia coli]
7359	GM_128_B2_B02_MR	g18559	BLASTN	789	9e-29	74	G.max gene for catalase
7360	GM_128_B2_B02_T7	g2995405	BLASTX	522	9e-49	64	(Y12432) polyprotein [Ananas comosus]
7361	GM_128_B2_B04_T7	g2462058	BLASTX	220	2e-17	41	(Y13389) reverse transcriptase [Antirrhinum majus]
7362	GM_128_B2_B06_MR	g3695395	BLASTX	228	3e-17	44	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
7363	GM_128_B2_B07_MR	g3600036	BLASTX	139	5e-12	87	(AF080119) contains similarity to protein kinase domains (Pfam: pkinase.hmm, score: 227.04) [Arabidopsis thaliana]
7364	GM_128_B2_B10_MR	g3513745	BLASTX	247	1e-18	35	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
7365	GM_128_B2_B10_T7	g343945	BLASTN	390	1e-11	62	Yeast (S.cerevisiae) mitochondrial var1 gene, 5' flank.
7366	GM_128_B2_B12_T7	g4063760	BLASTX	369	7e-32	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7367	GM_128_B2_C04_T7	g505129	BLASTN	448	3e-13	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
7368	GM_128_B2_C06_MR	g2522230	BLASTX	324	2e-28	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
7369	GM_128_B2_C08_MR	g2443320	BLASTX	434	9e-39	50	(D85597) polyprotein [Oryza australiensis]
7370	GM_128_B2_C10_MR	g4038037	BLASTX	178	1e-11	27	(AC005936) hypothetical protein [Arabidopsis thaliana]
7371	GM_128_B2_C10_T7	g170029	BLASTN	399	5e-11	64	Glycine max cv. Dare nodulin 26 gene fragment.
7372	GM_128_B2_C11_MR	g2558658	BLASTX	191	8e-17	37	(AC002354) No definition line found [Arabidopsis thaliana]
7373	GM_128_B2_D08_T7	g3548804	BLASTX	378	3e-33	57	(AC005313) unknown protein [Arabidopsis thaliana]
7374	GM_128_B2_D11_T7	g2970554	BLASTN	482	9e-15	85	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
7375	GM_128_B2_E01_MR	g3135274	BLASTX	271	3e-22	42	(AC003058) putative beta-1,3-endoglucanase [Arabidopsis thaliana]
7376	GM_128_B2_E01_T7	g2522228	BLASTX	464	3e-43	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
7377	GM_128_B2_E02_T7	g4139038	BLASTX	166	5e-10	40	(AF072272) resistance protein candidate RGC2K [Lactuca sativa]
7378	GM_128_B2_E05_MR	g2213582	BLASTX	447	4e-40	56	(AC000348) T7N9.2 [Arabidopsis thaliana]
7379	GM_128_B2_E05_T7	g170080	BLASTN	463	6e-14	73	Soybean seed lectin gene transposable element tgm1.
7380	GM_128_B2_E06_MR	g507910	BLASTN	629	8e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7381	GM_128_B2_E06_T7	g18559	BLASTN	596	5e-20	70	G.max gene for catalase
7382	GM_128_B2_E07_T7	g3142328	BLASTN	735	3e-26	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7383	GM_128_B2_E09_T7	g3777527	BLASTX	697	1e-66	91	(AF053008) gag-pol polyprotein [Glycine max]
7384	GM_128_B2_E11_MR	g3892709	BLASTX	176	1e-11	82	(AL033545) putative protein [Arabidopsis thaliana]
7385	GM_128_B2_E12_T7	g3319362	BLASTX	296	3e-26	49	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
7386	GM_128_B2_F05_MR	g2564750	BLASTN	372	9e-10	64	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
7387	GM_128_B2_F05_T7	g1806143	BLASTN	348	7e-09	72	M.sativa mRNA for cdc2 kinase homologue, cdc2MsE.
7388	GM_128_B2_F10_MR	g3128209	BLASTX	680	4e-66	80	(AC004077) unknown protein [Arabidopsis thaliana]
7389	GM_128_B2_F12_MR	g505129	BLASTN	362	2e-09	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
7390	GM_128_B2_F12_T7	g2522230	BLASTX	200	3e-15	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
7391	GM_128_B2_G02_MR	g169910	BLASTN	615	3e-21	87	Soybean actin 3 gene (SAc3), complete cds.
7392	GM_128_B2_G02_T7	g3873182	BLASTN	437	1e-12	63	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7393	GM_128_B2_G03_T7	g99922	BLASTX	317	1e-27	60	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
7394	GM_128_B2_G06_T7	g4056456	BLASTX	290	7e-25	80	(AC005990) Strong similarity to gb U20808 auxin-induced protein from Vigna radiata and a member of the zinc-binding dehydrogenase family PF 00107. ESTs gb T43674, gb H77006 and gb AA395179 come from this gene. [Arabidopsis thaliana]
7395	GM_128_B2_G07_MR	g2995405	BLASTX	204	1e-37	66	(Y12432) polyprotein [Ananas comosus]
7396	GM_128_B2_G11_T7	g421955	BLASTX	369	3e-33	56	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
7397	GM_128_B2_G12_T7	g3757517	BLASTX	149	2e-10	34	(AC005167) putative salt-inducible protein [Arabidopsis thaliana]
7398	GM_128_B2_H05_T7	g507910	BLASTN	471	1e-14	77	Glycine max BSR-101 satellite SB92 genomic sequence.
7399	GM_128_B2_H09_MR	g1785729	BLASTN	621	5e-21	61	A.thaliana mitochondrial genome, part B
7400	GM_128_B2_H09_T7	g3941729	BLASTN	405	3e-11	61	Homo sapiens chromosome 7 BAC clone F5, complete sequence [Homo sapiens]
7401	GM_129_A1_D10_MR	g905360	BLASTN	423	3e-12	88	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
7402	GM_129_A1_E07_MR	g2443320	BLASTX	157	3e-09	48	(D85597) polyprotein [Oryza australiensis]
7403	GM_129_A2_A05_MR	g3777526	BLASTN	450	2e-13	66	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
7404	GM_129_A2_A07_T7	g13606	BLASTN	283	9e-10	68	Yeast mitochondrial gene for transfer RNA-Trp >gi 343974 gb K03310 YSTMTTGWX Saccharomyces cerevisiae mitochondrial Trp-tRNA gene.
7405	GM_129_A2_A08_MR	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7406	GM_129_A2_A08_T7	g507910	BLASTN	375	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7407	GM_129_A2_A11_T7	g3758836	BLASTN	361	3e-09	61	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
7408	GM_129_A2_A12_T7	g2642431	BLASTX	320	2e-26	48	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
7409	GM_129_A2_B01_MR	g2894587	BLASTN	383	3e-10	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-112, complete sequence [Plasmodium falciparum]
7410	GM_129_A2_B02_MR	g3845327	BLASTN	289	3e-10	63	Plasmodium falciparum chromosome 2, section 68 of 73 of the complete sequence
7411	GM_129_A2_B03_MR	g3097320	BLASTN	717	2e-25	77	Glycine max gene for Bd 30K, complete cds
7412	GM_129_A2_B09_MR	g155854	BLASTN	414	4e-12	61	Babesia bigemina antigen (Bbg 1.1) mRNA, 3' end.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7413	GM_129_A2_B10_T7	g3426334	BLASTN	375	6e-10	60	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
7414	GM_129_A2_B11_MR	g134646	BLASTX	201	3e-19	92	SUPEROXIDE DISMUTASE, CHLOROPLAST PRECURSOR (FE) gi 169955 (M64267) Fe-superoxide dismutase [Glycine max] gi 228415 prf 1803527A Fe superoxide dismutase [Glycine max]
7415	GM_129_A2_B12_MR	g4063760	BLASTX	332	6e-28	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7416	GM_129_A2_B12_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7417	GM_129_A2_C06_T7	g2129709	BLASTX	236	1e-17	42	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
7418	GM_129_A2_C07_T7	g2522227	BLASTX	183	2e-13	38	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
7419	GM_129_A2_C12_T7	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7420	GM_129_A2_D01_T7	g3549652	BLASTX	269	4e-21	54	(AJ224982) MAP3K epsilon protein kinase [Arabidopsis thaliana]
7421	GM_129_A2_D02_T7	g4063760	BLASTX	148	2e-09	32	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7422	GM_129_A2_D04_MR	g3097320	BLASTN	427	3e-12	63	Glycine max gene for Bd 30K, complete cds
7423	GM_129_A2_D05_T7	g2160694	BLASTX	246	2e-21	83	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
7424	GM_129_A2_D06_T7	g3097320	BLASTN	564	2e-18	73	Glycine max gene for Bd 30K, complete cds
7425	GM_129_A2_D09_MR	g2129618	BLASTX	243	1e-18	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7426	GM_129_A2_D10_MR	g3142328	BLASTN	1138	1e-44	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7427	GM_129_A2_E02_MR	g3097320	BLASTN	470	3e-14	70	Glycine max gene for Bd 30K, complete cds
7428	GM_129_A2_E04_MR	g507910	BLASTN	576	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
7429	GM_129_A2_E04_T7	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
7430	GM_129_A2_E07_MR	g3810596	BLASTX	273	8e-22	49	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
7431	GM_129_A2_E08_MR	g905361	BLASTX	334	9e-29	78	(U22103) gag-protease polyprotein [Glycine max]
7432	GM_129_A2_E08_T7	g507910	BLASTN	433	6e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
7433	GM_129_A2_E09_T7	g2132182	BLASTX	262	4e-21	83	hypothetical protein YPL086c - yeast (Saccharomyces cerevisiae) gi 1151240 (U43281) Lpg22p [Saccharomyces cerevisiae]
7434	GM_129_A2_E12_T7	g2443320	BLASTX	178	9e-16	42	(D85597) polyprotein [Oryza australiensis]
7435	GM_129_A2_F01_MR	g3204134	BLASTX	193	4e-29	96	(AJ006771) beta-galactosidase [Cicer arietinum]
7436	GM_129_A2_F07_T7	g1769899	BLASTX	189	4e-22	73	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7437	GM_129_A2_F08_MR	g2522226	BLASTN	691	2e-24	66	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
7438	GM_129_A2_F10_MR	g4063760	BLASTX	390	4e-34	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7439	GM_129_A2_F11_MR	g1167523	BLASTX	91	5e-09	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
7440	GM_129_A2_F12_T7	g3645899	BLASTX	146	1e-13	41	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7441	GM_129_A2_G05_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7442	GM_129_A2_G05_T7	g507910	BLASTN	361	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7443	GM_129_A2_H01_MR	g3142328	BLASTN	691	3e-24	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7444	GM_129_A2_H04_T7	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7445	GM_129_A2_H05_T7	g3645899	BLASTX	213	8e-28	51	(U68408) 5' end not determined experimentally [Zea mays]
7446	GM_129_A2_H06_MR	g507910	BLASTN	604	1e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
7447	GM_129_A2_H06_T7	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7448	GM_129_B1_A01_MR	g2522227	BLASTX	150	1e-17	41	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
7449	GM_129_B1_A03_MR	g507910	BLASTN	401	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7450	GM_129_B1_A03_T7	g507910	BLASTN	371	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7451	GM_129_B1_A06_MR	g3142328	BLASTN	625	3e-21	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7452	GM_129_B1_A06_T7	g3599418	BLASTN	467	4e-14	70	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7453	GM_129_B1_A07_MR	g3845197	BLASTN	365	2e-09	57	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
7454	GM_129_B1_A07_T7	g1769897	BLASTX	317	3e-27	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7455	GM_129_B1_A08_MR	g2129618	BLASTX	184	4e-14	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7456	GM_129_B1_A09_MR	g4063760	BLASTX	536	9e-50	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7457	GM_129_B1_A11_T7	g3688600	BLASTX	174	2e-11	58	(AB009030) beta-Amyrin Synthase [Panax ginseng]
7458	GM_129_B1_A12_T7	g18559	BLASTN	355	5e-09	66	G.max gene for catalase
7459	GM_129_B1_B02_MR	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7460	GM_129_B1_B02_T7	g507910	BLASTN	366	6e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7461	GM_129_B1_B03_T7	g507910	BLASTN	369	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7462	GM_129_B1_B05_MR	g2244916	BLASTX	154	3e-09	21	(Z97339) hypothetical protein [Arabidopsis thaliana]
7463	GM_129_B1_B05_T7	g3097320	BLASTN	476	2e-14	69	Glycine max gene for Bd 30K, complete cds
7464	GM_129_B1_B06_MR	g255576	BLASTN	333	7e-09	66	small auxin up RNA gene cluster: orf 6B [Glycine max=soybeans, cv. Wayne, Genomic, 665 nt]
7465	GM_129_B1_B11_MR	g3142328	BLASTN	1290	2e-51	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7466	GM_129_B1_B12_MR	g4159702	BLASTN	579	4e-19	69	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2N11, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7467	GM_129_B1_C01_T7	g3513745	BLASTX	214	3e-15	28	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
7468	GM_129_B1_C02_T7	g2801677	BLASTN	748	1e-27	72	Glycine max telomere-associated sequence STAS6
7469	GM_129_B1_C08_MR	g2982571	BLASTN	384	2e-10	59	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-97, complete sequence [Plasmodium falciparum]
7470	GM_129_B1_C10_MR	g507910	BLASTN	414	4e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7471	GM_129_B1_C10_T7	g507910	BLASTN	403	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7472	GM_129_B1_C11_MR	g905361	BLASTX	723	1e-70	96	(U22103) gag-protease polyprotein [Glycine max]
7473	GM_129_B1_D03_MR	g1040717	BLASTN	396	4e-19	67	D.polychroa microsatellite sequence (clone Dp ch1 F3)
7474	GM_129_B1_D03_T7	g130582	BLASTX	422	2e-37	62	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
7475	GM_129_B1_D11_MR	g535454	BLASTX	196	1e-14	43	(U13940) cysteine proteinase [Alnus glutinosa]
7476	GM_129_B1_D11_T7	g535454	BLASTX	182	6e-13	58	(U13940) cysteine proteinase [Alnus glutinosa]
7477	GM_129_B1_D12_T7	g3142328	BLASTN	769	7e-28	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7478	GM_129_B1_E01_MR	g507910	BLASTN	387	7e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7479	GM_129_B1_E01_T7	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7480	GM_129_B1_E02_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7481	GM_129_B1_E06_MR	g4063756	BLASTN	529	7e-17	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
7482	GM_129_B1_E10_MR	g3947433	BLASTN	468	4e-14	64	Homo sapiens BAC clone RG060P12 from 7q21, complete sequence [Homo sapiens]
7483	GM_129_B1_E12_T7	g1171583	BLASTN	356	5e-09	63	P.falciparum complete gene map of plastid-like DNA (IR-A)
7484	GM_129_B1_F05_MR	g3645899	BLASTX	292	9e-24	62	(U68408) 5' end not determined experimentally [Zea mays]
7485	GM_129_B1_G04_T7	g18559	BLASTN	886	4e-33	75	G.max gene for catalase
7486	GM_129_B1_G06_MR	g3599418	BLASTN	355	5e-09	64	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7487	GM_129_B1_G08_MR	g507910	BLASTN	353	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7488	GM_129_B1_G08_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7489	GM_129_B1_G10_T7	g507910	BLASTN	380	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7490	GM_129_B1_G11_MR	g507910	BLASTN	515	1e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
7491	GM_129_B1_G11_T7	g4063760	BLASTX	288	3e-23	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7492	GM_129_B1_G12_MR	g1654140	BLASTX	260	2e-20	69	(U37840) lipoxygenase [Lycopersicon esculentum]
7493	GM_129_B1_H01_MR	g1174779	BLASTX	249	7e-20	88	TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR gi 166894 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]
7494	GM_129_B1_H03_T7	g2129613	BLASTX	135	8e-10	42	homeotic protein BEL1 - Arabidopsis thaliana gi 1122533 (U39944) BELL1 [Arabidopsis thaliana]
7495	GM_129_B1_H08_MR	g4115365	BLASTX	277	5e-22	50	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
7496	GM_129_B1_H09_MR	g3142328	BLASTN	1987	2e-83	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7497	GM_129_B1_H10_MR	g507910	BLASTN	515	1e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
7498	GM_129_B1_H10_T7	g4063760	BLASTX	281	2e-22	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7499	GM_129_B1_H11_T7	g3097320	BLASTN	432	2e-12	69	Glycine max gene for Bd 30K, complete cds
7500	GM_129_B1_H12_MR	g2500199	BLASTX	185	6e-38	100	RAC-LIKE GTP BINDING PROTEIN RHO1 gi 477010 pir A47525 ras-related small GTP-binding protein Rho1Ps - garden pea gi 1263170 (L19093) GTP-binding protein [Pisum sativum]
7501	GM_129_B2_A01_T7	g3645899	BLASTX	297	1e-29	49	(U68408) 5' end not determined experimentally [Zea mays]
7502	GM_129_B2_A05_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7503	GM_129_B2_A05_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7504	GM_129_B2_B01_MR	g2960069	BLASTX	155	2e-09	60	(Y12777) acyl-CoA synthetase-like protein [Homo sapiens]
7505	GM_129_B2_B08_MR	g4140712	BLASTX	197	6e-15	38	(AF110183) putative integrase [Oryza sativa]
7506	GM_129_B2_C09_MR	g2462749	BLASTX	289	6e-24	62	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]
7507	GM_129_B2_D02_MR	g2924729	BLASTN	362	3e-09	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]
7508	GM_129_B2_D08_T7	g2708743	BLASTX	241	4e-18	36	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
7509	GM_129_B2_D11_T7	g3777527	BLASTX	520	3e-56	95	(AF053008) gag-pol polyprotein [Glycine max]
7510	GM_129_B2_D12_MR	g218268	BLASTN	437	3e-13	78	Glycine max pol gene for reverse transcriptase, partial sequence
7511	GM_129_B2_E02_MR	g18559	BLASTN	694	2e-24	75	G.max gene for catalase
7512	GM_129_B2_E03_MR	g218269	BLASTX	247	3e-20	71	(D12839) reverse transcriptase [Glycine max]
7513	GM_129_B2_E04_T7	g3142330	BLASTX	593	6e-57	84	(U96295) envelope-like [Glycine max]
7514	GM_129_B2_E09_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7515	GM_129_B2_E10_T7	g4138185	BLASTN	418	1e-12	67	M.fuscata microsatellite DNA, MFGT22 region
7516	GM_129_B2_E11_MR	g1335695	BLASTX	208	5e-22	46	(X02600) unidentified open reading frame II (146 aa) [Drosophila melanogaster]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7517	GM_129_B2_E12_MR	g4115365	BLASTX	164	5e-10	43	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
7518	GM_129_B2_F04_T7	g1171583	BLASTN	360	3e-09	61	P.falciparum complete gene map of plastid-like DNA (IR-A)
7519	GM_129_B2_F08_T7	g3033389	BLASTX	242	2e-18	38	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
7520	GM_129_B2_F11_MR	g3777527	BLASTX	295	8e-24	45	(AF053008) gag-pol polyprotein [Glycine max]
7521	GM_129_B2_G01_MR	g117188	BLASTX	312	5e-27	50	CYTOCHROME P450 LXXIA1 (ARP-2) gi 81423 pir A35867 cytochrome P450 71A1 - avocado
7522	GM_129_B2_G07_MR	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7523	GM_129_B2_G07_T7	g507910	BLASTN	348	4e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7524	GM_129_B2_G08_T7	g4092470	BLASTN	713	4e-25	71	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
7525	GM_129_B2_G09_T7	g4063760	BLASTX	247	1e-25	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7526	GM_129_B2_G12_T7	g454847	BLASTN	411	1e-11	75	Glycine max ribosomal protein S11 gene, complete cds
7527	GM_129_B2_H03_T7	g3097320	BLASTN	528	7e-17	71	Glycine max gene for Bd 30K, complete cds
7528	GM_129_B2_H08_MR	g3142328	BLASTN	559	6e-40	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7529	GM_129_B2_H09_MR	g4063760	BLASTX	201	5e-14	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7530	GM_129_B2_H11_MR	g507910	BLASTN	389	6e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
7531	GM_129_B2_H12_T7	g2462058	BLASTX	286	2e-24	51	(Y13389) reverse transcriptase [Antirrhinum majus]
7532	GM_130_A1_A01_MR	g507910	BLASTN	501	5e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
7533	GM_130_A1_B09_MR	g13373	BLASTN	395	1e-11	61	Terminal inverted repeat from Paramecium mitochondrion >gi 342968 gb J01432 PARMTDIN1 paramecium species 1 mitochondria dimer initiation region dna.
7534	GM_130_A1_B11_MR	g3777527	BLASTX	229	1e-19	63	(AF053008) gag-pol polyprotein [Glycine max]
7535	GM_130_A1_C02_MR	g3097320	BLASTN	710	4e-25	81	Glycine max gene for Bd 30K, complete cds
7536	GM_130_A1_C04_MR	g1644402	BLASTX	174	8e-12	49	(U73524) putative ATP/GTP-binding protein [Homo sapiens]
7537	GM_130_A1_E06_MR	g1483218	BLASTX	130	5e-13	43	(X99793) induced upon wounding stress [Arabidopsis thaliana]
7538	GM_130_A1_G11_MR	g3845197	BLASTN	394	9e-11	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
7539	GM_130_B1_A01_T7	g4050011	BLASTN	425	3e-12	64	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
7540	GM_130_B1_A02_MR	g2624372	BLASTN	375	6e-10	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-64, complete sequence [Plasmodium falciparum]
7541	GM_130_B1_A02_T7	g3250687	BLASTX	127	4e-14	40	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
7542	GM_130_B1_A03_MR	g18559	BLASTN	412	1e-11	70	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7543	GM_130_B1_A05_T7	g3979928	BLASTN	400	5e-11	63	Caenorhabditis elegans cosmid Y18D10A, complete sequence [Caenorhabditis elegans]
7544	GM_130_B1_A06_T7	g21059	BLASTN	425	4e-13	66	P.vulgaris PvVPE2 mRNA for pectin esterase.
7545	GM_130_B1_A07_MR	g507910	BLASTN	359	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7546	GM_130_B1_A11_MR	g2522226	BLASTN	483	7e-15	63	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
7547	GM_130_B1_B04_T7	g3738114	BLASTN	359	3e-09	65	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
7548	GM_130_B1_B06_MR	g3142379	BLASTX	299	1e-25	67	(AF053008) envelope-like [Glycine max]
7549	GM_130_B1_B07_T7	g629693	BLASTX	183	7e-13	45	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
7550	GM_130_B1_B08_T7	g3021268	BLASTX	329	1e-27	44	(AL022347) putative protein [Arabidopsis thaliana]
7551	GM_130_B1_B10_MR	g2522228	BLASTX	222	4e-17	55	(AB007466) reverse transcriptase-like protein [Vicia faba]
7552	GM_130_B1_B10_T7	g1769898	BLASTX	239	2e-18	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7553	GM_130_B1_B12_T7	g3033400	BLASTX	216	5e-34	93	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]
7554	GM_130_B1_C02_MR	g3645899	BLASTX	206	1e-14	42	(U68408) 5' end not determined experimentally [Zea mays]
7555	GM_130_B1_C02_T7	g2708743	BLASTX	203	4e-14	31	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
7556	GM_130_B1_C04_T7	g3513747	BLASTX	204	2e-18	33	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
7557	GM_130_B1_C08_MR	g2194123	BLASTX	125	1e-15	70	(AC002062) Similar to Secale chloroplast ribosomal protein L12 (gb SCL121A). EST gb H36579 comes from this gene. [Arabidopsis thaliana]
7558	GM_130_B1_D01_T7	g2995405	BLASTX	574	2e-54	59	(Y12432) polyprotein [Ananas comosus]
7559	GM_130_B1_D02_MR	g3492857	BLASTN	454	2e-13	65	Homo sapiens 12q24.2 PAC RPCI1-157K6 (Roswell Park Cancer Institute Human PAC library) complete sequence [Homo sapiens]
7560	GM_130_B1_D04_MR	g1666236	BLASTX	166	3e-11	39	(U76261) unknown [Hordeum vulgare]
7561	GM_130_B1_D05_MR	g3777527	BLASTX	338	2e-28	45	(AF053008) gag-pol polyprotein [Glycine max]
7562	GM_130_B1_D07_T7	g4038056	BLASTX	399	2e-35	51	(AC005897) putative transposon [Arabidopsis thaliana]
7563	GM_130_B1_D09_MR	g2429543	BLASTX	173	5e-11	43	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]
7564	GM_130_B1_D11_MR	g3250687	BLASTX	158	2e-10	34	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
7565	GM_130_B1_E01_MR	g2462936	BLASTX	303	3e-26	46	(Y12321) open reading frame 2 [Brassica oleracea]
7566	GM_130_B1_E03_MR	g100488	BLASTX	199	5e-14	44	TNP2 protein - garden snapdragon

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7567	GM_130_B1_E04_MR	g3406033	BLASTN	393	1e-10	67	Homo sapiens 12p13.3 RPCI4-773N5 (Roswell Park Cancer Institute Human PAC library) complete sequence [Homo sapiens]
7568	GM_130_B1_E05_T7	g3176806	BLASTN	389	2e-11	62	Homo sapiens allele 17 fragile site locus (FRA10B) minisatellite, 5' sequence
7569	GM_130_B1_E08_MR	g99755	BLASTX	381	3e-34	51	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
7570	GM_130_B1_E11_MR	g1066856	BLASTN	459	1e-13	87	Glycine max acetyl coenzyme A carboxylase (ACCase-B) gene, 5' end of cds.
7571	GM_130_B1_F01_MR	g1666236	BLASTX	191	5e-14	30	(U76261) unknown [Hordeum vulgare]
7572	GM_130_B1_F02_T7	g3687234	BLASTX	182	5e-12	35	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
7573	GM_130_B1_F03_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7574	GM_130_B1_F03_T7	g3777527	BLASTX	794	4e-77	98	(AF053008) gag-pol polyprotein [Glycine max]
7575	GM_130_B1_F05_MR	g2828184	BLASTN	545	1e-17	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN9, complete sequence [Arabidopsis thaliana]
7576	GM_130_B1_F07_MR	g2642431	BLASTX	335	4e-28	50	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
7577	GM_130_B1_F10_T7	g507910	BLASTN	578	2e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
7578	GM_130_B1_F11_T7	g18559	BLASTN	464	5e-14	76	G.max gene for catalase
7579	GM_130_B1_F12_MR	g2443320	BLASTX	452	1e-40	48	(D85597) polyprotein [Oryza australiensis]
7580	GM_130_B1_G05_MR	g507910	BLASTN	365	7e-10	69	Glycine max BSR-101 satellite SB92 genomic sequence.
7581	GM_130_B1_G05_T7	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
7582	GM_130_B1_G10_MR	g1431738	BLASTN	676	9e-24	76	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
7583	GM_130_B1_G12_MR	g2239134	BLASTX	168	7e-15	65	(Y13729) NDH-A protein [Hordeum vulgare]
7584	GM_130_B1_H01_MR	g4063756	BLASTN	478	1e-14	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
7585	GM_130_B1_H02_MR	g1666236	BLASTX	240	1e-19	32	(U76261) unknown [Hordeum vulgare]
7586	GM_130_B1_H02_T7	g3980359	BLASTN	372	9e-10	60	Human DNA sequence from clone 344I7 on chromosome Xp11.21-11.3. Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8, KRT8) pseudogene, ESTs and a GSS, complete sequence [Homo sapiens]
7587	GM_130_B1_H03_T7	g1142701	BLASTN	1299	2e-52	84	Glycine max satellite STR120-A.3.
7588	GM_130_B1_H04_T7	g905361	BLASTX	219	2e-16	30	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7589	GM_130_B1_H05_MR	g100484	BLASTX	325	1e-27	43	hypothetical protein - garden snapdragon
7590	GM_130_B1_H06_T7	g2465923	BLASTX	175	3e-21	79	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]
7591	GM_130_B1_H08_MR	g3063461	BLASTX	168	1e-10	33	(AC003981) F22O13.23 [Arabidopsis thaliana]
7592	GM_130_B1_H10_MR	g629693	BLASTX	150	3e-15	36	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
7593	GM_130_B1_H11_MR	g2979597	BLASTN	716	3e-25	65	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
7594	GM_130_B1_H12_MR	g3695395	BLASTX	230	6e-19	40	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
7595	GM_130_B1_H12_T7	g3777527	BLASTX	687	1e-65	96	(AF053008) gag-pol polyprotein [Glycine max]
7596	GM_130_B2_A01_MR	g2129618	BLASTX	172	3e-12	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7597	GM_130_B2_A05_MR	g905361	BLASTX	305	1e-25	96	(U22103) gag-protease polyprotein [Glycine max]
7598	GM_130_B2_A06_MR	g507910	BLASTN	339	1e-08	69	Glycine max BSR-101 satellite SB92 genomic sequence.
7599	GM_130_B2_A06_T7	g507910	BLASTN	415	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7600	GM_130_B2_A07_T7	g3142328	BLASTN	844	3e-31	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7601	GM_130_B2_A08_T7	g905361	BLASTX	524	1e-49	96	(U22103) gag-protease polyprotein [Glycine max]
7602	GM_130_B2_A11_T7	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7603	GM_130_B2_B05_MR	g11565	BLASTN	556	1e-18	91	Soybean chloroplast psb A gene coding for photosystem II thylakoid membrane protein
7604	GM_130_B2_B07_MR	g4063760	BLASTX	272	1e-21	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7605	GM_130_B2_C01_T7	g2462058	BLASTX	266	3e-22	52	(Y13389) reverse transcriptase [Antirrhinum majus]
7606	GM_130_B2_C03_MR	g2997694	BLASTX	196	7e-15	38	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
7607	GM_130_B2_C06_T7	g3142328	BLASTN	586	1e-19	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7608	GM_130_B2_C07_MR	g100484	BLASTX	340	3e-29	52	hypothetical protein - garden snapdragon
7609	GM_130_B2_C07_T7	g18559	BLASTN	366	1e-09	75	G.max gene for catalase
7610	GM_130_B2_C08_T7	g3142328	BLASTN	700	1e-24	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7611	GM_130_B2_C09_T7	g3142328	BLASTN	1306	3e-52	83	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7612	GM_130_B2_C10_T7	g507910	BLASTN	720	6e-26	88	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7613	GM_130_B2_C12_MR	g507910	BLASTN	561	1e-18	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7614	GM_130_B2_D02_MR	g2522227	BLASTX	199	3e-15	51	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
7615	GM_130_B2_D03_T7	g4063760	BLASTX	537	8e-50	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7616	GM_130_B2_D07_MR	g3763850	BLASTN	524	1e-16	65	Glycine max GmENOD93 gene for early nodulin, complete cds
7617	GM_130_B2_D11_MR	g505129	BLASTN	361	2e-09	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
7618	GM_130_B2_E05_MR	g2129618	BLASTX	218	6e-16	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7619	GM_130_B2_E05_T7	g2244803	BLASTX	208	2e-19	42	(Z97336) reverse transcriptase-like protein [Arabidopsis thaliana]
7620	GM_130_B2_E07_MR	g1066856	BLASTN	456	1e-13	67	Glycine max acetyl coenzyme A carboxylase (ACCase-B) gene, 5' end of cds.
7621	GM_130_B2_E09_MR	g3599418	BLASTN	559	3e-18	83	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7622	GM_130_B2_E12_MR	g18559	BLASTN	361	3e-09	68	G.max gene for catalase
7623	GM_130_B2_F07_MR	g4063760	BLASTX	557	5e-52	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7624	GM_130_B2_F10_MR	g3097320	BLASTN	428	2e-12	72	Glycine max gene for Bd 30K, complete cds
7625	GM_130_B2_G05_T7	g130398	BLASTX	187	1e-12	38	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 297) gi 85089 pir B24872 retrovirus-related pol polyprotein homolog - fruit fly (Drosophila melanogaster) transposon 297
7626	GM_130_B2_H04_MR	g3777527	BLASTX	669	1e-66	97	(AF053008) gag-pol polyprotein [Glycine max]
7627	GM_130_B2_H06_MR	g3097320	BLASTN	480	1e-14	77	Glycine max gene for Bd 30K, complete cds
7628	GM_130_B2_H09_T7	g905361	BLASTX	432	1e-39	95	(U22103) gag-protease polyprotein [Glycine max]
7629	GM_131_A1_A05_T7	g1769898	BLASTX	241	1e-18	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7630	GM_131_A1_B03_MR	g2276311	BLASTN	367	1e-09	65	Human DNA sequence from PAC 431A14 on chromosome 6p21. Contains CYCLOPHILIN (PEPTIDYLPROLYL ISOMERASE) like and CIP1 (WAF1, CDKNA1, CDKN1, MDA-6, SDI1, PIC1, CAP20) genes. Contains probable GTPase and receptor genes and E...
7631	GM_131_A1_D01_MR	g3650039	BLASTX	149	8e-09	57	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
7632	GM_131_A1_D02_MR	g3204133	BLASTN	416	7e-12	84	Cicer arietinum mRNA for beta-galactosidase, partial
7633	GM_131_A1_E09_T7	g507910	BLASTN	384	9e-11	77	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7634	GM_131_A1_F01_MR	g3695395	BLASTX	174	2e-11	46	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
7635	GM_131_A1_G06_T7	g3097836	BLASTN	434	1e-12	62	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
7636	GM_131_A1_H01_MR	g130582	BLASTX	155	4e-09	63	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
7637	GM_131_B1_A09_T7	g100484	BLASTX	364	7e-32	56	hypothetical protein - garden snapdragon
7638	GM_131_B1_B02_T7	g3845197	BLASTN	410	2e-11	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
7639	GM_131_B1_B07_T7	g3097320	BLASTN	586	2e-19	75	Glycine max gene for Bd 30K, complete cds
7640	GM_131_B1_C01_T7	g1871202	BLASTN	372	9e-10	67	Human chromosome 16p13 BAC clone CIT987SK-3H8 complete sequence [Homo sapiens]
7641	GM_131_B1_C03_T7	g2979574	BLASTN	484	8e-15	64	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence [Homo sapiens]
7642	GM_131_B1_C07_T7	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
7643	GM_131_B1_C11_T7	g2961349	BLASTX	225	1e-16	50	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
7644	GM_131_B1_D11_T7	g3142328	BLASTN	939	1e-35	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7645	GM_131_B1_F07_T7	g3097320	BLASTN	458	1e-13	73	Glycine max gene for Bd 30K, complete cds
7646	GM_131_B1_G07_T7	g18559	BLASTN	348	1e-08	74	G.max gene for catalase
7647	GM_131_B1_G09_T7	g3023281	BLASTX	377	1e-38	61	HIGH AFFINITY AMMONIUM TRANSPORTER gi 2065194 gnl PID e223603 (X95098) ammonium transporter [Lycopersicon esculentum]
7648	GM_131_B1_H01_T7	g4063760	BLASTX	377	9e-33	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7649	GM_131_B2_A01_MR	g3142328	BLASTN	777	3e-28	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7650	GM_131_B2_A06_MR	g3142328	BLASTN	1225	1e-48	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7651	GM_131_B2_A07_MR	g505129	BLASTN	351	1e-11	73	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
7652	GM_131_B2_A09_MR	g3845298	BLASTN	403	3e-11	67	Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7653	GM_131_B2_A10_MR	g1769898	BLASTX	336	5e-29	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7654	GM_131_B2_B06_MR	g2995405	BLASTX	333	3e-28	45	(Y12432) polyprotein [Ananas comosus]
7655	GM_131_B2_B11_MR	g1769897	BLASTX	179	4e-12	32	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7656	GM_131_B2_C11_T7	g3777527	BLASTX	636	3e-60	95	(AF053008) gag-pol polyprotein [Glycine max]
7657	GM_131_B2_D01_MR	g100488	BLASTX	128	8e-09	37	TNP2 protein - garden snapdragon
7658	GM_131_B2_D04_T7	g1091678	BLASTX	140	1e-11	36	activator-like transposable element [Pennisetum glaucum]
7659	GM_131_B2_D06_MR	g541825	BLASTX	124	6e-11	80	protein kinase - spinach gi 457711 (Z30332) protein kinase [Spinacia oleracea]
7660	GM_131_B2_D10_T7	g3142328	BLASTN	1727	2e-71	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7661	GM_131_B2_D12_T7	g3645899	BLASTX	173	3e-15	41	(U68408) 5' end not determined experimentally [Zea mays]
7662	GM_131_B2_E01_MR	g3097320	BLASTN	620	5e-21	80	Glycine max gene for Bd 30K, complete cds
7663	GM_131_B2_E03_T7	g3645899	BLASTX	275	3e-27	49	(U68408) 5' end not determined experimentally [Zea mays]
7664	GM_131_B2_E04_T7	g2194136	BLASTX	370	6e-32	48	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
7665	GM_131_B2_E06_MR	g3142328	BLASTN	1621	1e-66	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7666	GM_131_B2_E09_T7	g3779026	BLASTX	324	5e-27	47	(AC005171) putative retrotransposon [Arabidopsis thaliana]
7667	GM_131_B2_E11_T7	g3650039	BLASTX	136	5e-14	36	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
7668	GM_131_B2_F01_MR	g4038056	BLASTX	294	4e-24	50	(AC005897) putative transposon [Arabidopsis thaliana]
7669	GM_131_B2_F06_T7	g3947433	BLASTN	439	9e-13	73	Homo sapiens BAC clone RG060P12 from 7q21, complete sequence [Homo sapiens]
7670	GM_131_B2_G03_T7	g2815075	BLASTN	380	4e-10	60	Caenorhabditis elegans cosmid Y38H8A, complete sequence [Caenorhabditis elegans]
7671	GM_131_B2_G05_MR	g1769898	BLASTX	331	2e-28	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7672	GM_131_B2_G05_T7	g3319351	BLASTX	207	1e-14	38	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
7673	GM_131_B2_G07_MR	g4126312	BLASTN	456	1e-13	63	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
7674	GM_131_B2_G09_MR	g18559	BLASTN	448	3e-13	70	G.max gene for catalase
7675	GM_131_B2_G09_T7	g2522228	BLASTX	124	3e-10	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
7676	GM_131_B2_G11_MR	g3738114	BLASTN	466	5e-14	66	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7677	GM_131_B2_G12_T7	g3777527	BLASTX	334	6e-31	74	(AF053008) gag-pol polyprotein [Glycine max]
7678	GM_131_B2_H03_MR	g2213606	BLASTN	420	6e-12	58	Genomic sequence for Arabidopsis thaliana BAC F21J9, complete sequence [Arabidopsis thaliana]
7679	GM_131_B2_H04_MR	g507910	BLASTN	373	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7680	GM_131_B2_H06_MR	g2245044	BLASTX	174	2e-20	52	(Z97342) similarity to reverse transcriptase - Arabidopsis thaliana retrotransposon 2 (fragment) [Arabidopsis thaliana]
7681	GM_132_A1_A10_T7	g3882355	BLASTX	189	1e-13	77	(U92460) pdr1 [Arabidopsis thaliana]
7682	GM_132_A1_E03_T7	g507910	BLASTN	569	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
7683	GM_132_A1_F01_MR	g1658456	BLASTN	350	2e-09	66	Gossypium barbadense strain Giza 84, gypsy retrotransposon, reverse transcriptase gene, partial cds.
7684	GM_132_A1_F03_MR	g342952	BLASTN	409	2e-12	64	paramecium species 1,168 mt dna dimer: replication init. region.
7685	GM_132_A1_F04_T7	g2522227	BLASTX	207	5e-16	54	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
7686	GM_132_A1_F12_T7	g3452140	BLASTX	191	2e-14	73	(AJ004901) resistance protein [Glycine max]
7687	GM_132_A1_H01_T7	g3582328	BLASTX	170	6e-11	39	(AC005496) hypothetical protein [Arabidopsis thaliana]
7688	GM_132_A1_H02_T7	g3298547	BLASTX	180	4e-12	42	(AC004681) putative condensin protein [Arabidopsis thaliana]
7689	GM_132_A1_H11_T7	g3142328	BLASTN	692	2e-24	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7690	GM_132_A2_A02_T7	g3097320	BLASTN	1011	9e-39	78	Glycine max gene for Bd 30K, complete cds
7691	GM_132_A2_A05_MR	g905361	BLASTX	697	5e-68	93	(U22103) gag-protease polyprotein [Glycine max]
7692	GM_132_A2_A05_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7693	GM_132_A2_A11_MR	g3645899	BLASTX	155	2e-12	50	(U68408) 5' end not determined experimentally [Zea mays]
7694	GM_132_A2_A11_T7	g3777527	BLASTX	313	9e-33	49	(AF053008) gag-pol polyprotein [Glycine max]
7695	GM_132_A2_B03_T7	g3513745	BLASTX	213	4e-15	33	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
7696	GM_132_A2_B04_T7	g1769898	BLASTX	176	4e-17	52	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7697	GM_132_A2_B05_MR	g507910	BLASTN	550	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
7698	GM_132_A2_B05_T7	g4063760	BLASTX	219	7e-16	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7699	GM_132_A2_C01_MR	g18559	BLASTN	1004	2e-38	73	G.max gene for catalase
7700	GM_132_A2_C02_MR	g3608155	BLASTX	117	2e-13	60	(AC005314) putative RNA helicase [Arabidopsis thaliana]
7701	GM_132_A2_C02_T7	g3377834	BLASTX	216	6e-16	36	(AF075598) No definition line found [Arabidopsis thaliana]
7702	GM_132_A2_C03_T7	g422418	BLASTX	228	6e-17	43	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
7703	GM_132_A2_C05_T7	g3645899	BLASTX	280	2e-22	57	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7704	GM_132_A2_C07_T7	g3241916	BLASTN	505	9e-16	68	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15N18, complete sequence [Arabidopsis thaliana]
7705	GM_132_A2_C08_T7	g4006831	BLASTX	229	9e-27	41	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
7706	GM_132_A2_C09_MR	g3777527	BLASTX	289	3e-23	52	(AF053008) gag-pol polyprotein [Glycine max]
7707	GM_132_A2_D02_MR	g343022	BLASTN	733	3e-26	83	Pea chloroplast photosystem II gene encoding the D2 and 44kd chlorophyll a-binding proteins, complete cds.
7708	GM_132_A2_D03_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7709	GM_132_A2_D03_T7	g507910	BLASTN	623	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7710	GM_132_A2_D06_MR	g131301	BLASTX	246	3e-20	86	PHOTOSYSTEM II D2 PROTEIN (PHOTOSYSTEM Q(A) PROTEIN) gi 72664 pir F2NTD2 photosystem II protein D2 - common tobacco chloroplast gi 1076691 pir S52397 photosystem II protein D2 - garden snapdragon chloroplast gi 11824 (Z00044) PSII D2 protein [Nicotiana tabacum] gi 669100 (X84155) photosystem I subunit [Antirrhinum majus] gi 225284 prf 1211235V photosystem II D2 protein [Nicotiana tabacum]
7711	GM_132_A2_D10_MR	g99922	BLASTX	272	1e-28	66	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
7712	GM_132_A2_E05_T7	g1785701	BLASTX	103	2e-09	33	(Y08501) orf154 [Arabidopsis thaliana]
7713	GM_132_A2_E08_T7	g3810596	BLASTX	138	7e-09	32	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
7714	GM_132_A2_F03_MR	g4038057	BLASTX	179	7e-12	39	(AC005897) hypothetical protein [Arabidopsis thaliana]
7715	GM_132_A2_F04_T7	g3608144	BLASTX	118	2e-13	72	(AC005314) unknown protein [Arabidopsis thaliana]
7716	GM_132_A2_F06_T7	g3599418	BLASTN	493	2e-15	88	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7717	GM_132_A2_F08_T7	g1769898	BLASTX	399	5e-36	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7718	GM_132_A2_G01_T7	g1666236	BLASTX	294	3e-25	34	(U76261) unknown [Hordeum vulgare]
7719	GM_132_A2_G02_MR	g2160169	BLASTX	143	6e-18	48	(AC000132) No definition line found [Arabidopsis thaliana]
7720	GM_132_A2_G03_MR	g3777527	BLASTX	240	5e-18	38	(AF053008) gag-pol polyprotein [Glycine max]
7721	GM_132_A2_G06_T7	g3176795	BLASTN	430	4e-13	60	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
7722	GM_132_A2_G08_T7	g4160362	BLASTN	357	4e-09	61	Saccharomyces cerevisiae complete mitochondrial genome
7723	GM_132_A2_H09_MR	g3834323	BLASTX	192	5e-14	42	(AC005679) F9K20.25 [Arabidopsis thaliana]
7724	GM_132_A2_H10_MR	g18559	BLASTN	427	3e-12	74	G.max gene for catalase
7725	GM_132_B1_A03_T7	g507910	BLASTN	629	8e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
7726	GM_132_B1_A04_T7	g2791289	BLASTX	358	1e-30	49	(AJ000387) protease [Drosophila melanogaster]
7727	GM_132_B1_A11_T7	g507910	BLASTN	404	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7728	GM_132_B1_A12_T7	g2506276	BLASTX	225	5e-17	64	RUBISCO SUBUNIT BINDING-PROTEIN ALPHA SUBUNIT PRECURSOR (60 KD CHAPERONIN ALPHA SUBUNIT) (CPN-60 ALPHA) gi 2129561 pir S71235 chaperonin-60 alpha chain - Arabidopsis thaliana gi 1223910 (U49357) chaperonin-60 alpha subunit [Arabidopsis thaliana]
7729	GM_132_B1_B01_T7	g2129618	BLASTX	161	1e-11	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7730	GM_132_B1_B02_MR	g3449327	BLASTN	419	7e-12	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]
7731	GM_132_B1_B03_MR	g3810596	BLASTX	255	7e-20	46	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
7732	GM_132_B1_B05_MR	g3810596	BLASTX	179	9e-12	45	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
7733	GM_132_B1_B06_MR	g2443320	BLASTX	252	2e-19	47	(D85597) polyprotein [Oryza australiensis]
7734	GM_132_B1_B10_MR	g507910	BLASTN	435	5e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
7735	GM_132_B1_B11_T7	g1326016	BLASTX	188	1e-12	58	TY3-2 orfB
7736	GM_132_B1_C05_MR	g4063760	BLASTX	321	8e-27	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7737	GM_132_B1_C06_MR	g2660670	BLASTX	360	4e-31	76	(AC002342) putative Cu2+-transporting ATPase [Arabidopsis thaliana]
7738	GM_132_B1_C06_T7	g2827663	BLASTX	149	8e-09	35	(AL021637) membrane-associated salt-inducible-like protein [Arabidopsis thaliana]
7739	GM_132_B1_C07_MR	g3142300	BLASTX	284	9e-23	65	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb L29224 from S. cerevisiae. ESTs gb R64908 and gb T88158, gb N38703 and gb AA651043 come from this gene. [Arabidopsis thaliana]
7740	GM_132_B1_C08_MR	g507910	BLASTN	435	5e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
7741	GM_132_B1_C08_T7	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7742	GM_132_B1_C10_MR	g507910	BLASTN	678	5e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
7743	GM_132_B1_C11_T7	g170605	BLASTN	546	4e-18	64	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
7744	GM_132_B1_D01_T7	g3142328	BLASTN	812	8e-30	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7745	GM_132_B1_D02_MR	g3645899	BLASTX	196	2e-14	46	(U68408) 5' end not determined experimentally [Zea mays]
7746	GM_132_B1_D04_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7747	GM_132_B1_D04_T7	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7748	GM_132_B1_D06_MR	g2129618	BLASTX	161	7e-10	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7749	GM_132_B1_D10_MR	g18559	BLASTN	352	6e-09	65	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7750	GM_132_B1_E01_MR	g3142328	BLASTN	494	2e-15	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7751	GM_132_B1_E05_T7	g2995405	BLASTX	147	2e-10	44	(Y12432) polyprotein [Ananas comosus]
7752	GM_132_B1_E10_MR	g2244915	BLASTX	228	5e-17	40	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
7753	GM_132_B1_E11_MR	g1769898	BLASTX	225	4e-17	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7754	GM_132_B1_F02_T7	g2995405	BLASTX	410	3e-40	65	(Y12432) polyprotein [Ananas comosus]
7755	GM_132_B1_F03_MR	g99922	BLASTX	368	9e-43	76	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
7756	GM_132_B1_F05_MR	g2462749	BLASTX	226	4e-17	57	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]
7757	GM_132_B1_F06_MR	g3599418	BLASTN	380	3e-10	72	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7758	GM_132_B1_G02_T7	g1769898	BLASTX	334	8e-29	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7759	GM_132_B1_G03_MR	g3047103	BLASTX	146	7e-09	84	(AF058919) regions of weak similarity to l-asparaginase [Arabidopsis thaliana]
7760	GM_132_B1_G08_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7761	GM_132_B1_G08_T7	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7762	GM_132_B1_G10_MR	g3810596	BLASTX	300	1e-24	51	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
7763	GM_132_B1_H06_T7	g507910	BLASTN	622	2e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7764	GM_132_B1_H07_T7	g3377856	BLASTX	351	5e-30	53	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 19.54) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 12.35) [Arabidopsis thaliana]
7765	GM_132_B1_H08_T7	g1703318	BLASTX	111	4e-13	65	ANNEXIN-LIKE PROTEIN RJ4 gi 1362037 pir S56674 annexin homolog RJ4 (clone RJ4) - garden strawberry (fragment) gi 643076 (U19941) annexin [Fragaria x ananassa]
7766	GM_132_B1_H10_T7	g4038037	BLASTX	155	4e-09	29	(AC005936) hypothetical protein [Arabidopsis thaliana]
7767	GM_132_B1_H11_T7	g2584827	BLASTN	399	6e-11	60	Arabidopsis thaliana chromosome 1 BAC F12F1 sequence, complete sequence [Arabidopsis thaliana]
7768	GM_132_B2_A02_T7	g3777527	BLASTX	229	7e-17	76	(AF053008) gag-pol polyprotein [Glycine max]
7769	GM_132_B2_A04_MR	g507910	BLASTN	529	3e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
7770	GM_132_B2_A08_MR	g507910	BLASTN	406	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7771	GM_132_B2_B03_T7	g2522227	BLASTX	199	3e-15	52	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
7772	GM_132_B2_B06_MR	g3461836	BLASTX	206	8e-19	72	(AC005315) putative protein kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7773	GM_132_B2_B09_MR	g3142328	BLASTN	813	7e-30	98	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7774	GM_132_B2_B12_MR	g3142328	BLASTN	1330	2e-53	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7775	GM_132_B2_C01_MR	g4063760	BLASTX	156	3e-09	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7776	GM_132_B2_C02_T7	g421955	BLASTX	183	2e-21	52	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
7777	GM_132_B2_C03_MR	g2462058	BLASTX	385	7e-35	54	(Y13389) reverse transcriptase [Antirrhinum majus]
7778	GM_132_B2_C04_MR	g3738114	BLASTN	398	6e-11	59	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
7779	GM_132_B2_C07_MR	g1142703	BLASTN	903	3e-34	91	Glycine max satellite STR120-B.1.
7780	GM_132_B2_C09_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7781	GM_132_B2_C10_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7782	GM_132_B2_C10_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7783	GM_132_B2_D03_MR	g3023751	BLASTX	177	3e-14	64	70 KD PEPTIDYLPROLYL ISOMERASE (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE) gi 1076772 pir S55383 peptidylprolyl isomerase (EC 5.2.1.8) - wheat gi 854626 (X86903) peptidylprolyl isomerase [Triticum aestivum]
7784	GM_132_B2_D10_T7	g1769898	BLASTX	200	1e-24	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7785	GM_132_B2_D12_MR	g18559	BLASTN	1098	9e-43	75	G.max gene for catalase
7786	GM_132_B2_E05_MR	g100484	BLASTX	244	3e-22	46	hypothetical protein - garden snapdragon
7787	GM_132_B2_E05_T7	g3777527	BLASTX	541	4e-50	91	(AF053008) gag-pol polyprotein [Glycine max]
7788	GM_132_B2_E08_MR	g3097320	BLASTN	415	9e-12	72	Glycine max gene for Bd 30K, complete cds
7789	GM_132_B2_F02_T7	g1480927	BLASTN	395	6e-11	79	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
7790	GM_132_B2_F03_T7	g18737	BLASTN	374	6e-10	81	Glycine max RPRP3 gene for repetitive proline-rich protein 3
7791	GM_132_B2_F05_MR	g99755	BLASTX	406	4e-37	53	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
7792	GM_132_B2_F07_MR	g3820757	BLASTN	400	3e-11	65	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
7793	GM_132_B2_G01_MR	g508826	BLASTN	362	2e-09	64	Drosophila melanogaster Oregon-R mitochondrial A+T region.
7794	GM_132_B2_G02_T7	g18559	BLASTN	769	8e-28	79	G.max gene for catalase
7795	GM_132_B2_G05_MR	g3047068	BLASTX	192	3e-13	39	(AF058825) similar to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7796	GM_132_B2_G10_MR	g1167523	BLASTX	107	7e-17	46	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
7797	GM_132_B2_G11_MR	g2995405	BLASTX	493	1e-45	69	(Y12432) polyprotein [Ananas comosus]
7798	GM_132_B2_H02_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7799	GM_132_B2_H09_MR	g3097320	BLASTN	465	5e-14	68	Glycine max gene for Bd 30K, complete cds
7800	GM_133_A1_A02_T7	g507910	BLASTN	539	1e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
7801	GM_133_A1_A05_T7	g905361	BLASTX	116	9e-13	31	(U22103) gag-protease polyprotein [Glycine max]
7802	GM_133_A1_B09_T7	g507910	BLASTN	395	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7803	GM_133_A1_B10_T7	g3097320	BLASTN	837	7e-31	79	Glycine max gene for Bd 30K, complete cds
7804	GM_133_A1_B11_MR	g2443320	BLASTX	193	4e-13	36	(D85597) polyprotein [Oryza australiensis]
7805	GM_133_A1_B12_MR	g99922	BLASTX	324	2e-28	76	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
7806	GM_133_A1_C01_T7	g3097320	BLASTN	467	4e-14	70	Glycine max gene for Bd 30K, complete cds
7807	GM_133_A1_C06_MR	g4038056	BLASTX	266	4e-21	47	(AC005897) putative transposon [Arabidopsis thaliana]
7808	GM_133_A1_C12_T7	g4063760	BLASTX	173	7e-18	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7809	GM_133_A1_D05_T7	g3695395	BLASTX	104	1e-10	51	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
7810	GM_133_A1_D06_MR	g507910	BLASTN	522	6e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
7811	GM_133_A1_E07_T7	g2464905	BLASTX	240	1e-19	59	(Z99708) minor allergen [Arabidopsis thaliana]
7812	GM_133_A1_E12_T7	g728905	BLASTX	202	5e-14	46	PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC RETICULUM CA2+-ATPASE) gi 1078206 pir S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) gi 171114 (L01795) ATPase [Saccharomyces cerevisiae] gi 595560 (U12980) Drs2p: Membrane spanning Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae]
7813	GM_133_A1_F02_T7	g2522228	BLASTX	239	5e-19	57	(AB007466) reverse transcriptase-like protein [Vicia faba]
7814	GM_133_A1_F04_T7	g18559	BLASTN	705	6e-25	76	G.max gene for catalase
7815	GM_133_A1_F12_T7	g3777527	BLASTX	252	4e-29	53	(AF053008) gag-pol polyprotein [Glycine max]
7816	GM_133_A1_G02_MR	g2129618	BLASTX	185	2e-12	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7817	GM_133_A1_G03_MR	g4038056	BLASTX	194	2e-23	49	(AC005897) putative transposon [Arabidopsis thaliana]
7818	GM_133_A1_G04_MR	g170606	BLASTN	494	1e-15	65	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
7819	GM_133_A1_G08_T7	g3097320	BLASTN	504	9e-16	78	Glycine max gene for Bd 30K, complete cds
7820	GM_133_A1_H02_MR	g3142328	BLASTN	789	7e-58	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7821	GM_133_A1_H05_MR	g294042	BLASTN	409	2e-11	62	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
7822	GM_133_A1_H10_T7	g2264307	BLASTN	774	6e-28	73	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MED24, complete sequence [Arabidopsis thaliana]
7823	GM_133_A2_A02_MR	g2995405	BLASTX	407	3e-36	68	(Y12432) polyprotein [Ananas comosus]
7824	GM_133_A2_A05_MR	g3650039	BLASTX	152	4e-09	36	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
7825	GM_133_A2_A06_MR	g629693	BLASTX	305	2e-26	60	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
7826	GM_133_A2_B03_MR	g18559	BLASTN	511	4e-16	71	G.max gene for catalase
7827	GM_133_A2_B06_T7	g629693	BLASTX	283	4e-24	61	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
7828	GM_133_A2_B11_MR	g3777527	BLASTX	497	2e-45	92	(AF053008) gag-pol polyprotein [Glycine max]
7829	GM_133_A2_B11_T7	g3142379	BLASTX	310	6e-27	66	(AF053008) envelope-like [Glycine max]
7830	GM_133_A2_C02_T7	g3810595	BLASTX	279	3e-22	42	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
7831	GM_133_A2_C03_MR	g1685003	BLASTX	230	8e-18	40	(U32643) immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]
7832	GM_133_A2_C04_MR	g3645899	BLASTX	133	4e-11	43	(U68408) 5' end not determined experimentally [Zea mays]
7833	GM_133_A2_C04_T7	g3142379	BLASTX	260	3e-21	59	(AF053008) envelope-like [Glycine max]
7834	GM_133_A2_C05_MR	g132086	BLASTX	290	7e-25	100	RIBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN 1 PRECURSOR gi 68053 pir RKSYS ribulose-bisphosphate carboxylase (EC 4.1.1.39) small chain precursor SRS1 - soybean gi 18742 (V00458) rubpcase [Glycine max]
7835	GM_133_A2_C06_T7	g3097320	BLASTN	1180	2e-46	82	Glycine max gene for Bd 30K, complete cds
7836	GM_133_A2_C08_MR	g507910	BLASTN	424	2e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
7837	GM_133_A2_C08_T7	g507910	BLASTN	447	1e-13	78	Glycine max BSR-101 satellite SB92 genomic sequence.
7838	GM_133_A2_C09_T7	g2895634	BLASTN	395	4e-11	64	Zerene eurydice large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
7839	GM_133_A2_C11_MR	g3845281	BLASTN	324	5e-09	65	Plasmodium falciparum chromosome 2, section 56 of 73 of the complete sequence
7840	GM_133_A2_D02_T7	g1666236	BLASTX	200	5e-15	37	(U76261) unknown [Hordeum vulgare]
7841	GM_133_A2_D07_T7	g3395443	BLASTX	291	6e-25	47	(AC004683) putative ammonium transporter, 3' partial [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7842	GM_133_A2_D08_T7	g3600054	BLASTX	169	3e-11	34	(AF080120) No definition line found [Arabidopsis thaliana]
7843	GM_133_A2_D09_MR	g1888357	BLASTX	177	2e-11	67	(X98130) alpha-mannosidase [Arabidopsis thaliana] gi 1890154 gnl PID e307744 (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]
7844	GM_133_A2_D09_T7	g2323254	BLASTN	373	8e-10	64	Human Chromosome X, complete sequence [Homo sapiens]
7845	GM_133_A2_E02_MR	g507910	BLASTN	609	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7846	GM_133_A2_E02_T7	g4063756	BLASTN	361	3e-09	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
7847	GM_133_A2_E03_MR	g3810596	BLASTX	212	3e-15	34	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
7848	GM_133_A2_E05_MR	g3599418	BLASTN	1118	1e-43	87	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
7849	GM_133_A2_F02_T7	g18559	BLASTN	715	2e-25	73	G.max gene for catalase
7850	GM_133_A2_F03_MR	g1142701	BLASTN	975	9e-38	81	Glycine max satellite STR120-A.3.
7851	GM_133_A2_F05_T7	g507910	BLASTN	577	2e-19	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7852	GM_133_A2_F09_MR	g1619300	BLASTX	168	6e-12	47	(X95269) LRR protein [Lycopersicon esculentum]
7853	GM_133_A2_F11_T7	g1524341	BLASTN	362	8e-10	73	S.douglasii mitochondrial tRNAPro and tRNAtrp genes
7854	GM_133_A2_F12_T7	g2522230	BLASTX	239	2e-19	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
7855	GM_133_A2_G01_MR	g905361	BLASTX	194	1e-13	40	(U22103) gag-protease polyprotein [Glycine max]
7856	GM_133_A2_G04_MR	g507910	BLASTN	404	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7857	GM_133_A2_G04_T7	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
7858	GM_133_A2_G05_T7	g1813979	BLASTX	325	1e-28	76	(Y10860) hypothetical protein [Musa acuminata]
7859	GM_133_A2_G08_T7	g3142328	BLASTN	961	1e-36	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7860	GM_133_A2_G10_MR	g2765817	BLASTX	157	9e-10	75	(Z95352) AtMlo-h1 [Arabidopsis thaliana]
7861	GM_133_A2_G11_T7	g4063760	BLASTX	281	1e-22	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7862	GM_133_A2_H05_MR	g4063760	BLASTX	423	1e-37	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7863	GM_133_A2_H08_T7	g4063760	BLASTX	225	1e-16	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7864	GM_133_B1_A04_MR	g3695387	BLASTX	151	1e-08	50	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
7865	GM_133_B1_A07_T7	g3820757	BLASTN	387	1e-10	66	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
7866	GM_133_B1_A08_T7	g1769898	BLASTX	183	2e-12	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7867	GM_133_B1_A09_T7	g507910	BLASTN	420	2e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7868	GM_133_B1_B04_MR	g2995405	BLASTX	309	1e-25	63	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7869	GM_133_B1_C02_T7	g2462134	BLASTX	187	5e-13	39	(Y13368) reverse transcriptase [Beta vulgaris]
7870	GM_133_B1_C03_MR	g4063760	BLASTX	309	2e-25	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7871	GM_133_B1_C03_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7872	GM_133_B1_C05_MR	g2502084	BLASTN	623	4e-22	77	Vigna radiata adenosine triphosphatase mRNA, partial cds
7873	GM_133_B1_C05_T7	g4056421	BLASTX	352	2e-31	76	(AC005322) Similar to gb Z30094 basic transcripion factor 2, 44 kD subunit from Homo sapiens. EST gb W43325 comes from this gene. [Arabidopsis thaliana]
7874	GM_133_B1_C11_MR	g3097320	BLASTN	1258	6e-50	84	Glycine max gene for Bd 30K, complete cds
7875	GM_133_B1_D03_MR	g3777527	BLASTX	313	2e-27	71	(AF053008) gag-pol polyprotein [Glycine max]
7876	GM_133_B1_D04_T7	g3513747	BLASTX	182	8e-12	44	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
7877	GM_133_B1_D12_T7	g2129473	BLASTX	238	2e-19	48	arabinogalactan-like protein - loblolly pine gi 607774 (U09556) arabinogalactan-like protein [Pinus taeda]
7878	GM_133_B1_E01_T7	g2642431	BLASTX	156	5e-09	38	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
7879	GM_133_B1_E02_MR	g2505878	BLASTX	298	7e-25	62	(Y12776) gene5; most likely [Arabidopsis thaliana]
7880	GM_133_B1_E02_T7	g2252836	BLASTX	201	3e-14	52	(AF013293) contains weak similarity to S. cerevisiae BOB1 protein (PIR:S45444) [Arabidopsis thaliana]
7881	GM_133_B1_E06_MR	g3319362	BLASTX	234	1e-17	43	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
7882	GM_133_B1_E06_T7	g3513747	BLASTX	283	2e-22	51	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
7883	GM_133_B1_E07_T7	g507910	BLASTN	573	3e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
7884	GM_133_B1_E11_T7	g3882297	BLASTX	135	9e-09	67	(AB018331) KIAA0788 protein [Homo sapiens]
7885	GM_133_B1_F03_MR	g3810596	BLASTX	247	5e-19	35	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
7886	GM_133_B1_F04_MR	g3142328	BLASTN	891	2e-33	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7887	GM_133_B1_F04_T7	g3142328	BLASTN	870	2e-32	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7888	GM_133_B1_F07_MR	g3097320	BLASTN	556	4e-18	72	Glycine max gene for Bd 30K, complete cds
7889	GM_133_B1_F08_T7	g3461846	BLASTX	155	5e-09	44	(AC005315) putative zinc-finger protein [Arabidopsis thaliana]
7890	GM_133_B1_F09_T7	g507910	BLASTN	442	2e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7891	GM_133_B1_F11_MR	g2443320	BLASTX	196	2e-13	39	(D85597) polyprotein [Oryza australiensis]
7892	GM_133_B1_F12_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7893	GM_133_B1_G02_T7	g18559	BLASTN	803	2e-29	77	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7894	GM_133_B1_G03_MR	g641905	BLASTX	241	1e-19	59	(U19267) cysteine proteinase [Zinnia elegans]
7895	GM_133_B1_G06_MR	g132674	BLASTX	86	6e-13	40	50S RIBOSOMAL PROTEIN L14 gi 94724 pir S15437 ribosomal protein L14 - Thermus aquaticus gi 48104 (X56552) ribosomal protein L14 [Thermus aquaticus] gi 755806 (Z37993) ribosomal protein L14 [Thermus thermophilus]
7896	GM_133_B1_G10_MR	g18559	BLASTN	835	8e-31	78	G.max gene for catalase
7897	GM_133_B1_H05_T7	g629693	BLASTX	275	3e-23	60	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
7898	GM_133_B1_H11_MR	g3510505	BLASTX	210	6e-15	48	(AF030881) pol polyprotein [Fugu rubripes]
7899	GM_133_B2_A03_MR	g3695387	BLASTX	283	8e-23	72	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
7900	GM_133_B2_A03_T7	g3142328	BLASTN	847	2e-31	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7901	GM_133_B2_A04_MR	g3097320	BLASTN	639	7e-22	73	Glycine max gene for Bd 30K, complete cds
7902	GM_133_B2_A07_MR	g507910	BLASTN	422	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7903	GM_133_B2_A07_T7	g18559	BLASTN	924	7e-35	78	G.max gene for catalase
7904	GM_133_B2_A10_T7	g3930515	BLASTX	121	7e-09	47	(AF059674) putative gag protein [Nicotiana tabacum]
7905	GM_133_B2_B01_T7	g3650039	BLASTX	220	2e-16	42	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
7906	GM_133_B2_B02_T7	g1142701	BLASTN	1267	6e-51	84	Glycine max satellite STR120-A.3.
7907	GM_133_B2_B04_MR	g507910	BLASTN	666	2e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
7908	GM_133_B2_B07_MR	g2443320	BLASTX	262	6e-26	53	(D85597) polyprotein [Oryza australiensis]
7909	GM_133_B2_B07_T7	g2995405	BLASTX	410	1e-36	63	(Y12432) polyprotein [Ananas comosus]
7910	GM_133_B2_C06_MR	g18559	BLASTN	871	2e-32	75	G.max gene for catalase
7911	GM_133_B2_C07_T7	g2995405	BLASTX	312	2e-28	47	(Y12432) polyprotein [Ananas comosus]
7912	GM_133_B2_D08_MR	g3645899	BLASTX	139	7e-18	48	(U68408) 5' end not determined experimentally [Zea mays]
7913	GM_133_B2_D10_MR	g2924777	BLASTX	247	6e-19	39	(AC002334) putative receptor protein kinase [Arabidopsis thaliana]
7914	GM_133_B2_E01_MR	g2129618	BLASTX	216	1e-15	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7915	GM_133_B2_E02_MR	g4063760	BLASTX	433	8e-39	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7916	GM_133_B2_E02_T7	g507910	BLASTN	436	4e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
7917	GM_133_B2_E05_MR	g4063760	BLASTX	163	5e-17	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7918	GM_133_B2_E05_T7	g3142328	BLASTN	1775	1e-73	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7919	GM_133_B2_E07_MR	g2982291	BLASTX	146	1e-09	57	(AF051230) heat shock protein [Picea mariana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7920	GM_133_B2_E09_MR	g1769897	BLASTX	317	3e-27	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7921	GM_133_B2_E12_T7	g507910	BLASTN	419	3e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
7922	GM_133_B2_F01_T7	g4063760	BLASTX	472	7e-43	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7923	GM_133_B2_F02_T7	g3777527	BLASTX	626	4e-59	96	(AF053008) gag-pol polyprotein [Glycine max]
7924	GM_133_B2_F05_MR	g4063760	BLASTX	255	1e-19	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7925	GM_133_B2_G02_T7	g3142328	BLASTN	961	1e-36	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
7926	GM_133_B2_G03_MR	g2769655	BLASTN	525	1e-16	66	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
7927	GM_133_B2_G04_MR	g1769897	BLASTX	233	6e-18	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7928	GM_133_B2_H05_T7	g18559	BLASTN	786	1e-28	75	G.max gene for catalase
7929	GM_133_B2_H09_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7930	GM_133_B2_H09_T7	g3777527	BLASTX	584	1e-54	94	(AF053008) gag-pol polyprotein [Glycine max]
7931	GM_133_B2_H10_MR	g4063760	BLASTX	122	8e-09	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7932	GM_133_B2_H11_T7	g421954	BLASTX	259	1e-20	46	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
7933	GM_134_A1_A06_MR	g507910	BLASTN	378	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
7934	GM_134_A1_A10_T7	g4063760	BLASTX	258	4e-20	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7935	GM_134_A1_B01_MR	g507910	BLASTN	423	2e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
7936	GM_134_A1_B01_T7	g507910	BLASTN	383	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7937	GM_134_A1_B04_MR	g3097320	BLASTN	552	6e-18	75	Glycine max gene for Bd 30K, complete cds
7938	GM_134_A1_B07_MR	g18695	BLASTN	474	1e-14	75	Soybean nodulin 22 gene
7939	GM_134_A1_B08_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7940	GM_134_A1_B08_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
7941	GM_134_A1_B12_T7	g2522228	BLASTX	154	1e-09	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
7942	GM_134_A1_C08_MR	g169934	BLASTN	1501	1e-61	99	G.max (soybean) atpH gene encoding CFO-ATPase subunit III, chloroplast gene encoding chloroplast protein, complete cds.
7943	GM_134_A1_C09_MR	g3337361	BLASTX	240	6e-20	56	(AC004481) ankyrin-like protein [Arabidopsis thaliana]
7944	GM_134_A1_C11_T7	g2190419	BLASTX	250	1e-19	48	(Y13632) dem [Lycopersicon esculentum]
7945	GM_134_A1_D01_MR	g3777527	BLASTX	708	7e-68	96	(AF053008) gag-pol polyprotein [Glycine max]
7946	GM_134_A1_D03_MR	g507910	BLASTN	380	1e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
7947	GM_134_A1_D10_T7	g3894383	BLASTX	278	3e-22	47	(AF053993) disease resistance protein [Lycopersicon esculentum]
7948	GM_134_A1_D11_MR	g3746069	BLASTX	224	2e-16	35	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7949	GM_134_A1_E08_MR	g3869063	BLASTN	489	5e-15	66	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17O22, complete sequence [Arabidopsis thaliana]
7950	GM_134_A1_E11_MR	g3746069	BLASTX	200	7e-14	33	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
7951	GM_134_A1_F04_T7	g3426334	BLASTN	590	1e-19	67	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
7952	GM_134_A1_F07_MR	g2462058	BLASTX	258	2e-21	42	(Y13389) reverse transcriptase [Antirrhinum majus]
7953	GM_134_A1_F10_T7	g3097320	BLASTN	526	9e-17	74	Glycine max gene for Bd 30K, complete cds
7954	GM_134_A1_G01_T7	g3721855	BLASTN	381	3e-10	70	Panax ginseng OSCPNY2 mRNA for beta-Amyrin Synthase, complete cds
7955	GM_134_A1_G04_MR	g3549652	BLASTX	144	8e-09	90	(AJ224982) MAP3K epsilon protein kinase [Arabidopsis thaliana]
7956	GM_134_A1_G05_T7	g345511	BLASTX	179	7e-12	34	retrovirus-related copia polyprotein - fruit fly (Drosophila simulans) (fragments)
7957	GM_134_A1_G06_MR	g2129618	BLASTX	212	3e-15	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
7958	GM_134_A1_G10_T7	g3513745	BLASTX	196	3e-13	39	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
7959	GM_134_A1_H01_T7	g2462058	BLASTX	353	2e-31	54	(Y13389) reverse transcriptase [Antirrhinum majus]
7960	GM_134_A1_H06_MR	g4038056	BLASTX	277	3e-22	43	(AC005897) putative transposon [Arabidopsis thaliana]
7961	GM_134_A1_H06_T7	g1769898	BLASTX	156	1e-09	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
7962	GM_134_A1_H07_MR	g2765817	BLASTX	157	8e-10	64	(Z95352) AtMlo-h1 [Arabidopsis thaliana]
7963	GM_134_A1_H10_MR	g3097320	BLASTN	1320	9e-53	82	Glycine max gene for Bd 30K, complete cds
7964	GM_134_A1_H11_T7	g2522228	BLASTX	165	1e-24	70	(AB007466) reverse transcriptase-like protein [Vicia faba]
7965	GM_134_A2_A01_MR	g2995405	BLASTX	331	4e-28	53	(Y12432) polyprotein [Ananas comosus]
7966	GM_134_A2_A04_MR	g3810596	BLASTX	244	1e-18	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
7967	GM_134_A2_A06_MR	g4038056	BLASTX	141	1e-13	32	(AC005897) putative transposon [Arabidopsis thaliana]
7968	GM_134_A2_A07_T7	g2351064	BLASTN	723	1e-25	73	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDJ22
7969	GM_134_A2_A11_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
7970	GM_134_A2_A11_T7	g507910	BLASTN	492	1e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
7971	GM_134_A2_B03_T7	g3097320	BLASTN	764	1e-27	76	Glycine max gene for Bd 30K, complete cds
7972	GM_134_A2_B04_MR	g170080	BLASTN	285	1e-09	63	Soybean seed lectin gene transposable element tgm1.
7973	GM_134_A2_B08_T7	g3097320	BLASTN	896	2e-33	79	Glycine max gene for Bd 30K, complete cds
7974	GM_134_A2_B12_MR	g18559	BLASTN	794	6e-29	73	G.max gene for catalase
7975	GM_134_A2_B12_T7	g2828185	BLASTN	391	1e-10	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUD21, complete sequence [Arabidopsis thaliana]
7976	GM_134_A2_C03_T7	g18559	BLASTN	793	6e-29	77	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
7977	GM_134_A2_C06_MR	g3645899	BLASTX	213	4e-22	49	(U68408) 5' end not determined experimentally [Zea mays]
7978	GM_134_A2_D01_MR	g2995405	BLASTX	328	9e-28	52	(Y12432) polyprotein [Ananas comosus]
7979	GM_134_A2_D02_T7	g507910	BLASTN	392	4e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
7980	GM_134_A2_D03_MR	g3002939	BLASTX	102	3e-14	100	(AF043426) RNA polymerase II second largest subunit [Peperomia caperata]
7981	GM_134_A2_D04_MR	g1707007	BLASTX	231	2e-17	37	(U78721) hypothetical protein [Arabidopsis thaliana]
7982	GM_134_A2_D05_T7	g1076755	BLASTX	492	1e-45	80	protein kinase - rice gi 450300 (L27821) protein kinase [Oryza sativa]
7983	GM_134_A2_D08_MR	g169934	BLASTN	1257	2e-50	90	G.max (soybean) atpH gene encoding CFO-ATPase subunit III, chloroplast gene encoding chloroplast protein, complete cds.
7984	GM_134_A2_E02_MR	g18559	BLASTN	460	8e-14	68	G.max gene for catalase
7985	GM_134_A2_E06_T7	g18683	BLASTN	397	5e-11	74	G.max N-20t gene
7986	GM_134_A2_E07_MR	g3097320	BLASTN	525	1e-16	78	Glycine max gene for Bd 30K, complete cds
7987	GM_134_A2_E08_T7	g3097320	BLASTN	681	8e-24	75	Glycine max gene for Bd 30K, complete cds
7988	GM_134_A2_E09_T7	g3269281	BLASTX	272	9e-22	49	(AL030978) putative protein [Arabidopsis thaliana]
7989	GM_134_A2_F02_MR	g3845197	BLASTN	357	4e-09	65	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
7990	GM_134_A2_F04_MR	g2582971	BLASTX	156	4e-12	54	(D83711) TKRP125 [Nicotiana tabacum]
7991	GM_134_A2_F05_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
7992	GM_134_A2_F06_MR	g1666236	BLASTX	167	3e-11	30	(U76261) unknown [Hordeum vulgare]
7993	GM_134_A2_F10_T7	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
7994	GM_134_A2_F11_MR	g3777527	BLASTX	409	6e-36	60	(AF053008) gag-pol polyprotein [Glycine max]
7995	GM_134_A2_F11_T7	g1167523	BLASTX	189	1e-12	47	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
7996	GM_134_A2_G01_MR	g1171499	BLASTX	282	5e-24	69	(Z68913) reverse transcriptase [Beta vulgaris]
7997	GM_134_A2_G01_T7	g1658457	BLASTX	225	6e-18	61	(U75248) reverse transcriptase [Gossypium barbadense]
7998	GM_134_A2_G03_MR	g4063760	BLASTX	383	2e-33	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
7999	GM_134_A2_G05_MR	g4056428	BLASTX	163	3e-10	73	(AC005322) Similar to gb U43629 integral membrane protein from Beta vulgaris and a member of sugar transporter family PF 00083. [Arabidopsis thaliana]
8000	GM_134_A2_G06_T7	g2407789	BLASTN	431	2e-12	63	Glycine max grr1 (grr1) mRNA, complete cds
8001	GM_134_A2_G07_MR	g2462134	BLASTX	117	5e-14	44	(Y13368) reverse transcriptase [Beta vulgaris]
8002	GM_134_A2_G09_T7	g18559	BLASTN	860	6e-32	79	G.max gene for catalase
8003	GM_134_A2_H01_T7	g18559	BLASTN	554	4e-18	72	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8004	GM_134_A2_H06_T7	g2129618	BLASTX	210	4e-15	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8005	GM_134_A2_H07_T7	g3777527	BLASTX	490	1e-44	87	(AF053008) gag-pol polyprotein [Glycine max]
8006	GM_134_B1_A05_MR	g3142328	BLASTN	1023	2e-39	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8007	GM_134_B1_A09_MR	g507910	BLASTN	484	3e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8008	GM_134_B1_A11_T7	g343938	BLASTN	349	9e-09	61	Yeast (S.cerevisiae) mitochondrial Ser-tRNA and ATPase proteolipid genes.
8009	GM_134_B1_B03_MR	g3142328	BLASTN	1645	9e-68	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8010	GM_134_B1_B04_MR	g1666236	BLASTX	172	7e-12	28	(U76261) unknown [Hordeum vulgare]
8011	GM_134_B1_B06_T7	g18559	BLASTN	796	5e-29	74	G.max gene for catalase
8012	GM_134_B1_B08_MR	g2895632	BLASTN	244	7e-10	72	Speyeria mormonia large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
8013	GM_134_B1_B10_T7	g507910	BLASTN	409	7e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8014	GM_134_B1_B12_T7	g507910	BLASTN	573	3e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
8015	GM_134_B1_C03_T7	g1167523	BLASTX	226	1e-17	43	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
8016	GM_134_B1_C05_MR	g13619	BLASTN	356	7e-10	63	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
8017	GM_134_B1_C05_T7	g1931643	BLASTX	210	1e-15	47	(U95973) DnaJ isolog [Arabidopsis thaliana]
8018	GM_134_B1_D01_MR	g2982303	BLASTX	168	1e-14	71	(AF051236) hypothetical protein [Picea mariana]
8019	GM_134_B1_D01_T7	g3834323	BLASTX	188	5e-25	63	(AC005679) F9K20.25 [Arabidopsis thaliana]
8020	GM_134_B1_D04_MR	g1170897	BLASTX	308	1e-41	75	MALATE DEHYDROGENASE, GLYOXYSOMAL PRECURSOR gi 1076276 pir S52039 NAD-malate dehydrogenase - cucumber gi 695311 (L31900) glyoxysomal malate dehydrogenase [Cucumis sativus]
8021	GM_134_B1_D04_T7	g13767	BLASTN	452	3e-14	62	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8022	GM_134_B1_D05_MR	g13764	BLASTN	388	2e-11	65	Torulopsis glabrata mitochondrial DNA for ATPase 8 downstream of cytochrome oxidase 1 gene >gi 343953 gb M11874 YSLMTIG03 Yeast (T.glabrata) mitochondrial DNA between cytochrome oxidase subunit I and ATPase subunit 8 genes.
8023	GM_134_B1_D05_T7	g2499498	BLASTX	319	1e-43	86	PHOSPHOGLYCERATE KINASE, CYTOSOLIC gi 1161602 gnl PID e151093 (Z48976) phosphoglycerate kinase (PGK) [Nicotiana tabacum]
8024	GM_134_B1_D08_MR	g2129618	BLASTX	180	7e-12	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8025	GM_134_B1_D08_T7	g13584	BLASTN	399	2e-11	61	Yeast mitochondrial oxi3 gene exon 1 for cytochrome c oxidase subunit I
8026	GM_134_B1_D11_MR	g3142328	BLASTN	1413	4e-57	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8027	GM_134_B1_D11_T7	g3650039	BLASTX	155	2e-09	33	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
8028	GM_134_B1_E01_MR	g1666236	BLASTX	161	1e-10	28	(U76261) unknown [Hordeum vulgare]
8029	GM_134_B1_E03_T7	g2213632	BLASTX	159	3e-10	43	(AC000103) F21J9.24 [Arabidopsis thaliana]
8030	GM_134_B1_E04_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8031	GM_134_B1_E04_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8032	GM_134_B1_E08_MR	g1431738	BLASTN	558	2e-18	93	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
8033	GM_134_B1_F02_MR	g905361	BLASTX	544	2e-55	94	(U22103) gag-protease polyprotein [Glycine max]
8034	GM_134_B1_F03_MR	g3142379	BLASTX	333	2e-29	60	(AF053008) envelope-like [Glycine max]
8035	GM_134_B1_F05_T7	g2129618	BLASTX	153	5e-09	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8036	GM_134_B1_F07_MR	g505129	BLASTN	282	1e-10	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
8037	GM_134_B1_F08_T7	g3096920	BLASTX	107	6e-09	34	(AL023094) putative ketoacyl-CoA synthase [Arabidopsis thaliana]
8038	GM_134_B1_F10_MR	g2435558	BLASTN	375	7e-10	64	Caenorhabditis elegans cosmid F52D1
8039	GM_134_B1_F11_T7	g507910	BLASTN	542	7e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
8040	GM_134_B1_G01_T7	g1769898	BLASTX	146	8e-13	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8041	GM_134_B1_G03_MR	g507910	BLASTN	367	6e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8042	GM_134_B1_G10_MR	g1666236	BLASTX	144	9e-09	28	(U76261) unknown [Hordeum vulgare]
8043	GM_134_B1_G11_MR	g18768	BLASTN	482	2e-15	68	Soybean Tgm6 transposable element 3' end
8044	GM_134_B1_H05_T7	g507910	BLASTN	508	2e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8045	GM_134_B1_H08_MR	g18559	BLASTN	792	7e-29	73	G.max gene for catalase
8046	GM_135_A1_A03_MR	g100484	BLASTX	310	5e-26	56	hypothetical protein - garden snapdragon
8047	GM_135_A1_A04_MR	g170606	BLASTN	743	4e-27	70	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
8048	GM_135_A1_A06_T7	g1213629	BLASTX	245	2e-19	51	(X95991) pectinesterase [Prunus persica]
8049	GM_135_A1_A09_MR	g1871173	BLASTN	450	3e-13	61	Arabidopsis thaliana chromosome II BAC T06D20 genomic sequence, complete sequence
8050	GM_135_A1_A10_T7	g629693	BLASTX	153	1e-09	45	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8051	GM_135_A1_B04_MR	g2335186	BLASTN	387	2e-10	61	Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence [Homo sapiens]
8052	GM_135_A1_B05_MR	g2443320	BLASTX	167	3e-10	39	(D85597) polyprotein [Oryza australiensis]
8053	GM_135_A1_B10_T7	g1769898	BLASTX	394	9e-38	67	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8054	GM_135_A1_B11_MR	g1710401	BLASTX	307	8e-27	83	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) gi 1044912 (X92443) ribonucleotide reductase R2 [Nicotiana tabacum]
8055	GM_135_A1_B12_T7	g2129618	BLASTX	178	1e-11	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8056	GM_135_A1_C09_T7	g2443889	BLASTX	163	4e-10	45	similar to S-linalool synthase gp U58314 1491939 [Arabidopsis thaliana]
8057	GM_135_A1_C11_MR	g1666236	BLASTX	205	1e-15	35	(U76261) unknown [Hordeum vulgare]
8058	GM_135_A1_C11_T7	g629693	BLASTX	311	4e-27	60	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8059	GM_135_A1_C12_MR	g3869065	BLASTN	389	1e-10	67	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]
8060	GM_135_A1_C12_T7	g2598587	BLASTX	124	5e-10	86	(Y15366) cycloartenol synthase [Medicago truncatula]
8061	GM_135_A1_D01_T7	g3319372	BLASTX	207	7e-16	37	(AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]
8062	GM_135_A1_D02_MR	g2583121	BLASTX	144	3e-09	77	(AC002387) putative phosphotransferase [Arabidopsis thaliana]
8063	GM_135_A1_D07_MR	g3241935	BLASTN	477	2e-14	63	Arabidopsis thaliana chromosome IV from 19 cM, complete sequence [Arabidopsis thaliana]
8064	GM_135_A1_D09_T7	g507910	BLASTN	362	9e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8065	GM_135_A1_D12_MR	g3645899	BLASTX	351	4e-30	61	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8066	GM_135_A1_E05_T7	g1006806	BLASTN	757	1e-27	70	Vigna radiata 1-aminocyclopropane-1-carboxylic acid synthase (VRACS7) mRNA, complete cds.
8067	GM_135_A1_F01_MR	g100484	BLASTX	262	2e-22	51	hypothetical protein - garden snapdragon
8068	GM_135_A1_F05_T7	g170083	BLASTN	419	3e-12	70	Soybean (clone E15) urease (ure) gene, exons 2,3 and 4 and partial cds.
8069	GM_135_A1_F08_T7	g2129618	BLASTX	227	6e-17	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8070	GM_135_A1_F11_T7	g3777527	BLASTX	140	2e-18	62	(AF053008) gag-pol polyprotein [Glycine max]
8071	GM_135_A1_G01_MR	g3142328	BLASTN	1175	3e-46	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8072	GM_135_A1_G04_T7	g4039114	BLASTN	470	3e-14	66	Glycine max alcohol-dehydrogenase (Adh-2) gene, partial cds
8073	GM_135_A1_G07_T7	g99922	BLASTX	361	2e-32	72	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
8074	GM_135_A1_G12_T7	g4115357	BLASTX	143	3e-12	39	(AC005957) hypothetical protein [Arabidopsis thaliana]
8075	GM_135_A1_H01_MR	g2760165	BLASTN	675	2e-23	73	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]
8076	GM_135_A1_H02_MR	g507910	BLASTN	500	6e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
8077	GM_135_A1_H03_MR	g4063760	BLASTX	404	7e-40	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8078	GM_135_A1_H05_T7	g3513747	BLASTX	173	8e-11	45	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
8079	GM_135_A1_H08_T7	g99922	BLASTX	535	8e-51	71	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
8080	GM_135_A1_H10_MR	g100484	BLASTX	298	1e-24	58	hypothetical protein - garden snapdragon
8081	GM_135_A1_H11_T7	g556672	BLASTN	349	8e-09	71	S.cereale (Halo) chloroplast mRNA for heat-shock protein
8082	GM_135_B1_A07_T7	g13767	BLASTN	405	4e-12	69	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
8083	GM_135_B1_A08_MR	g2522228	BLASTX	304	2e-26	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
8084	GM_135_B1_B02_MR	g3645899	BLASTX	251	2e-19	47	(U68408) 5' end not determined experimentally [Zea mays]
8085	GM_135_B1_B09_T7	g3337367	BLASTX	196	4e-14	36	(AC004481) hypothetical protein [Arabidopsis thaliana]
8086	GM_135_B1_B10_MR	g3142328	BLASTN	956	2e-36	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8087	GM_135_B1_B12_T7	g507910	BLASTN	536	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8088	GM_135_B1_C02_MR	g559276	BLASTN	405	2e-11	63	Saccharomyces cerevisiae mitochondrion transfer RNA-Ser1 (tRNA-Ser) gene and varI gene, complete cds.
8089	GM_135_B1_C07_T7	g18559	BLASTN	913	2e-34	76	G.max gene for catalase
8090	GM_135_B1_C09_T7	g3650035	BLASTX	172	6e-11	51	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
8091	GM_135_B1_C11_T7	g1934969	BLASTN	369	1e-09	65	P.falciparum mRNA for AARP1 protein, partial
8092	GM_135_B1_C12_T7	g3142328	BLASTN	878	8e-33	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8093	GM_135_B1_D10_T7	g3645899	BLASTX	327	2e-27	52	(U68408) 5' end not determined experimentally [Zea mays]
8094	GM_135_B1_D11_MR	g905361	BLASTX	425	7e-39	96	(U22103) gag-protease polyprotein [Glycine max]
8095	GM_135_B1_D12_MR	g2462134	BLASTX	205	5e-15	37	(Y13368) reverse transcriptase [Beta vulgaris]
8096	GM_135_B1_D12_T7	g3097320	BLASTN	705	7e-25	81	Glycine max gene for Bd 30K, complete cds
8097	GM_135_B1_E03_T7	g18559	BLASTN	355	5e-09	72	G.max gene for catalase
8098	GM_135_B1_E04_T7	g1142703	BLASTN	275	1e-13	75	Glycine max satellite STR120-B.1.
8099	GM_135_B1_E06_MR	g4063760	BLASTX	364	2e-31	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8100	GM_135_B1_E11_MR	g3097320	BLASTN	543	2e-17	75	Glycine max gene for Bd 30K, complete cds
8101	GM_135_B1_E12_T7	g3097320	BLASTN	874	2e-32	78	Glycine max gene for Bd 30K, complete cds
8102	GM_135_B1_F03_MR	g3777527	BLASTX	139	9e-09	41	(AF053008) gag-pol polyprotein [Glycine max]
8103	GM_135_B1_F03_T7	g1785740	BLASTX	114	7e-09	31	(Y08502) orf170 [Arabidopsis thaliana]
8104	GM_135_B1_F04_MR	g2245073	BLASTN	406	3e-11	68	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8
8105	GM_135_B1_F06_MR	g984307	BLASTN	1137	3e-47	91	Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precurso...
8106	GM_135_B1_F08_T7	g4115563	BLASTX	220	1e-16	41	(AB013598) UDP-glucose:anthocyanin 5-O-glucosyltransferase [Verbena x hybrida]
8107	GM_135_B1_F11_MR	g3688172	BLASTX	162	1e-11	50	(AL031804) putative protein [Arabidopsis thaliana]
8108	GM_135_B1_F12_MR	g18559	BLASTN	856	9e-32	75	G.max gene for catalase
8109	GM_135_B1_F12_T7	g2462936	BLASTX	171	3e-12	35	(Y12321) open reading frame 2 [Brassica oleracea]
8110	GM_135_B1_G08_MR	g4063760	BLASTX	420	3e-37	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8111	GM_135_B1_G08_T7	g507910	BLASTN	400	2e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8112	GM_135_B1_G11_MR	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
8113	GM_135_B1_G11_T7	g507910	BLASTN	647	1e-22	86	Glycine max BSR-101 satellite SB92 genomic sequence.
8114	GM_135_B1_H07_MR	g3643588	BLASTN	493	3e-15	67	Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8115	GM_135_B1_H09_MR	g905361	BLASTX	414	1e-37	92	(U22103) gag-protease polyprotein [Glycine max]
8116	GM_135_B1_H09_T7	g417499	BLASTX	155	3e-09	76	AUTOANTIGEN PM-SCL gi 284357 pir A43920 nucleolar 100K polymyositis-scleroderma protein 2 - human gi 179283 (L01457) PM-Scl autoantigen [Homo sapiens]
8117	GM_135_B1_H10_MR	g507910	BLASTN	695	8e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
8118	GM_135_B1_H10_T7	g507910	BLASTN	559	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
8119	GM_135_B1_H11_MR	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
8120	GM_136_A1_A03_MR	g3047068	BLASTX	194	2e-13	38	(AF058825) similar to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
8121	GM_136_A1_A09_MR	g2522228	BLASTX	373	1e-33	66	(AB007466) reverse transcriptase-like protein [Vicia faba]
8122	GM_136_A1_A11_MR	g1666236	BLASTX	198	8e-15	33	(U76261) unknown [Hordeum vulgare]
8123	GM_136_A1_B01_MR	g3924609	BLASTX	127	1e-12	46	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
8124	GM_136_A1_B03_MR	g3513745	BLASTX	214	3e-15	39	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
8125	GM_136_A1_B05_MR	g2995405	BLASTX	315	2e-26	52	(Y12432) polyprotein [Ananas comosus]
8126	GM_136_A1_B05_T7	g3142379	BLASTX	273	1e-22	80	(AF053008) envelope-like [Glycine max]
8127	GM_136_A1_B07_T7	g3426334	BLASTN	367	1e-09	59	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
8128	GM_136_A1_C03_MR	g18559	BLASTN	1161	1e-45	86	G.max gene for catalase
8129	GM_136_A1_C05_T7	g3777527	BLASTX	508	6e-50	95	(AF053008) gag-pol polyprotein [Glycine max]
8130	GM_136_A1_D03_MR	g100484	BLASTX	242	1e-18	47	hypothetical protein - garden snapdragon
8131	GM_136_A1_D04_T7	g2961349	BLASTX	237	7e-18	52	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
8132	GM_136_A1_D07_MR	g629693	BLASTX	131	6e-10	54	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8133	GM_136_A1_D11_MR	g18559	BLASTN	767	9e-28	75	G.max gene for catalase
8134	GM_136_A1_D12_T7	g3097320	BLASTN	431	2e-12	72	Glycine max gene for Bd 30K, complete cds
8135	GM_136_A1_E01_T7	g3777527	BLASTX	350	1e-29	79	(AF053008) gag-pol polyprotein [Glycine max]
8136	GM_136_A1_E02_T7	g905361	BLASTX	288	9e-24	73	(U22103) gag-protease polyprotein [Glycine max]
8137	GM_136_A1_E06_MR	g18559	BLASTN	396	6e-11	73	G.max gene for catalase
8138	GM_136_A1_E12_MR	g905361	BLASTX	313	2e-26	74	(U22103) gag-protease polyprotein [Glycine max]
8139	GM_136_A1_F01_MR	g3522945	BLASTX	175	1e-11	47	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]
8140	GM_136_A1_F01_T7	g4140712	BLASTX	159	6e-11	33	(AF110183) putative integrase [Oryza sativa]
8141	GM_136_A1_F04_T7	g2522227	BLASTX	211	2e-16	54	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
8142	GM_136_A1_F06_T7	g1769898	BLASTX	254	4e-20	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8143	GM_136_A1_F07_MR	g3250687	BLASTX	251	1e-20	41	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
8144	GM_136_A1_F07_T7	g2245104	BLASTX	226	1e-16	64	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
8145	GM_136_A1_F08_T7	g1769898	BLASTX	298	7e-25	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8146	GM_136_A1_F11_MR	g507910	BLASTN	467	2e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
8147	GM_136_A1_G01_MR	g507910	BLASTN	620	2e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8148	GM_136_A1_G07_MR	g3645899	BLASTX	216	1e-15	45	(U68408) 5' end not determined experimentally [Zea mays]
8149	GM_136_A1_G08_T7	g1769897	BLASTX	167	7e-11	33	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8150	GM_136_A1_G09_T7	g4038056	BLASTX	270	2e-21	49	(AC005897) putative transposon [Arabidopsis thaliana]
8151	GM_136_A1_G10_T7	g507910	BLASTN	398	2e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
8152	GM_136_A1_H01_MR	g1666236	BLASTX	189	9e-14	29	(U76261) unknown [Hordeum vulgare]
8153	GM_136_A1_H05_T7	g3810596	BLASTX	200	5e-14	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
8154	GM_136_A1_H07_MR	g4063760	BLASTX	351	6e-30	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8155	GM_136_A1_H09_MR	g100484	BLASTX	326	1e-27	54	hypothetical protein - garden snapdragon
8156	GM_136_A2_A05_T7	g629693	BLASTX	342	2e-30	55	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8157	GM_136_A2_A07_MR	g4038056	BLASTX	216	1e-15	44	(AC005897) putative transposon [Arabidopsis thaliana]
8158	GM_136_A2_A08_T7	g1666236	BLASTX	208	6e-16	30	(U76261) unknown [Hordeum vulgare]
8159	GM_136_A2_A11_MR	g18559	BLASTN	821	3e-30	77	G.max gene for catalase
8160	GM_136_A2_B05_T7	g170080	BLASTN	679	8e-24	97	Soybean seed lectin gene transposable element tgm1.
8161	GM_136_A2_B10_MR	g3097320	BLASTN	500	1e-15	72	Glycine max gene for Bd 30K, complete cds
8162	GM_136_A2_C04_MR	g4063760	BLASTX	316	3e-26	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8163	GM_136_A2_C12_MR	g13536	BLASTN	403	2e-11	68	Yeast (S. cerevisiae) mitochondrial genes for several tRNAs (Thr(2), Cys(2) and His). >gi 343930 gb K00537 YSCMTTGO1 Yeast (S.cerevisiae) mitochondrial cap-oxi1 region: Thr-2, Cys-2 and His-tRNA genes.
8164	GM_136_A2_C12_T7	g2842479	BLASTX	162	2e-10	57	(AL021749) hypothetical protein [Arabidopsis thaliana]
8165	GM_136_A2_D01_T7	g4038056	BLASTX	399	2e-35	51	(AC005897) putative transposon [Arabidopsis thaliana]
8166	GM_136_A2_D02_T7	g2104945	BLASTN	431	2e-12	76	Glycine max copia-like retrotransposon Tgmr, complete sequence
8167	GM_136_A2_D03_MR	g2688299	BLASTX	191	7e-23	56	(AE001145) prolyl-tRNA synthetase (proS) [Borrelia burgdorferi]
8168	GM_136_A2_D07_MR	g4063760	BLASTX	249	4e-19	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8169	GM_136_A2_D07_T7	g507910	BLASTN	660	3e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
8170	GM_136_A2_D08_MR	g3142328	BLASTN	785	1e-28	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8171	GM_136_A2_D09_MR	g507910	BLASTN	350	3e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8172	GM_136_A2_D09_T7	g507910	BLASTN	380	1e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
8173	GM_136_A2_E04_MR	g3004543	BLASTN	325	6e-09	62	Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence, complete sequence.
8174	GM_136_A2_E04_T7	g662904	BLASTX	118	4e-10	59	nitrate reductase (NADH) [Cichorium intybus]
8175	GM_136_A2_E05_T7	g18695	BLASTN	399	4e-11	71	Soybean nodulin 22 gene
8176	GM_136_A2_E07_T7	g18559	BLASTN	350	8e-09	72	G.max gene for catalase
8177	GM_136_A2_E09_MR	g2244804	BLASTX	213	7e-16	48	(Z97336) Ste20-like kinase homolog [Arabidopsis thaliana]
8178	GM_136_A2_F07_MR	g2642431	BLASTX	160	2e-09	47	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
8179	GM_136_A2_F09_T7	g3426334	BLASTN	349	9e-09	66	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
8180	GM_136_A2_G01_MR	g2522227	BLASTX	162	6e-11	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
8181	GM_136_A2_G04_MR	g1171583	BLASTN	387	2e-10	68	P.falciparum complete gene map of plastid-like DNA (IR-A)
8182	GM_136_A2_H08_T7	g421955	BLASTX	273	5e-23	54	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
8183	GM_136_A2_H09_MR	g99922	BLASTX	494	2e-46	72	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
8184	GM_136_A2_H10_MR	g3128195	BLASTX	176	4e-12	81	(AC004521) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana] gi 3341673 (AC003672) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana]
8185	GM_136_B1_A01_MR	g99755	BLASTX	185	6e-21	48	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
8186	GM_136_B1_A04_T7	g18695	BLASTN	401	3e-11	71	Soybean nodulin 22 gene
8187	GM_136_B1_B04_MR	g507910	BLASTN	659	4e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
8188	GM_136_B1_B06_T7	g18660	BLASTN	635	8e-22	77	G.max hsp22 gene for low MW heat shock protein
8189	GM_136_B1_B07_MR	g212878	BLASTN	393	6e-11	66	Gallus gallus vitellogenin gene coding for phosvitin, exons 23 and 24.
8190	GM_136_B1_B08_MR	g507910	BLASTN	477	6e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
8191	GM_136_B1_B08_T7	g507910	BLASTN	491	1e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8192	GM_136_B1_B11_MR	g1666236	BLASTX	199	6e-15	30	(U76261) unknown [Hordeum vulgare]
8193	GM_136_B1_C06_T7	g3777527	BLASTX	389	1e-39	96	(AF053008) gag-pol polyprotein [Glycine max]
8194	GM_136_B1_C11_T7	g2129618	BLASTX	193	3e-13	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8195	GM_136_B1_D02_MR	g905361	BLASTX	333	1e-28	79	(U22103) gag-protease polyprotein [Glycine max]
8196	GM_136_B1_D03_MR	g4063760	BLASTX	105	7e-11	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8197	GM_136_B1_D04_MR	g4063760	BLASTX	299	2e-24	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8198	GM_136_B1_D05_MR	g1360090	BLASTX	121	1e-09	66	(X95576) C1C-Nt1 gene product [Nicotiana tabacum]
8199	GM_136_B1_D06_MR	g1142702	BLASTN	437	3e-13	73	Glycine max satellite STR120-A.4.
8200	GM_136_B1_D11_MR	g547684	BLASTX	583	6e-56	95	HEAT SHOCK PROTEIN 82 gi 100336 pir S18865 heat shock protein 82 - common tobacco (fragment) gi 19880 (X63195) heat shock protein 82 [Nicotiana tabacum]
8201	GM_136_B1_D11_T7	g905361	BLASTX	387	1e-34	82	(U22103) gag-protease polyprotein [Glycine max]
8202	GM_136_B1_E05_MR	g507910	BLASTN	378	2e-10	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8203	GM_136_B1_E07_MR	g421955	BLASTX	178	3e-12	44	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
8204	GM_136_B1_E11_MR	g1813979	BLASTX	286	2e-27	58	(Y10860) hypothetical protein [Musa acuminata]
8205	GM_136_B1_F01_MR	g3845197	BLASTN	357	4e-09	65	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
8206	GM_136_B1_F01_T7	g3097320	BLASTN	912	3e-34	79	Glycine max gene for Bd 30K, complete cds
8207	GM_136_B1_F06_MR	g3777527	BLASTX	242	7e-35	77	(AF053008) gag-pol polyprotein [Glycine max]
8208	GM_136_B1_F08_T7	g507910	BLASTN	435	5e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8209	GM_136_B1_F12_MR	g2315153	BLASTX	173	8e-12	72	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
8210	GM_136_B1_F12_T7	g3645899	BLASTX	319	1e-26	58	(U68408) 5' end not determined experimentally [Zea mays]
8211	GM_136_B1_G02_MR	g905361	BLASTX	426	5e-39	96	(U22103) gag-protease polyprotein [Glycine max]
8212	GM_136_B1_G04_MR	g2522227	BLASTX	227	3e-18	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
8213	GM_136_B1_G07_T7	g1236920	BLASTN	356	4e-09	64	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
8214	GM_136_B1_G09_T7	g3947733	BLASTX	329	1e-28	53	(AJ009719) NL25 [Solanum tuberosum]
8215	GM_136_B1_G10_T7	g99922	BLASTX	494	2e-46	74	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
8216	GM_136_B1_H01_MR	g1666236	BLASTX	156	4e-10	32	(U76261) unknown [Hordeum vulgare]
8217	GM_136_B1_H02_T7	g3645899	BLASTX	216	4e-18	47	(U68408) 5' end not determined experimentally [Zea mays]
8218	GM_136_B1_H07_MR	g4063760	BLASTX	449	2e-40	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8219	GM_137_A1_A09_T7	g3047086	BLASTX	126	4e-12	46	(AF058914) similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31) [Arabidopsis thaliana]
8220	GM_137_A1_C07_T7	g2618605	BLASTN	534	4e-17	79	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8221	GM_137_A1_C10_T7	g3386613	BLASTX	92	4e-10	94	(AC004665) putative ATP-dependent RNA helicase [Arabidopsis thaliana]
8222	GM_137_A1_D09_T7	g507910	BLASTN	568	5e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8223	GM_137_A1_E03_T7	g4038056	BLASTX	269	2e-21	54	(AC005897) putative transposon [Arabidopsis thaliana]
8224	GM_137_A1_E05_T7	g507910	BLASTN	355	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
8225	GM_137_A1_E07_T7	g2443320	BLASTX	114	2e-11	52	(D85597) polyprotein [Oryza australiensis]
8226	GM_137_A1_E10_T7	g507910	BLASTN	550	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
8227	GM_137_A1_F07_T7	g3142328	BLASTN	972	4e-37	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8228	GM_137_A1_F09_T7	g507910	BLASTN	387	7e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8229	GM_137_A1_G01_T7	g3599418	BLASTN	358	3e-09	75	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
8230	GM_137_A1_G06_T7	g18559	BLASTN	762	2e-27	71	G.max gene for catalase
8231	GM_137_A1_G08_T7	g3550090	BLASTX	147	6e-16	48	(AF072640) reverse transcriptase [Lycopersicon esculentum]
8232	GM_137_A1_G09_T7	g905361	BLASTX	189	4e-13	39	(U22103) gag-protease polyprotein [Glycine max]
8233	GM_137_A1_H04_T7	g18559	BLASTN	868	3e-32	74	G.max gene for catalase
8234	GM_137_A1_H06_T7	g3319362	BLASTX	169	1e-10	35	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
8235	GM_137_A1_H08_T7	g3930515	BLASTX	115	3e-10	46	(AF059674) putative gag protein [Nicotiana tabacum]
8236	GM_137_A1_H11_T7	g18559	BLASTN	871	2e-32	75	G.max gene for catalase
8237	GM_137_A2_A08_MR	g4063760	BLASTX	206	2e-14	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8238	GM_137_A2_A09_T7	g2264320	BLASTN	436	1e-12	60	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
8239	GM_137_A2_B03_MR	g533086	BLASTX	278	1e-23	75	(U07605) precursor delta-9-stearoyl-acyl carrier protein desaturase [Thunbergia alata]
8240	GM_137_A2_B07_T7	g3269291	BLASTX	141	1e-14	69	(AL030978) putative receptor protein kinase [Arabidopsis thaliana]
8241	GM_137_A2_B09_T7	g4063760	BLASTX	155	4e-09	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8242	GM_137_A2_B12_MR	g2129618	BLASTX	100	3e-11	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8243	GM_137_A2_C04_T7	g507910	BLASTN	356	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8244	GM_137_A2_D04_T7	g4038056	BLASTX	186	2e-12	50	(AC005897) putative transposon [Arabidopsis thaliana]
8245	GM_137_A2_E06_MR	g1480927	BLASTN	986	4e-38	86	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
8246	GM_137_A2_F10_MR	g100484	BLASTX	183	4e-14	48	hypothetical protein - garden snapdragon

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8247	GM_137_A2_F10_T7	g130582	BLASTX	153	8e-09	42	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
8248	GM_137_A2_G06_T7	g3097320	BLASTN	383	3e-10	72	Glycine max gene for Bd 30K, complete cds
8249	GM_137_A2_G10_T7	g3777527	BLASTX	429	6e-41	90	(AF053008) gag-pol polyprotein [Glycine max]
8250	GM_137_A2_H10_T7	g4063756	BLASTN	404	3e-11	73	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
8251	GM_137_A2_H12_T7	g507910	BLASTN	550	3e-18	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8252	GM_137_B1_A05_T7	g100484	BLASTX	314	2e-26	54	hypothetical protein - garden snapdragon
8253	GM_137_B1_A09_MR	g507910	BLASTN	391	5e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8254	GM_137_B1_B01_T7	g2961384	BLASTX	181	1e-23	67	(AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]
8255	GM_137_B1_B05_T7	g9933	BLASTN	380	3e-10	64	P.falciparum pfc2 gene for p34cdc2 protein kinase
8256	GM_137_B1_B06_T7	g3046854	BLASTN	376	6e-10	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]
8257	GM_137_B1_B08_T7	g2522228	BLASTX	382	1e-34	61	(AB007466) reverse transcriptase-like protein [Vicia faba]
8258	GM_137_B1_B12_MR	g2443320	BLASTX	199	1e-13	51	(D85597) polyprotein [Oryza australiensis]
8259	GM_137_B1_C11_T7	g507910	BLASTN	508	2e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
8260	GM_137_B1_C12_MR	g507910	BLASTN	382	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8261	GM_137_B1_D06_T7	g3426334	BLASTN	416	8e-12	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
8262	GM_137_B1_D07_MR	g99730	BLASTX	245	2e-19	51	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
8263	GM_137_B1_D07_T7	g4063756	BLASTN	449	3e-13	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
8264	GM_137_B1_E02_MR	g507910	BLASTN	366	6e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8265	GM_137_B1_E02_T7	g3142328	BLASTN	755	3e-27	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8266	GM_137_B1_E04_MR	g3319363	BLASTX	276	4e-22	54	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 33.26) [Arabidopsis thaliana]
8267	GM_137_B1_E04_T7	g3645899	BLASTX	351	4e-30	62	(U68408) 5' end not determined experimentally [Zea mays]
8268	GM_137_B1_E11_MR	g2104945	BLASTN	400	4e-11	66	Glycine max copia-like retrotransposon Tgmr, complete sequence
8269	GM_137_B1_F01_MR	g507910	BLASTN	476	7e-15	74	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8270	GM_137_B1_F03_MR	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8271	GM_137_B1_F06_T7	g18559	BLASTN	614	8e-21	76	G.max gene for catalase
8272	GM_137_B1_F07_MR	g4092470	BLASTN	459	1e-13	66	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
8273	GM_137_B1_F08_MR	g3695395	BLASTX	199	3e-14	43	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
8274	GM_137_B1_F08_T7	g3645899	BLASTX	170	9e-11	36	(U68408) 5' end not determined experimentally [Zea mays]
8275	GM_137_B1_F12_T7	g3142328	BLASTN	741	1e-26	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8276	GM_137_B1_G02_T7	g18559	BLASTN	836	7e-31	73	G.max gene for catalase
8277	GM_137_B1_G10_T7	g18559	BLASTN	1156	2e-45	91	G.max gene for catalase
8278	GM_137_B1_H01_MR	g2443320	BLASTX	241	3e-18	49	(D85597) polyprotein [Oryza australiensis]
8279	GM_137_B1_H02_T7	g2828182	BLASTN	417	8e-12	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOJ9, complete sequence [Arabidopsis thaliana]
8280	GM_137_B1_H04_MR	g1480927	BLASTN	882	3e-33	84	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
8281	GM_137_B1_H06_MR	g4063760	BLASTX	135	4e-15	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8282	GM_137_B2_A04_MR	g507910	BLASTN	541	8e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
8283	GM_137_B2_A04_T7	g4063760	BLASTX	335	3e-28	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8284	GM_137_B2_A05_MR	g507910	BLASTN	356	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
8285	GM_137_B2_A06_MR	g469192	BLASTN	377	4e-10	65	Arabidopsis thaliana mRNA for amidophosphoribosyltransferase, complete cds
8286	GM_137_B2_A07_MR	g2982251	BLASTX	192	2e-14	70	(AF051208) putative RNA-binding protein [Picea mariana]
8287	GM_137_B2_A11_MR	g3097320	BLASTN	455	1e-13	70	Glycine max gene for Bd 30K, complete cds
8288	GM_137_B2_B01_MR	g4063760	BLASTX	414	1e-36	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8289	GM_137_B2_B01_T7	g507910	BLASTN	385	9e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8290	GM_137_B2_B02_MR	g18559	BLASTN	371	9e-10	72	G.max gene for catalase
8291	GM_137_B2_B02_T7	g629693	BLASTX	157	4e-10	32	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8292	GM_137_B2_B03_T7	g2443320	BLASTX	339	1e-28	52	(D85597) polyprotein [Oryza australiensis]
8293	GM_137_B2_B05_MR	g100484	BLASTX	246	4e-19	44	hypothetical protein - garden snapdragon
8294	GM_137_B2_B09_T7	g4063760	BLASTX	153	7e-09	33	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8295	GM_137_B2_B12_MR	g2651310	BLASTX	272	4e-22	48	(AC002336) putative PTR2-B peptide transporter [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8296	GM_137_B2_B12_T7	g3377848	BLASTX	213	4e-16	51	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
8297	GM_137_B2_C01_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8298	GM_137_B2_C01_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8299	GM_137_B2_C03_MR	g2344903	BLASTX	287	1e-24	75	(AC002388) triacyglycerol lipase isolog [Arabidopsis thaliana] gi 3341700 (AC003672) putative triacyglycerol lipase [Arabidopsis thaliana]
8300	GM_137_B2_C04_MR	g3142379	BLASTX	261	2e-21	59	(AF053008) envelope-like [Glycine max]
8301	GM_137_B2_C05_T7	g3097320	BLASTN	1111	3e-43	82	Glycine max gene for Bd 30K, complete cds
8302	GM_137_B2_C12_T7	g629693	BLASTX	251	1e-20	56	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8303	GM_137_B2_D11_MR	g2342684	BLASTX	399	2e-36	56	(AC000106) F7G19.14 [Arabidopsis thaliana]
8304	GM_137_B2_D12_T7	g1871187	BLASTX	197	1e-13	84	(U90439) unknown protein [Arabidopsis thaliana]
8305	GM_137_B2_E03_MR	g3935183	BLASTX	253	8e-23	66	(AC004557) F17L21.26 [Arabidopsis thaliana]
8306	GM_137_B2_E07_T7	g1769898	BLASTX	370	9e-33	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8307	GM_137_B2_E08_MR	g3241917	BLASTN	463	7e-14	65	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19B1, complete sequence [Arabidopsis thaliana]
8308	GM_137_B2_E09_MR	g3449334	BLASTN	311	4e-10	73	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]
8309	GM_137_B2_E09_T7	g2980777	BLASTX	198	3e-14	55	(AL022198) putative protein [Arabidopsis thaliana]
8310	GM_137_B2_F02_T7	g2443348	BLASTX	309	2e-36	81	(AB001379) cytochrome P450 [Glycyrrhiza echinata]
8311	GM_137_B2_F03_MR	g1168471	BLASTX	196	5e-24	78	PROTEIN KINASE APK1B gi 2160295 gnl PID d1001485 (D10152) protein tyrosine-serine-threonine kinase [Arabidopsis thaliana]
8312	GM_137_B2_F09_T7	g3319362	BLASTX	429	2e-38	66	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
8313	GM_137_B2_F11_MR	g3236250	BLASTX	251	1e-20	95	(AC004684) hypothetical protein [Arabidopsis thaliana]
8314	GM_137_B2_G01_T7	g2995405	BLASTX	330	5e-28	55	(Y12432) polyprotein [Ananas comosus]
8315	GM_137_B2_G02_T7	g3645899	BLASTX	359	6e-31	57	(U68408) 5' end not determined experimentally [Zea mays]
8316	GM_137_B2_G03_T7	g3033389	BLASTX	206	1e-14	42	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
8317	GM_137_B2_G06_MR	g1167523	BLASTX	358	1e-30	55	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
8318	GM_137_B2_G11_T7	g4063760	BLASTX	171	3e-13	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8319	GM_137_B2_G12_T7	g1915988	BLASTN	353	5e-09	66	Tritrichomonas foetus putative protein tyrosine phosphatase, complete cds, and putative serine/threonine protein kinase genes, partial cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8320	GM_137_B2_H04_MR	g507910	BLASTN	596	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8321	GM_137_B2_H06_MR	g905361	BLASTX	652	3e-63	97	(U22103) gag-protease polyprotein [Glycine max]
8322	GM_137_B2_H07_T7	g2764526	BLASTN	472	3e-14	61	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
8323	GM_137_B2_H10_T7	g3645899	BLASTX	341	5e-29	56	(U68408) 5' end not determined experimentally [Zea mays]
8324	GM_138_A2_A02_MR	g343945	BLASTN	380	4e-11	60	Yeast (S.cerevisiae) mitochondrial var1 gene, 5' flank.
8325	GM_138_A2_A05_MR	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8326	GM_138_A2_A05_T7	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
8327	GM_138_A2_A06_MR	g2970554	BLASTN	354	6e-09	70	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
8328	GM_138_A2_A07_T7	g4063760	BLASTX	298	1e-25	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8329	GM_138_A2_A11_MR	g2522228	BLASTX	452	5e-42	55	(AB007466) reverse transcriptase-like protein [Vicia faba]
8330	GM_138_A2_A12_MR	g3264544	BLASTN	605	3e-20	62	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
8331	GM_138_A2_B11_MR	g905361	BLASTX	787	2e-77	95	(U22103) gag-protease polyprotein [Glycine max]
8332	GM_138_A2_B11_T7	g18768	BLASTN	525	2e-17	66	Soybean Tgm6 transposable element 3' end
8333	GM_138_A2_C03_T7	g1871180	BLASTX	243	7e-20	80	(U90439) unknown protein [Arabidopsis thaliana]
8334	GM_138_A2_C04_MR	g4003339	BLASTN	365	2e-09	62	Homo sapiens chromosome 10 clone CIT-HSP-1287C20, complete sequence [Homo sapiens]
8335	GM_138_A2_C09_MR	g3097320	BLASTN	430	2e-12	72	Glycine max gene for Bd 30K, complete cds
8336	GM_138_A2_C12_T7	g3645899	BLASTX	184	7e-24	42	(U68408) 5' end not determined experimentally [Zea mays]
8337	GM_138_A2_D02_T7	g3097320	BLASTN	925	7e-35	81	Glycine max gene for Bd 30K, complete cds
8338	GM_138_A2_D03_T7	g343945	BLASTN	363	2e-10	58	Yeast (S.cerevisiae) mitochondrial var1 gene, 5' flank.
8339	GM_138_A2_D04_MR	g4063760	BLASTX	389	4e-34	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8340	GM_138_A2_D06_MR	g4160362	BLASTN	363	2e-09	61	Saccharomyces cerevisiae complete mitochondrial genome
8341	GM_138_A2_D06_T7	g342953	BLASTN	514	3e-17	68	paramecium species 4.51a mt dna dimer: replication init. region.
8342	GM_138_A2_D08_T7	g100484	BLASTX	320	4e-27	43	hypothetical protein - garden snapdragon
8343	GM_138_A2_D09_MR	g507910	BLASTN	389	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8344	GM_138_A2_E03_MR	g3337395	BLASTN	508	7e-16	62	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
8345	GM_138_A2_E05_MR	g3510505	BLASTX	264	1e-20	40	(AF030881) pol polyprotein [Fugu rubripes]
8346	GM_138_A2_E07_MR	g3599418	BLASTN	476	1e-14	93	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
8347	GM_138_A2_E07_T7	g505129	BLASTN	356	4e-09	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8348	GM_138_A2_E08_MR	g2995405	BLASTX	459	2e-44	57	(Y12432) polyprotein [Ananas comosus]
8349	GM_138_A2_E10_MR	g4063756	BLASTN	546	1e-17	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
8350	GM_138_A2_E12_MR	g3097320	BLASTN	439	8e-13	74	Glycine max gene for Bd 30K, complete cds
8351	GM_138_A2_F02_MR	g3845089	BLASTN	366	2e-09	60	Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence
8352	GM_138_A2_F02_T7	g1666236	BLASTX	265	3e-22	34	(U76261) unknown [Hordeum vulgare]
8353	GM_138_A2_F05_MR	g99755	BLASTX	458	1e-42	51	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
8354	GM_138_A2_F06_T7	g3142328	BLASTN	2143	1e-90	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8355	GM_138_A2_F12_MR	g2224933	BLASTX	806	2e-79	86	(AF004216) ethylene-insensitive3 [Arabidopsis thaliana] gi 2224935 (AF004217) ethylene-insensitive3 [Arabidopsis thaliana]
8356	GM_138_A2_G02_MR	g505129	BLASTN	430	2e-12	68	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
8357	GM_138_A2_G02_T7	g4115365	BLASTX	127	4e-09	29	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
8358	GM_138_A2_G08_MR	g3097836	BLASTN	427	3e-12	60	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
8359	GM_138_A2_G10_MR	g4156152	BLASTN	389	1e-10	62	Homo sapiens clone DJ56J10, complete sequence [Homo sapiens]
8360	GM_138_A2_H02_T7	g3319362	BLASTX	380	3e-33	43	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
8361	GM_138_A2_H04_MR	g2979562	BLASTX	193	9e-24	71	(AC003680) unknown protein [Arabidopsis thaliana] gi 3386623 (AC004665) unknown protein [Arabidopsis thaliana]
8362	GM_138_A2_H05_MR	g99922	BLASTX	203	7e-20	82	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
8363	GM_138_A2_H07_MR	g2911063	BLASTN	351	8e-09	68	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSAII project)
8364	GM_138_B2_A03_T7	g3777527	BLASTX	553	3e-51	90	(AF053008) gag-pol polyprotein [Glycine max]
8365	GM_138_B2_B04_MR	g3777527	BLASTX	384	2e-33	93	(AF053008) gag-pol polyprotein [Glycine max]
8366	GM_138_B2_B04_T7	g905361	BLASTX	550	2e-52	98	(U22103) gag-protease polyprotein [Glycine max]
8367	GM_138_B2_B07_MR	g2961349	BLASTX	174	4e-11	46	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
8368	GM_138_B2_B08_T7	g1769898	BLASTX	387	1e-34	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8369	GM_138_B2_B09_T7	g1431738	BLASTN	493	2e-15	79	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8370	GM_138_B2_C08_MR	g3142289	BLASTX	249	4e-27	53	(AC002411) Strong similarity to beta-keto-Coa synthase gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
8371	GM_138_B2_C09_T7	g4063760	BLASTX	435	6e-39	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8372	GM_138_B2_C11_T7	g3176798	BLASTN	381	5e-11	62	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite, 5' sequence
8373	GM_138_B2_C12_MR	g1769898	BLASTX	196	7e-14	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8374	GM_138_B2_D01_T7	g2443320	BLASTX	257	7e-20	49	(D85597) polyprotein [Oryza australiensis]
8375	GM_138_B2_D02_MR	g100484	BLASTX	234	8e-18	62	hypothetical protein - garden snapdragon
8376	GM_138_B2_D05_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8377	GM_138_B2_D07_T7	g2522227	BLASTX	127	9e-09	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
8378	GM_138_B2_D09_MR	g4063760	BLASTX	189	2e-14	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8379	GM_138_B2_D10_MR	g507910	BLASTN	551	3e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
8380	GM_138_B2_D11_T7	g1709885	BLASTX	183	8e-13	55	PHYTOENE SYNTHASE PRECURSOR gi 1086122 pir S54135 phytoene synthase - Narcissus pseudonarcissus gi 780275 (X78814) phytoene synthase [Narcissus pseudonarcissus]
8381	GM_138_B2_E02_T7	g3599418	BLASTN	503	9e-16	71	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
8382	GM_138_B2_E04_T7	g3327393	BLASTX	151	2e-13	35	(AC004483) hypothetical protein [Arabidopsis thaliana]
8383	GM_138_B2_E08_MR	g507910	BLASTN	497	7e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8384	GM_138_B2_E08_T7	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8385	GM_138_B2_E10_MR	g3777527	BLASTX	424	1e-46	98	(AF053008) gag-pol polyprotein [Glycine max]
8386	GM_138_B2_E12_MR	g507910	BLASTN	356	2e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8387	GM_138_B2_E12_T7	g507910	BLASTN	390	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8388	GM_138_B2_F06_MR	g3142328	BLASTN	1334	2e-53	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8389	GM_138_B2_F10_T7	g629693	BLASTX	214	2e-16	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8390	GM_138_B2_G04_T7	g3599418	BLASTN	829	1e-30	77	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
8391	GM_138_B2_G07_MR	g3176806	BLASTN	345	2e-09	68	Homo sapiens allele 17 fragile site locus (FRA10B) minisatellite, 5' sequence
8392	GM_138_B2_G09_MR	g3777527	BLASTX	220	2e-17	53	(AF053008) gag-pol polyprotein [Glycine max]
8393	GM_138_B2_G10_T7	g507910	BLASTN	386	8e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8394	GM_138_B2_G12_MR	g3445210	BLASTX	197	8e-19	50	(AC004786) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]
8395	GM_138_B2_H01_MR	g1351780	BLASTX	94	7e-11	71	HYPOTHETICAL 23.2 KD PROTEIN (ORF 203) gi 984311 (U26948) unknown [Glycine max]
8396	GM_138_B2_H03_T7	g12212	BLASTN	1049	1e-45	93	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
8397	GM_138_B2_H04_T7	g3907448	BLASTN	393	1e-10	65	Homo sapiens chromosome 18, clone hRPK.24_A_23, complete sequence [Homo sapiens]
8398	GM_138_B2_H10_MR	g1184075	BLASTX	132	2e-09	50	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
8399	GM_138_B2_H10_T7	g2429543	BLASTX	221	5e-21	53	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]
8400	GM_139_A1_A05_T7	g13767	BLASTN	362	3e-10	63	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
8401	GM_139_A1_B09_MR	g2443320	BLASTX	173	6e-14	52	(D85597) polyprotein [Oryza australiensis]
8402	GM_139_A1_C08_T7	g3142328	BLASTN	867	3e-32	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8403	GM_139_A1_D11_T7	g3097320	BLASTN	931	4e-35	80	Glycine max gene for Bd 30K, complete cds
8404	GM_139_A1_F04_T7	g2642431	BLASTX	166	4e-10	42	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
8405	GM_139_A1_F11_MR	g3184270	BLASTN	554	5e-18	74	Arabidopsis thaliana chromosome II BAC T8K22 genomic sequence, complete sequence.
8406	GM_139_A1_G08_T7	g4092470	BLASTN	600	5e-20	68	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
8407	GM_139_A1_G11_T7	g905361	BLASTX	235	5e-18	95	(U22103) gag-protease polyprotein [Glycine max]
8408	GM_139_A1_H02_T7	g1881384	BLASTX	246	3e-20	57	(AB001585) reverse transcriptase [Solanum melongena]
8409	GM_139_A1_H07_T7	g4063760	BLASTX	198	1e-13	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8410	GM_139_A2_A02_MR	g4063760	BLASTX	502	4e-46	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8411	GM_139_A2_A05_MR	g3142328	BLASTN	1033	7e-40	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8412	GM_139_A2_A08_MR	g4063760	BLASTX	358	1e-32	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8413	GM_139_A2_B04_MR	g130582	BLASTX	347	2e-29	55	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
8414	GM_139_A2_C01_T7	g3645899	BLASTX	100	1e-08	42	(U68408) 5' end not determined experimentally [Zea mays]
8415	GM_139_A2_C11_MR	g3097320	BLASTN	479	1e-14	71	Glycine max gene for Bd 30K, complete cds
8416	GM_139_A2_D02_MR	g2522228	BLASTX	226	2e-22	63	(AB007466) reverse transcriptase-like protein [Vicia faba]
8417	GM_139_A2_D03_T7	g3142328	BLASTN	398	5e-11	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8418	GM_139_A2_E05_MR	g3142379	BLASTX	268	4e-22	59	(AF053008) envelope-like [Glycine max]
8419	GM_139_A2_E10_T7	g507910	BLASTN	470	1e-14	77	Glycine max BSR-101 satellite SB92 genomic sequence.
8420	GM_139_A2_F12_T7	g3097320	BLASTN	350	8e-09	72	Glycine max gene for Bd 30K, complete cds
8421	GM_139_A2_G05_T7	g507910	BLASTN	352	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
8422	GM_139_A2_G08_T7	g3142379	BLASTX	256	8e-21	80	(AF053008) envelope-like [Glycine max]
8423	GM_139_A2_G11_T7	g2995405	BLASTX	329	7e-28	65	(Y12432) polyprotein [Ananas comosus]
8424	GM_139_A2_H07_MR	g3810596	BLASTX	261	1e-20	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
8425	GM_139_A2_H10_T7	g3550435	BLASTN	418	7e-12	63	Hordeum vulgare Hotr1 gene
8426	GM_139_B1_A01_T7	g456383	BLASTN	372	5e-10	74	Blastocrithidia culicis ATCC 30268 kinetoplast (MURF1) and apocytochrome B (cytB) genes, partial cds, and ATPase subunit 6 (MURF4) gene, complete pre-RNA-edited DNA sequence.
8427	GM_139_B1_A09_T7	g18559	BLASTN	314	4e-11	71	G.max gene for catalase
8428	GM_139_B1_A12_MR	g733521	BLASTN	351	7e-09	67	Dictyostelium discoideum phosphatidylinositol-4,5-diphosphate 3-kinase (PIK2) mRNA, complete cds.
8429	GM_139_B1_B07_MR	g4063756	BLASTN	450	3e-13	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
8430	GM_139_B1_B07_T7	g3142330	BLASTX	457	2e-42	91	(U96295) envelope-like [Glycine max]
8431	GM_139_B1_B12_T7	g2052034	BLASTN	385	2e-10	68	Human DNA sequence from PAC 450C20 on chromosome X
8432	GM_139_B1_C10_MR	g2129618	BLASTX	185	2e-12	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8433	GM_139_B1_D02_T7	g1785739	BLASTX	159	6e-11	37	(Y08502) orf240b [Arabidopsis thaliana]
8434	GM_139_B1_D06_MR	g3142328	BLASTN	961	1e-36	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8435	GM_139_B1_D08_MR	g3097320	BLASTN	634	1e-21	76	Glycine max gene for Bd 30K, complete cds
8436	GM_139_B1_D09_T7	g1435023	BLASTX	215	6e-17	70	(D26578) DNA-binding protein [Daucus carota]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8437	GM_139_B1_E04_T7	g4063760	BLASTX	192	5e-13	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8438	GM_139_B1_E06_T7	g4063760	BLASTX	243	2e-18	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8439	GM_139_B1_E08_T7	g2673917	BLASTX	205	4e-14	50	(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]
8440	GM_139_B1_E09_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8441	GM_139_B1_E09_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8442	GM_139_B1_F03_T7	g4063760	BLASTX	281	2e-22	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8443	GM_139_B1_F06_MR	g4063760	BLASTX	270	2e-21	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8444	GM_139_B1_F11_T7	g507910	BLASTN	591	4e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
8445	GM_139_B1_F12_T7	g3097320	BLASTN	558	3e-18	77	Glycine max gene for Bd 30K, complete cds
8446	GM_139_B1_G02_T7	g3695387	BLASTX	137	1e-13	70	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
8447	GM_139_B1_G07_T7	g507910	BLASTN	625	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
8448	GM_139_B1_G09_MR	g507910	BLASTN	532	2e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
8449	GM_139_B1_G09_T7	g507910	BLASTN	573	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8450	GM_139_B1_G11_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8451	GM_139_B1_G11_T7	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8452	GM_139_B1_H05_T7	g100484	BLASTX	259	2e-20	58	hypothetical protein - garden snapdragon
8453	GM_139_B1_H06_T7	g3142328	BLASTN	760	2e-27	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8454	GM_139_B1_H08_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8455	GM_139_B1_H08_T7	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8456	GM_139_B1_H11_MR	g2443320	BLASTX	212	4e-15	42	(D85597) polyprotein [Oryza australiensis]
8457	GM_139_B1_H11_T7	g2501353	BLASTX	220	1e-23	89	TRANSKETOLASE, CHLOROPLAST (TK) gi 1084440 pir S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) gi 664901 (Z46646) transketolase [Craterostigma plantagineum]
8458	GM_139_B1_H12_MR	g3461838	BLASTX	226	8e-17	43	(AC005315) putative receptor protein kinase [Arabidopsis thaliana]
8459	GM_139_B2_A01_T71016172	g218269	BLASTX	180	3e-13	79	(D12839) reverse transcriptase [Glycine max]
8460	GM_139_B2_A07_MR	g4063760	BLASTX	351	6e-30	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8461	GM_139_B2_A10_T71016172	g2522230	BLASTX	152	3e-10	55	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8462	GM_139_B2_B10_MR	g507910	BLASTN	547	4e-18	84	Glycine max BSR-101 satellite SB92 genomic sequence.
8463	GM_139_B2_B11_T71016172	g2689221	BLASTX	187	4e-13	45	(Y10098) 7-ethoxycoumarin O-deethylase [Helianthus tuberosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8464	GM_139_B2_B12_T71 016172	g806299	BLASTX	95	2e-09	38	(M25427) unknown protein [Zea mays]
8465	GM_139_B2_C03_T71 016172	g1666236	BLASTX	160	2e-10	33	(U76261) unknown [Hordeum vulgare]
8466	GM_139_B2_C05_MR	g3319362	BLASTX	374	1e-32	70	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
8467	GM_139_B2_C07_T71 016172	g2443320	BLASTX	213	4e-15	43	(D85597) polyprotein [Oryza australiensis]
8468	GM_139_B2_C09_T71 016172	g320565	BLASTX	257	2e-21	50	transposon TA1-1 KAS-1 - Arabidopsis thaliana (fragment)
8469	GM_139_B2_C10_MR	g3142328	BLASTN	538	2e-17	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8470	GM_139_B2_D01_MR	g507910	BLASTN	426	1e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8471	GM_139_B2_D07_MR	g2264320	BLASTN	440	8e-13	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
8472	GM_139_B2_E04_T71 016172	g3142328	BLASTN	1380	1e-55	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8473	GM_139_B2_E09_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
8474	GM_139_B2_E09_T71 016172	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
8475	GM_139_B2_F01_T71 016172	g3777527	BLASTX	511	7e-47	98	(AF053008) gag-pol polyprotein [Glycine max]
8476	GM_139_B2_F02_MR	g2842477	BLASTX	152	3e-09	76	(AL021749) copper-binding protein-like [Arabidopsis thaliana]
8477	GM_139_B2_F03_MR	g3249105	BLASTX	168	4e-11	88	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
8478	GM_139_B2_F05_T71 016172	g1142702	BLASTN	497	6e-16	76	Glycine max satellite STR120-A.4.
8479	GM_139_B2_G01_MR	g3777527	BLASTX	168	3e-10	37	(AF053008) gag-pol polyprotein [Glycine max]
8480	GM_139_B2_G04_T71 016172	g507910	BLASTN	595	3e-20	84	Glycine max BSR-101 satellite SB92 genomic sequence.
8481	GM_139_B2_G05_MR	g3142328	BLASTN	1400	1e-56	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8482	GM_139_B2_G06_T71 016172	g18559	BLASTN	651	2e-22	77	G.max gene for catalase
8483	GM_139_B2_G07_MR	g2443320	BLASTX	275	9e-22	53	(D85597) polyprotein [Oryza australiensis]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8484	GM_139_B2_H12_T71 016172	g436919	BLASTN	353	6e-09	62	Arabidopsis thaliana Landsburg lipoxygenase 1 gene, complete cds.
8485	GM_140_A1_A01_MR	g3080423	BLASTX	302	8e-25	51	(AL022604) putative protein [Arabidopsis thaliana]
8486	GM_140_A1_A03_MR	g2738734	BLASTN	438	5e-13	66	Cryptosporidium parvum small subunit ribosomal RNA gene, partial sequence, internal transcribed spacer 1, putative 5.8S ribosomal RNA gene and internal transcribed spacer 2, complete sequence, and large subunit ribosomal...
8487	GM_140_A1_A05_MR	g2995405	BLASTX	266	6e-30	56	(Y12432) polyprotein [Ananas comosus]
8488	GM_140_A1_A11_MR	g3294511	BLASTN	370	1e-09	63	Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
8489	GM_140_A1_B01_T7	g18559	BLASTN	1250	1e-49	87	G.max gene for catalase
8490	GM_140_A1_B02_T7	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8491	GM_140_A1_B03_MR	g2443320	BLASTX	258	4e-26	60	(D85597) polyprotein [Oryza australiensis]
8492	GM_140_A1_B07_T7	g507910	BLASTN	398	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
8493	GM_140_A1_B10_T7	g1769898	BLASTX	125	9e-16	38	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8494	GM_140_A1_C07_T7	g1167523	BLASTX	305	5e-25	46	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
8495	GM_140_A1_C11_T7	g857399	BLASTX	172	1e-16	69	(D50871) mitotic cyclin b1-type [Glycine max]
8496	GM_140_A1_D01_MR	g2894495	BLASTN	353	6e-09	58	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-95, complete sequence [Plasmodium falciparum]
8497	GM_140_A1_D11_T7	g18695	BLASTN	801	1e-29	91	Soybean nodulin 22 gene
8498	GM_140_A1_D12_T7	g4063760	BLASTX	533	2e-49	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8499	GM_140_A1_E05_T7	g3810596	BLASTX	332	4e-28	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
8500	GM_140_A1_E10_T7	g1061420	BLASTX	539	2e-54	83	(U38965) p-type H+-ATPase [Vicia faba]
8501	GM_140_A1_E12_T7	g3142328	BLASTN	480	7e-25	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8502	GM_140_A1_F01_T7	g507910	BLASTN	446	1e-13	78	Glycine max BSR-101 satellite SB92 genomic sequence.
8503	GM_140_A1_F02_T7	g18559	BLASTN	2487	2e-106	90	G.max gene for catalase
8504	GM_140_A1_F05_MR	g3282250	BLASTX	348	3e-34	70	(AF009337) CDPK-related protein kinase [Tradescantia virginiana]
8505	GM_140_A1_F06_MR	g2522230	BLASTX	159	5e-11	32	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8506	GM_140_A1_F09_T7	g1666236	BLASTX	201	4e-15	31	(U76261) unknown [Hordeum vulgare]
8507	GM_140_A1_F12_MR	g1946355	BLASTX	137	2e-09	31	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] gi 2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]
8508	GM_140_A1_G01_T7	g2995405	BLASTX	473	2e-43	51	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8509	GM_140_A1_G03_T7	g3273387	BLASTN	394	9e-11	60	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
8510	GM_140_A1_G04_MR	g3142328	BLASTN	675	1e-23	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8511	GM_140_A1_G05_T7	g100484	BLASTX	483	6e-45	50	hypothetical protein - garden snapdragon
8512	GM_140_A1_G07_T7	g4160362	BLASTN	339	1e-12	65	Saccharomyces cerevisiae complete mitochondrial genome
8513	GM_140_A1_G08_T7	g3097320	BLASTN	490	4e-15	69	Glycine max gene for Bd 30K, complete cds
8514	GM_140_A1_G09_T7	g101042	BLASTX	158	3e-09	31	hypothetical protein Tf1 - fission yeast (Schizosaccharomyces pombe) gi 173477 (M38526) Tf1 protein [Schizosaccharomyces pombe]
8515	GM_140_A1_H05_T7	g2880057	BLASTX	271	2e-23	52	(AC002340) putative RNA helicase A, 5' partial [Arabidopsis thaliana]
8516	GM_140_A1_H07_T7	g1666236	BLASTX	157	8e-19	36	(U76261) unknown [Hordeum vulgare]
8517	GM_140_A1_H08_MR	g3645899	BLASTX	268	5e-46	55	(U68408) 5' end not determined experimentally [Zea mays]
8518	GM_140_A1_H10_T7	g3777527	BLASTX	878	6e-91	92	(AF053008) gag-pol polyprotein [Glycine max]
8519	GM_140_A1_H11_T7	g100484	BLASTX	215	9e-16	50	hypothetical protein - garden snapdragon
8520	GM_140_A1_H12_MR	g2995405	BLASTX	208	1e-22	51	(Y12432) polyprotein [Ananas comosus]
8521	GM_140_A2_A05_T7	g629693	BLASTX	171	1e-11	43	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8522	GM_140_A2_A12_T7	g3142379	BLASTX	152	2e-09	46	(AF053008) envelope-like [Glycine max]
8523	GM_140_A2_B02_T7	g4127445	BLASTN	461	7e-14	68	Arabidopsis thaliana ucp gene, exons 1-9
8524	GM_140_A2_B03_T7	g3142379	BLASTX	433	5e-40	75	(AF053008) envelope-like [Glycine max]
8525	GM_140_A2_B07_T7	g4127445	BLASTN	427	3e-12	67	Arabidopsis thaliana ucp gene, exons 1-9
8526	GM_140_A2_D01_T7	g1142703	BLASTN	582	8e-20	82	Glycine max satellite STR120-B.1.
8527	GM_140_A2_D02_T7	g3645899	BLASTX	187	7e-14	36	(U68408) 5' end not determined experimentally [Zea mays]
8528	GM_140_A2_D11_T7	g2522228	BLASTX	405	5e-37	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
8529	GM_140_A2_E02_T7	g2522230	BLASTX	105	9e-12	52	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8530	GM_140_A2_E05_T7	g3645899	BLASTX	282	2e-25	47	(U68408) 5' end not determined experimentally [Zea mays]
8531	GM_140_A2_E06_T7	g2244761	BLASTX	419	1e-38	54	(Z97335) similar to unknown protein - Arabidopsis thaliana [Arabidopsis thaliana]
8532	GM_140_A2_F03_T7	g117822	BLASTX	248	4e-24	66	CYTOCHROME B6 gi 65635 pir CBNT6 plastoquinol--plastocyanin reductase (EC 1.10.99.1) cytochrome b6 - common tobacco chloroplast gi 11858 (Z00044) cytochrome b6 [Nicotiana tabacum] gi 225226 prf 1211235BH cytochrome b6 [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8533	GM_140_A2_G01_T7	g3097320	BLASTN	390	1e-10	67	Glycine max gene for Bd 30K, complete cds
8534	GM_140_A2_H02_T7	g3777527	BLASTX	435	9e-39	84	(AF053008) gag-pol polyprotein [Glycine max]
8535	GM_140_A2_H05_T7	g320569	BLASTX	165	1e-11	46	transposon TNT1 - Arabidopsis thaliana (fragment)
8536	GM_140_A2_H11_T7	g3142328	BLASTN	1065	3e-41	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8537	GM_140_B1_A04_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
8538	GM_140_B1_A04_T7	g507910	BLASTN	387	7e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8539	GM_140_B1_A08_MR	g116054	BLASTX	190	2e-13	51	CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK) gi 280393 pir A43713 calcium-dependent protein kinase (EC 2.7.1.-) - soybean gi 169931 (M64987) Glycine max calcium dependent protein kinase mRNA. [Glycine max]
8540	GM_140_B1_A10_MR	g905361	BLASTX	487	1e-45	100	(U22103) gag-protease polyprotein [Glycine max]
8541	GM_140_B1_A11_MR	g1769898	BLASTX	325	8e-28	67	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8542	GM_140_B1_A11_T7	g81704	BLASTX	99	9e-12	43	S-locus-specific glycoprotein precursor - kale
8543	GM_140_B1_A12_MR	g18559	BLASTN	638	7e-22	74	G.max gene for catalase
8544	GM_140_B1_B01_T7	g2995405	BLASTX	394	7e-35	66	(Y12432) polyprotein [Ananas comosus]
8545	GM_140_B1_B03_T7	g218269	BLASTX	397	3e-36	93	(D12839) reverse transcriptase [Glycine max]
8546	GM_140_B1_B08_MR	g2995405	BLASTX	331	4e-28	60	(Y12432) polyprotein [Ananas comosus]
8547	GM_140_B1_C06_T7	g170029	BLASTN	365	2e-09	78	Glycine max cv. Dare nodulin 26 gene fragment.
8548	GM_140_B1_C10_MR	g2317908	BLASTX	214	6e-16	47	(U89959) Unknown protein [Arabidopsis thaliana]
8549	GM_140_B1_C12_T7	g3810596	BLASTX	224	1e-16	36	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
8550	GM_140_B1_D01_T7	g3142328	BLASTN	705	6e-25	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8551	GM_140_B1_D02_MR	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
8552	GM_140_B1_D12_MR	g913445	BLASTX	276	2e-23	56	(S75487) alcohol dehydrogenase ADH=alcohol dehydrogenase homolog {EC 1.1.1.1} [Lycopersicon esculentum=tomatoes, cv. red cherry, Peptide, 389 aa] [Lycopersicon esculentum]
8553	GM_140_B1_E06_MR	g3510347	BLASTN	476	2e-14	69	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]
8554	GM_140_B1_E06_T7	g871290	BLASTX	163	2e-23	53	(X69886) glycerol kinase [Homo sapiens]
8555	GM_140_B1_E08_T7	g2109275	BLASTX	165	5e-10	41	(U97106) downy mildew resistance protein RPP5 [Arabidopsis thaliana]
8556	GM_140_B1_E11_MR	g3047073	BLASTX	161	4e-10	42	(AF058825) contains similarity to retrotransposon-like proteins [Arabidopsis thaliana]
8557	GM_140_B1_F02_MR	g507910	BLASTN	567	5e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8558	GM_140_B1_F02_T7	g507910	BLASTN	481	4e-15	79	Glycine max BSR-101 satellite SB92 genomic sequence.
8559	GM_140_B1_F05_MR	g507910	BLASTN	349	4e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8560	GM_140_B1_F05_T7	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8561	GM_140_B1_F07_MR	g2330651	BLASTX	153	2e-12	69	(Y14559) topoisomerase II [Pisum sativum]
8562	GM_140_B1_F08_MR	g1171642	BLASTX	159	3e-10	61	PROBABLE SERINE/THREONINE-PROTEIN KINASE NAK gi 481206 pir S38326 protein kinase - Arabidopsis thaliana gi 166809 (L07248) protein kinase [Arabidopsis thaliana]
8563	GM_140_B1_F10_MR	g1843462	BLASTX	225	1e-17	53	(L10211) isoliquiritigenin 2'-O-methyltransferase [Medicago sativa]
8564	GM_140_B1_G05_MR	g1732513	BLASTX	160	4e-11	68	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]
8565	GM_140_B1_G06_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8566	GM_140_B1_G06_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
8567	GM_140_B1_G07_MR	g2443320	BLASTX	227	1e-16	60	(D85597) polyprotein [Oryza australiensis]
8568	GM_140_B1_G11_T7	g2335089	BLASTN	801	4e-29	73	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]
8569	GM_140_B1_H01_T7	g4063760	BLASTX	454	5e-41	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8570	GM_140_B1_H10_T7	g3335376	BLASTX	212	7e-16	42	(AC003028) putative ammonium transporter [Arabidopsis thaliana]
8571	GM_140_B1_H11_T7	g4063760	BLASTX	152	3e-12	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8572	GM_140_B2_A03_MR	g507910	BLASTN	358	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
8573	GM_140_B2_A12_T7	g4063760	BLASTX	165	4e-10	36	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8574	GM_140_B2_B05_T7	g2244965	BLASTX	161	5e-10	44	(Z97340) unnamed protein product [Arabidopsis thaliana]
8575	GM_140_B2_B06_MR	g507910	BLASTN	553	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
8576	GM_140_B2_B11_T7	g1769899	BLASTX	181	8e-18	72	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8577	GM_140_B2_C02_MR	g2995405	BLASTX	257	4e-20	54	(Y12432) polyprotein [Ananas comosus]
8578	GM_140_B2_C05_T7	g3645899	BLASTX	225	1e-16	48	(U68408) 5' end not determined experimentally [Zea mays]
8579	GM_140_B2_C06_T7	g100484	BLASTX	332	2e-28	58	hypothetical protein - garden snapdragon
8580	GM_140_B2_C07_MR	g3097320	BLASTN	435	1e-12	72	Glycine max gene for Bd 30K, complete cds
8581	GM_140_B2_C11_T7	g507910	BLASTN	458	4e-14	83	Glycine max BSR-101 satellite SB92 genomic sequence.
8582	GM_140_B2_D08_MR	g2829869	BLASTX	169	2e-11	96	(AC002396) pyruvate dehydrogenase E1 alpha subunit [Arabidopsis thaliana]
8583	GM_140_B2_D10_T7	g507910	BLASTN	555	2e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
8584	GM_140_B2_E02_T7	g3142328	BLASTN	1819	1e-75	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8585	GM_140_B2_E09_T7	g507910	BLASTN	372	3e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
8586	GM_140_B2_E12_T7	g4063760	BLASTX	126	8e-09	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8587	GM_140_B2_F02_T7	g1633547	BLASTN	491	4e-15	62	Human chromosome 12p13 sequence, complete sequence [Homo sapiens]
8588	GM_140_B2_G03_MR	g3650039	BLASTX	194	1e-13	53	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
8589	GM_140_B2_G03_T7	g3184508	BLASTN	469	4e-14	66	Homo sapiens chromosome 17, clone HRPC41C23, complete sequence [Homo sapiens]
8590	GM_140_B2_G07_T7	g130582	BLASTX	168	2e-10	40	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
8591	GM_140_B2_H01_T7	g4063760	BLASTX	224	4e-17	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8592	GM_140_B2_H04_MR	g3142328	BLASTN	710	4e-25	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8593	GM_140_B2_H04_T7	g99719	BLASTX	161	9e-10	35	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Landsberg) (fragment) gi 16384 (X53976) orf 2 [Arabidopsis thaliana]
8594	GM_140_B2_H09_MR	g3142328	BLASTN	1001	2e-38	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8595	GM_141_A1_A07_MR	g4038056	BLASTX	316	2e-26	51	(AC005897) putative transposon [Arabidopsis thaliana]
8596	GM_141_A1_A11_MR	g3786008	BLASTX	140	6e-09	50	(AC005499) unknown protein [Arabidopsis thaliana]
8597	GM_141_A1_B05_T7	g1495259	BLASTX	202	7e-15	38	(X97826) orf04 [Arabidopsis thaliana]
8598	GM_141_A1_B07_MR	g3776579	BLASTX	179	2e-11	82	(AC005388) Strong similarity to F22O13.22 gi 3063460 myosin homolog from A. thaliana BAC gb AC003981. [Arabidopsis thaliana]
8599	GM_141_A1_B09_MR	g3777527	BLASTX	248	3e-25	48	(AF053008) gag-pol polyprotein [Glycine max]
8600	GM_141_A1_B11_MR	g507910	BLASTN	371	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8601	GM_141_A1_C01_T7	g2708752	BLASTX	379	2e-34	69	(AC003952) putative histidine kinase [Arabidopsis thaliana]
8602	GM_141_A1_C04_MR	g2760832	BLASTX	115	4e-10	44	(AC003105) similar to barley ids-4 gene product [Arabidopsis thaliana]
8603	GM_141_A1_C06_MR	g507910	BLASTN	562	9e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
8604	GM_141_A1_C11_MR	g3142328	BLASTN	624	3e-21	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8605	GM_141_A1_D01_T7	g3777527	BLASTX	603	1e-56	98	(AF053008) gag-pol polyprotein [Glycine max]
8606	GM_141_A1_E04_MR	g905361	BLASTX	548	2e-58	95	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8607	GM_141_A1_F03_MR	g2522230	BLASTX	243	3e-28	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8608	GM_141_A1_F06_MR	g905361	BLASTX	182	2e-12	37	(U22103) gag-protease polyprotein [Glycine max]
8609	GM_141_A1_F09_MR	g342964	BLASTN	373	8e-11	61	paramecium species 5,311 mt dna dimer: replication init. region.
8610	GM_141_A1_F12_MR	g1277164	BLASTX	202	8e-21	93	(U51853) cysteine proteinase inhibitor [Glycine max]
8611	GM_141_A1_G01_T7	g3885341	BLASTX	162	5e-10	35	(AC005623) unknown protein [Arabidopsis thaliana]
8612	GM_141_A1_G03_MR	g3193290	BLASTX	405	2e-36	54	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabido...
8613	GM_141_A1_G04_T7	g1813979	BLASTX	134	4e-12	50	(Y10860) hypothetical protein [Musa acuminata]
8614	GM_141_A1_G06_T7	g886376	BLASTN	366	2e-09	60	Plasmodium falciparum (strain FCR3) variant-specific surface protein (var-2, var-3) genes, complete cds's.
8615	GM_141_A1_G12_MR	g99755	BLASTX	390	3e-35	45	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
8616	GM_141_A1_G12_T7	g2995405	BLASTX	150	1e-08	36	(Y12432) polyprotein [Ananas comosus]
8617	GM_141_A1_H04_MR	g3645899	BLASTX	202	3e-21	51	(U68408) 5' end not determined experimentally [Zea mays]
8618	GM_141_A1_H05_MR	g3645899	BLASTX	293	7e-24	56	(U68408) 5' end not determined experimentally [Zea mays]
8619	GM_141_A1_H08_T7	g3540184	BLASTX	311	8e-26	61	(AC004122) Similar to endoxylanases [Arabidopsis thaliana]
8620	GM_141_A2_C01_T7	g507910	BLASTN	425	1e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
8621	GM_141_A2_C11_T7	g3650039	BLASTX	257	2e-20	44	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
8622	GM_141_A2_E01_T7	g1666236	BLASTX	175	3e-12	28	(U76261) unknown [Hordeum vulgare]
8623	GM_141_A2_E05_MR	g2085783	BLASTN	507	7e-16	64	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
8624	GM_141_A2_F06_T7	g976178	BLASTX	112	2e-09	41	(L47183) reverse transcriptase [Arabidopsis thaliana]
8625	GM_141_A2_F08_T7	g3319351	BLASTX	208	3e-20	52	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
8626	GM_141_A2_G05_T7	g3097320	BLASTN	1455	7e-59	80	Glycine max gene for Bd 30K, complete cds
8627	GM_141_A2_G11_T7	g507910	BLASTN	526	4e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
8628	GM_141_A2_G12_MR	g3142328	BLASTN	412	1e-11	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8629	GM_141_A2_H03_T7	g2702365	BLASTX	319	5e-27	57	(AF036706) similar to S. cerevisiae Lpg15p (GB:U43281) [Caenorhabditis elegans]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8630	GM_141_A2_H06_T7	g3845197	BLASTN	522	1e-16	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
8631	GM_141_A2_H11_T7	g3142328	BLASTN	783	2e-28	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8632	GM_141_B1_A06_MR	g3283026	BLASTX	182	1e-13	45	putative transposase [Arabidopsis thaliana]
8633	GM_141_B1_A06_T7	g3184291	BLASTX	196	2e-13	51	(AC004136) putative DNA polymerase III gamma subunit [Arabidopsis thaliana]
8634	GM_141_B1_B07_MR	g4063760	BLASTX	170	3e-25	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8635	GM_141_B1_C06_MR	g507910	BLASTN	353	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
8636	GM_141_B1_C06_T7	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8637	GM_141_B1_C07_T7	g170606	BLASTN	586	8e-20	69	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
8638	GM_141_B1_C09_T7	g3142328	BLASTN	492	3e-15	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8639	GM_141_B1_C10_T7	g3645899	BLASTX	229	5e-17	53	(U68408) 5' end not determined experimentally [Zea mays]
8640	GM_141_B1_D10_T7	g913865	BLASTX	152	5e-09	93	branching enzyme II BEII [Zea mays, cultivar B73, endosperms, Peptide, 738 aa]
8641	GM_141_B1_E03_MR	g3142328	BLASTN	564	1e-18	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8642	GM_141_B1_E04_MR	g4115362	BLASTX	149	9e-09	50	(AC005957) hypothetical protein [Arabidopsis thaliana]
8643	GM_141_B1_E07_T7	g1345971	BLASTX	409	2e-37	88	OMEGA-3 FATTY ACID DESATURASE, CHLOROPLAST PRECURSOR gi 541947 pir JQ2339 omega-3 fatty acid desaturase (EC 1.14.99.-) GMD - soybean gi 408792 (L22965) omega-3 fatty acid desaturase [Glycine soja]
8644	GM_141_B1_F02_T7	g507910	BLASTN	407	9e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8645	GM_141_B1_F09_MR	g507910	BLASTN	472	1e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
8646	GM_141_B1_F09_T7	g507910	BLASTN	579	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8647	GM_141_B1_G02_T7	g3777527	BLASTX	176	3e-11	44	(AF053008) gag-pol polyprotein [Glycine max]
8648	GM_141_B1_G04_T7	g18559	BLASTN	589	1e-19	74	G.max gene for catalase
8649	GM_141_B1_G08_MR	g4063760	BLASTX	236	1e-17	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8650	GM_141_B1_G10_MR	g1498335	BLASTN	1369	6e-56	96	Glycine max actin (Soy120) gene, partial cds
8651	GM_141_B1_H04_MR	g507910	BLASTN	395	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8652	GM_141_B1_H06_MR	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
8653	GM_141_B1_H06_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
8654	GM_141_B1_H07_MR	g3096945	BLASTX	328	7e-29	78	(AL023094) putative auxin-regulated protein [Arabidopsis thaliana]
8655	GM_142_A1_A04_T7	g18559	BLASTN	544	1e-17	77	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8656	GM_142_A1_A05_MR	g226407	BLASTX	393	2e-34	46	retrotransposon del1-46 [Lilium henryi]
8657	GM_142_A1_A05_T7	g507910	BLASTN	711	2e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
8658	GM_142_A1_A06_MR	g1769899	BLASTX	203	1e-15	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8659	GM_142_A1_A10_MR	g3250688	BLASTX	216	5e-17	35	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
8660	GM_142_A1_A11_MR	g3876092	BLASTX	165	2e-10	47	(Z69635) Similarity to Drosophila white protein (SW:WHIT_DROME); cDNA EST EMBL:M89346 comes from this gene; cDNA EST yk311f2.3 comes from this gene; cDNA EST yk311f2.5 comes from this gene [Caenorhabditis elegans]
8661	GM_142_A1_A11_T7	g1150932	BLASTX	154	1e-09	80	(X88864) cyclin [Medicago sativa]
8662	GM_142_A1_B01_MR	g421894	BLASTX	226	1e-17	91	1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) 5 - mung bean (fragment) gi 297850 (Z12134) ACC synthase [Vigna radiata] gi 553115 (M94863) 1-aminocyclopropane-1-carboxylate synthase [Vigna radiata]
8663	GM_142_A1_B01_T7	g2244870	BLASTN	374	7e-10	66	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 3
8664	GM_142_A1_B03_MR	g629693	BLASTX	187	2e-13	34	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8665	GM_142_A1_B09_MR	g4160362	BLASTN	381	7e-15	66	Saccharomyces cerevisiae complete mitochondrial genome
8666	GM_142_A1_B10_MR	g1769898	BLASTX	172	1e-18	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8667	GM_142_A1_C06_MR	g93559	BLASTX	191	1e-12	33	ORF3 protein - rice tungro bacilliform virus gi 333967 (M65026) ORF3 [Rice tungro bacilliform virus]
8668	GM_142_A1_C11_MR	g507910	BLASTN	424	2e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
8669	GM_142_A1_C11_T7	g507910	BLASTN	369	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
8670	GM_142_A1_D02_T7	g4063760	BLASTX	218	8e-16	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8671	GM_142_A1_D05_T7	g3386534	BLASTX	174	8e-12	39	(AF078934) mariner transposase [Glycine max]
8672	GM_142_A1_D06_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8673	GM_142_A1_D09_MR	g2522230	BLASTX	216	5e-17	46	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8674	GM_142_A1_D10_T7	g1840106	BLASTN	352	2e-09	63	Human fragile site locus (FRA16B) minisatellite repeat
8675	GM_142_A1_D11_MR	g2258315	BLASTX	229	6e-17	42	(AF004878) resistance complex protein I2C-1 [Lycopersicon esculentum]
8676	GM_142_A1_D12_T7	g469153	BLASTN	372	8e-10	72	P.sativum (Birte) Lox1:Ps:2 gene.
8677	GM_142_A1_E09_MR	g905361	BLASTX	315	1e-26	75	(U22103) gag-protease polyprotein [Glycine max]
8678	GM_142_A1_E12_T7	g3953471	BLASTX	170	3e-11	54	(AC002328) F22O2.16 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8679	GM_142_A1_F01_MR	g2129618	BLASTX	196	1e-13	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8680	GM_142_A1_F03_T7	g343917	BLASTN	346	2e-09	69	yeast (s.cerevisiae) mitochondrial rep1 region & repetitive unit.
8681	GM_142_A1_F05_T7	g2522230	BLASTX	107	2e-13	32	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8682	GM_142_A1_F06_MR	g3142328	BLASTN	1474	6e-60	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8683	GM_142_A1_F08_MR	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
8684	GM_142_A1_F10_MR	g505129	BLASTN	398	5e-11	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
8685	GM_142_A1_F11_T7	g2995405	BLASTX	328	8e-28	61	(Y12432) polyprotein [Ananas comosus]
8686	GM_142_A1_G02_T7	g3810596	BLASTX	99	7e-11	29	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
8687	GM_142_A1_G06_MR	g1171591	BLASTN	364	2e-09	62	P.falciparum complete gene map of plastid-like DNA (IR-B)
8688	GM_142_A1_G07_MR	g18559	BLASTN	1448	1e-58	86	G.max gene for catalase
8689	GM_142_A1_G12_MR	g3777527	BLASTX	279	4e-22	96	(AF053008) gag-pol polyprotein [Glycine max]
8690	GM_142_A1_H01_MR	g3695393	BLASTX	209	8e-15	33	(AF096371) contains similarity to retroviral aspartyl proteases (Pfam: rvp.hmm, score: 11.80) [Arabidopsis thaliana]
8691	GM_142_A1_H02_MR	g4063760	BLASTX	237	8e-18	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8692	GM_142_A1_H02_T7	g4063760	BLASTX	309	2e-25	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8693	GM_142_A1_H04_MR	g3171875	BLASTN	389	2e-10	61	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.1...
8694	GM_142_A1_H06_MR	g4063760	BLASTX	190	1e-28	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8695	GM_142_A1_H06_T7	g507910	BLASTN	385	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8696	GM_142_A1_H07_MR	g1362108	BLASTX	199	4e-19	74	histone H3 homolog - common tobacco
8697	GM_142_A1_H08_MR	g1946355	BLASTX	196	1e-13	28	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] gi 2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]
8698	GM_142_A2_A03_MR	g3777527	BLASTX	338	1e-35	76	(AF053008) gag-pol polyprotein [Glycine max]
8699	GM_142_A2_A03_T7	g2443320	BLASTX	165	3e-23	53	(D85597) polyprotein [Oryza australiensis]
8700	GM_142_A2_B04_T7	g3810596	BLASTX	158	1e-09	53	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
8701	GM_142_A2_C11_MR	g3805850	BLASTX	237	3e-19	86	(AL031986) putative protein [Arabidopsis thaliana]
8702	GM_142_A2_E03_T7	g3599418	BLASTN	777	3e-28	85	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8703	GM_142_A2_E11_MR	g4063760	BLASTX	170	1e-10	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8704	GM_142_A2_F12_T7	g4063760	BLASTX	208	1e-14	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8705	GM_142_A2_H12_MR	g507910	BLASTN	430	8e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8706	GM_142_B1_A04_MR	g2465577	BLASTN	367	1e-09	69	Plasmodium falciparum microsatellite P4 sequence
8707	GM_142_B1_A05_T7	g4063760	BLASTX	525	1e-48	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8708	GM_142_B1_A11_MR	g3777527	BLASTX	423	2e-37	89	(AF053008) gag-pol polyprotein [Glycine max]
8709	GM_142_B1_B05_T7	g3777526	BLASTN	1155	3e-45	93	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
8710	GM_142_B1_B06_T7	g2829924	BLASTX	112	6e-10	48	(AC002291) Unknown protein [Arabidopsis thaliana]
8711	GM_142_B1_B11_MR	g3097320	BLASTN	538	2e-17	68	Glycine max gene for Bd 30K, complete cds
8712	GM_142_B1_C03_MR	g462669	BLASTX	195	1e-15	76	MYB-RELATED PROTEIN PP2 gi 99453 pir S24244 Pp2 protein - moss (Physcomitrella patens) gi 22638 (X67050) Pp2 [Physcomitrella patens]
8713	GM_142_B1_C05_T7	g2982459	BLASTX	225	6e-18	81	(AL022223) putative protein [Arabidopsis thaliana]
8714	GM_142_B1_C09_MR	g130582	BLASTX	330	1e-27	64	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
8715	GM_142_B1_C11_T7	g2618731	BLASTX	194	4e-14	44	(U49077) IAA21 [Arabidopsis thaliana]
8716	GM_142_B1_D01_MR	g2351176	BLASTX	253	2e-20	46	(D85222) S glycoprotein [Brassica rapa]
8717	GM_142_B1_D02_MR	g2995405	BLASTX	154	4e-09	44	(Y12432) polyprotein [Ananas comosus]
8718	GM_142_B1_D03_MR	g3142328	BLASTN	557	3e-18	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8719	GM_142_B1_D10_MR	g507910	BLASTN	514	1e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
8720	GM_142_B1_D10_T7	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
8721	GM_142_B1_E02_MR	g507910	BLASTN	403	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8722	GM_142_B1_E03_T7	g507910	BLASTN	375	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8723	GM_142_B1_E07_T7	g2827718	BLASTX	300	1e-24	45	(AL021684) retrotransposon - like protein [Arabidopsis thaliana]
8724	GM_142_B1_E10_T7	g2522228	BLASTX	359	7e-42	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
8725	GM_142_B1_F02_T7	g2522230	BLASTX	164	2e-11	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8726	GM_142_B1_F04_MR	g4063760	BLASTX	197	1e-13	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8727	GM_142_B1_F04_T7	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8728	GM_142_B1_F09_MR	g3777527	BLASTX	473	8e-43	95	(AF053008) gag-pol polyprotein [Glycine max]
8729	GM_142_B1_F11_MR	g3367534	BLASTX	465	4e-42	89	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis thaliana]
8730	GM_142_B1_F11_T7	g2506139	BLASTX	126	7e-14	73	COATOMER DELTA SUBUNIT (DELTA-COAT PROTEIN) (DELTA-COP) (ARCHAIN) gi 1314049 gnl PID e209222 (Z67962) archain/delta-COP [Oryza sativa]
8731	GM_142_B1_G03_T7	g1666236	BLASTX	261	9e-22	36	(U76261) unknown [Hordeum vulgare]
8732	GM_142_B1_G05_MR	g3142328	BLASTN	623	4e-23	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8733	GM_142_B1_G05_T7	g2244915	BLASTX	229	4e-17	36	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
8734	GM_142_B1_G07_T7	g3142328	BLASTN	1682	2e-69	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8735	GM_142_B1_G08_MR	g3193314	BLASTX	215	5e-16	51	(AF069299) contains similarity to Arabidopsis scarecrow (GB:U62798) [Arabidopsis thaliana]
8736	GM_142_B1_G08_T7	g3319351	BLASTX	209	9e-24	47	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
8737	GM_142_B1_G09_T7	g2228771	BLASTX	145	9e-09	47	(AF001453) Dc3 promoter-binding factor-1 [Helianthus annuus]
8738	GM_142_B1_G12_MR	g4063760	BLASTX	260	3e-20	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8739	GM_142_B1_G12_T7	g507910	BLASTN	589	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8740	GM_142_B1_H03_T7	g2522227	BLASTX	213	1e-16	53	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
8741	GM_142_B1_H04_MR	g905361	BLASTX	460	8e-43	93	(U22103) gag-protease polyprotein [Glycine max]
8742	GM_142_B1_H07_MR	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
8743	GM_142_B1_H08_T7	g18768	BLASTN	463	1e-14	69	Soybean Tgm6 transposable element 3' end
8744	GM_142_B2_A01_T7	g3097320	BLASTN	432	2e-12	67	Glycine max gene for Bd 30K, complete cds
8745	GM_142_B2_A02_MR	g3142328	BLASTN	665	4e-23	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8746	GM_142_B2_A02_T7	g4063760	BLASTX	392	3e-34	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8747	GM_142_B2_A04_T7	g3645899	BLASTX	296	3e-24	50	(U68408) 5' end not determined experimentally [Zea mays]
8748	GM_142_B2_B04_T7	g2462134	BLASTX	325	9e-31	52	(Y13368) reverse transcriptase [Beta vulgaris]
8749	GM_142_B2_B08_T7	g507910	BLASTN	420	2e-12	71	Glycine max BSR-101 satellite SB92 genomic sequence.
8750	GM_142_B2_B09_MR	g507910	BLASTN	398	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
8751	GM_142_B2_B09_T7	g507910	BLASTN	377	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
8752	GM_142_B2_C06_MR	g507910	BLASTN	533	2e-17	81	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8753	GM_142_B2_C09_MR	g3777527	BLASTX	696	1e-66	97	(AF053008) gag-pol polyprotein [Glycine max]
8754	GM_142_B2_C12_MR	g905361	BLASTX	193	2e-13	38	(U22103) gag-protease polyprotein [Glycine max]
8755	GM_142_B2_D08_MR	g4038056	BLASTX	277	3e-22	47	(AC005897) putative transposon [Arabidopsis thaliana]
8756	GM_142_B2_D10_MR	g1402883	BLASTX	280	2e-23	43	(X98130) unknown [Arabidopsis thaliana] gi 1495263 gnl PID e242837 (X97487) orf09 [Arabidopsis thaliana]
8757	GM_142_B2_D12_MR	g3142328	BLASTN	671	2e-23	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8758	GM_142_B2_D12_T7	g905361	BLASTX	98	1e-13	51	(U22103) gag-protease polyprotein [Glycine max]
8759	GM_142_B2_E08_T7	g3283026	BLASTX	185	1e-12	39	putative transposase [Arabidopsis thaliana]
8760	GM_142_B2_F03_T7	g1666236	BLASTX	183	4e-13	33	(U76261) unknown [Hordeum vulgare]
8761	GM_142_B2_F04_MR	g905361	BLASTX	432	1e-39	97	(U22103) gag-protease polyprotein [Glycine max]
8762	GM_142_B2_F05_MR	g3033400	BLASTX	318	2e-26	56	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]
8763	GM_142_B2_F09_T7	g3777527	BLASTX	192	8e-14	39	(AF053008) gag-pol polyprotein [Glycine max]
8764	GM_142_B2_F11_T7	g3135969	BLASTN	358	4e-09	64	Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family prot...
8765	GM_142_B2_G06_T7	g3269281	BLASTX	192	3e-13	48	(AL030978) putative protein [Arabidopsis thaliana]
8766	GM_142_B2_H03_MR	g4115942	BLASTX	170	4e-11	80	(AF118223) contains similarity to eukaryotic protein kinase domains (Pfam: PF00069, score=238.4, E= 1e-67, N=1) and EF hand domains (Pfam: PF00036, score=109.0, E=8.9e-29, N=5) [Arabidopsis thaliana]
8767	GM_143_A2_A07_MR	g421955	BLASTX	369	9e-36	64	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
8768	GM_143_A2_A09_MR	g2827663	BLASTX	390	7e-35	67	(AL021637) membrane-associated salt-inducible-like protein [Arabidopsis thaliana]
8769	GM_143_A2_A09_T7	g3738114	BLASTN	377	5e-10	64	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
8770	GM_143_A2_B08_MR	g507910	BLASTN	525	4e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
8771	GM_143_A2_B08_T7	g3777527	BLASTX	587	6e-55	95	(AF053008) gag-pol polyprotein [Glycine max]
8772	GM_143_A2_B09_MR	g13581	BLASTN	352	1e-09	62	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTCG10 Saccharomyces cerevisiae mitochondrion DNA segment.
8773	GM_143_A2_B09_T7	g1144554	BLASTN	357	6e-10	61	Anopheles merus 12S ribosomal RNA, D-loop, and tRNA-Ile mitochondrial genes, partial sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8774	GM_143_A2_C05_MR	g18767	BLASTN	339	2e-22	75	Soybean Tgm6 transposable element 5' end
8775	GM_143_A2_C07_T7	g2995405	BLASTX	203	2e-23	56	(Y12432) polyprotein [Ananas comosus]
8776	GM_143_A2_C10_MR	g3777527	BLASTX	290	3e-23	44	(AF053008) gag-pol polyprotein [Glycine max]
8777	GM_143_A2_C10_T7	g999189	BLASTN	367	1e-09	75	dihydrofolate reductase-thymidylate synthase=bifunctional enzyme [Glycine max, seedling, mRNA, 1794 nt]
8778	GM_143_A2_D02_MR	g3426334	BLASTN	546	1e-17	63	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
8779	GM_143_A2_D04_MR	g218269	BLASTX	157	9e-11	53	(D12839) reverse transcriptase [Glycine max]
8780	GM_143_A2_D07_T7	g4049350	BLASTX	208	4e-16	51	(AL034567) putative protein [Arabidopsis thaliana]
8781	GM_143_A2_D08_MR	g343898	BLASTN	238	4e-10	70	Yeast (S. Cerevisiae) mitochondrial hypersuppressive (HS) rho-mutant, rep2 DNA.
8782	GM_143_A2_D11_MR	g3097320	BLASTN	521	1e-16	80	Glycine max gene for Bd 30K, complete cds
8783	GM_143_A2_E02_MR	g3599418	BLASTN	1055	7e-41	84	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
8784	GM_143_A2_E04_T7	g2316016	BLASTX	278	5e-22	56	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
8785	GM_143_A2_E07_MR	g99755	BLASTX	338	2e-29	58	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
8786	GM_143_A2_E08_MR	g4063760	BLASTX	188	1e-12	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8787	GM_143_A2_E10_MR	g4063760	BLASTX	226	1e-16	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8788	GM_143_A2_E10_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8789	GM_143_A2_F09_T7	g1666236	BLASTX	156	4e-10	28	(U76261) unknown [Hordeum vulgare]
8790	GM_143_A2_F12_T7	g2244915	BLASTX	171	4e-12	37	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
8791	GM_143_A2_G02_MR	g3777527	BLASTX	696	1e-66	93	(AF053008) gag-pol polyprotein [Glycine max]
8792	GM_143_A2_G03_MR	g2522230	BLASTX	219	5e-27	44	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8793	GM_143_A2_G03_T7	g2129618	BLASTX	197	1e-13	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8794	GM_143_A2_G05_T7	g18559	BLASTN	772	6e-28	74	G.max gene for catalase
8795	GM_143_A2_G07_T7	g3287696	BLASTX	357	5e-31	65	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]
8796	GM_143_A2_G10_T7	g3687234	BLASTX	154	6e-09	49	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8797	GM_143_A2_H05_T7	g3763969	BLASTN	410	2e-11	64	Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE ...
8798	GM_143_A2_H09_T7	g1142699	BLASTN	573	1e-19	82	Glycine max satellite STR120-A.1.
8799	GM_143_B1_C09_MR	g3097320	BLASTN	466	5e-14	67	Glycine max gene for Bd 30K, complete cds
8800	GM_143_B1_E04_MR	g3777527	BLASTX	436	4e-43	90	(AF053008) gag-pol polyprotein [Glycine max]
8801	GM_143_B1_E05_MR	g507910	BLASTN	490	1e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
8802	GM_143_B1_E12_MR	g629693	BLASTX	159	3e-10	44	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
8803	GM_143_B1_F04_MR	g3047119	BLASTX	252	4e-23	60	(AF058919) No definition line found [Arabidopsis thaliana]
8804	GM_143_B1_F05_MR	g3097320	BLASTN	393	9e-11	66	Glycine max gene for Bd 30K, complete cds
8805	GM_143_B1_H04_MR	g1813979	BLASTX	173	3e-15	53	(Y10860) hypothetical protein [Musa acuminata]
8806	GM_143_B1_H09_MR	g2108140	BLASTN	379	8e-11	63	Malurus cyaneus microsatellite McyU8
8807	GM_143_B2_A03_T7	g308769	BLASTN	262	6e-10	64	Budworm mitochondrial partial transfer RNA-Met (tRNA-Met) gene, and partial 12S ribosomal RNA (12S rRNA) gene.
8808	GM_143_B2_A04_T7	g3645899	BLASTX	322	6e-27	49	(U68408) 5' end not determined experimentally [Zea mays]
8809	GM_143_B2_A05_T7	g3128136	BLASTN	382	8e-15	75	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1F13, complete sequence [Arabidopsis thaliana]
8810	GM_143_B2_A06_MR	g3142328	BLASTN	709	4e-25	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8811	GM_143_B2_A08_T7	g507910	BLASTN	397	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8812	GM_143_B2_B01_MR	g2522228	BLASTX	440	1e-40	70	(AB007466) reverse transcriptase-like protein [Vicia faba]
8813	GM_143_B2_B02_T7	g3098290	BLASTN	392	1e-11	60	Plasmodium falciparum sexual stage antigen (s16) gene, promoter and partial cds
8814	GM_143_B2_B03_T7	g3928097	BLASTX	184	1e-13	39	(AC005770) unknown protein, 5' partial [Arabidopsis thaliana]
8815	GM_143_B2_B09_T7	g4115365	BLASTX	155	5e-09	31	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
8816	GM_143_B2_B11_MR	g4063760	BLASTX	154	8e-10	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8817	GM_143_B2_C07_T7	g18559	BLASTN	779	3e-28	73	G.max gene for catalase
8818	GM_143_B2_C09_T7	g3645899	BLASTX	166	2e-20	46	(U68408) 5' end not determined experimentally [Zea mays]
8819	GM_143_B2_C11_MR	g4063760	BLASTX	202	4e-14	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8820	GM_143_B2_D01_MR	g1669680	BLASTN	451	2e-13	64	Human DNA sequence from PAC 293E14 contains ESTs, STS
8821	GM_143_B2_D01_T7	g2443320	BLASTX	301	2e-25	44	(D85597) polyprotein [Oryza australiensis]
8822	GM_143_B2_D02_MR	g1685091	BLASTX	185	5e-13	93	(U45243) diphenol oxidase [Nicotiana tabacum]
8823	GM_143_B2_D03_T7	g2462058	BLASTX	192	2e-14	43	(Y13389) reverse transcriptase [Antirrhinum majus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8824	GM_143_B2_D12_T7	g3645899	BLASTX	348	9e-30	58	(U68408) 5' end not determined experimentally [Zea mays]
8825	GM_143_B2_E01_T7	g99922	BLASTX	560	2e-53	71	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
8826	GM_143_B2_E10_T7	g4063760	BLASTX	434	8e-39	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8827	GM_143_B2_E12_T7	g4063756	BLASTN	444	5e-13	75	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
8828	GM_143_B2_F02_T7	g2959767	BLASTX	355	3e-30	43	(AJ002584) AtMRP4 [Arabidopsis thaliana]
8829	GM_143_B2_F04_T7	g3461840	BLASTX	284	1e-22	43	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
8830	GM_143_B2_F06_T7	g18559	BLASTN	956	3e-36	76	G.max gene for catalase
8831	GM_143_B2_F07_T7	g2522230	BLASTX	102	3e-09	33	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8832	GM_143_B2_G08_T7	g343036	BLASTN	389	3e-11	74	Pea chloroplast gene encoding Gly-tRNA, 3' end, and Arg-tRNA.
8833	GM_143_B2_G11_MR	g18559	BLASTN	529	6e-17	74	G.max gene for catalase
8834	GM_143_B2_G11_T7	g507910	BLASTN	518	8e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
8835	GM_143_B2_H06_T7	g4063760	BLASTX	108	1e-09	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8836	GM_144_A1_A06_MR	g3645899	BLASTX	150	6e-13	47	(U68408) 5' end not determined experimentally [Zea mays]
8837	GM_144_A1_A09_T7	g3319362	BLASTX	184	3e-14	51	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
8838	GM_144_A1_A10_MR	g507910	BLASTN	344	6e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8839	GM_144_A1_A12_T7	g1946279	BLASTX	183	1e-13	43	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
8840	GM_144_A1_B03_MR	g2288887	BLASTX	147	5e-13	63	(Y14325) mevalonate diphosphate decarboxylase [Arabidopsis thaliana] gi 3250736 gnl PID e1301175 (Y17593) mevalonate diphosphate decarboxylase [Arabidopsis thaliana]
8841	GM_144_A1_B04_MR	g2827514	BLASTX	184	2e-16	72	(AL021633) predicted protein [Arabidopsis thaliana]
8842	GM_144_A1_B08_T7	g3142328	BLASTN	505	7e-16	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8843	GM_144_A1_B11_MR	g3097320	BLASTN	938	2e-35	74	Glycine max gene for Bd 30K, complete cds
8844	GM_144_A1_B12_MR	g283035	BLASTX	121	1e-14	81	chaperonin hsp60 - maize gi 22248 (Z12114) mitochondrial chaperonin-60 [Zea mays]
8845	GM_144_A1_C03_MR	g905361	BLASTX	428	3e-39	96	(U22103) gag-protease polyprotein [Glycine max]
8846	GM_144_A1_C06_MR	g2995405	BLASTX	251	2e-19	50	(Y12432) polyprotein [Ananas comosus]
8847	GM_144_A1_C08_MR	g2656032	BLASTN	431	2e-12	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZF18
8848	GM_144_A1_D03_MR	g1769897	BLASTX	134	1e-09	35	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8849	GM_144_A1_D04_MR	g543632	BLASTX	141	7e-19	75	aldehyde reductase (EC 1.1.1.21), NADPH-dependent - bromegrass gi 167113 (L12042) aldose reductase-related protein [Bromus inermis]
8850	GM_144_A1_D06_MR	g2995405	BLASTX	460	5e-42	61	(Y12432) polyprotein [Ananas comosus]
8851	GM_144_A1_D08_T7	g4063760	BLASTX	195	3e-13	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8852	GM_144_A1_D11_MR	g2129618	BLASTX	172	5e-11	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8853	GM_144_A1_E09_MR	g3334667	BLASTX	430	1e-39	74	(Y10493) putative cytochrome P450 [Glycine max]
8854	GM_144_A1_E12_MR	g2995405	BLASTX	433	4e-39	67	(Y12432) polyprotein [Ananas comosus]
8855	GM_144_A1_F04_T7	g2879886	BLASTN	365	1e-09	60	Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes
8856	GM_144_A1_F06_MR	g3193221	BLASTN	375	6e-10	65	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
8857	GM_144_A1_F08_MR	g2995405	BLASTX	324	2e-27	50	(Y12432) polyprotein [Ananas comosus]
8858	GM_144_A1_G02_MR	g2276310	BLASTN	403	4e-11	63	Human DNA sequence from PAC 332O11 on chromosome 1q24-1q25. Contains ESTs and STSs
8859	GM_144_A1_G09_T7	g3142328	BLASTN	1134	2e-44	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8860	GM_144_A1_G11_MR	g3810595	BLASTX	162	1e-16	46	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
8861	GM_144_A1_G12_MR	g2191182	BLASTX	155	2e-09	50	(AF007271) similar to N. tabacum membrane-associated salt-inducible protein (PID:g473874) [Arabidopsis thaliana]
8862	GM_144_A1_H12_MR	g2827699	BLASTX	182	5e-12	72	(AL021684) predicted protein [Arabidopsis thaliana]
8863	GM_144_A2_A10_MR	g2738248	BLASTX	268	7e-26	96	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]
8864	GM_144_A2_B08_MR	g3777527	BLASTX	684	3e-65	98	(AF053008) gag-pol polyprotein [Glycine max]
8865	GM_144_A2_C10_MR	g1813979	BLASTX	335	1e-29	55	(Y10860) hypothetical protein [Musa acuminata]
8866	GM_144_A2_C12_MR	g3142328	BLASTN	1609	6e-73	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8867	GM_144_A2_D09_MR	g507910	BLASTN	378	2e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
8868	GM_144_A2_E07_MR	g2443320	BLASTX	295	6e-24	45	(D85597) polyprotein [Oryza australiensis]
8869	GM_144_A2_F01_MR	g2995405	BLASTX	489	4e-45	62	(Y12432) polyprotein [Ananas comosus]
8870	GM_144_A2_F03_MR	g4063756	BLASTN	393	1e-10	72	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
8871	GM_144_A2_F09_MR	g2275215	BLASTX	215	7e-17	65	(AC002337) hypothetical protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8872	GM_144_A2_F10_MR	g421954	BLASTX	329	4e-28	44	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
8873	GM_144_A2_G08_MR	g3171159	BLASTN	599	5e-20	65	Homo sapiens chromosome 21q22.3 PAC 21L13, complete sequence [Homo sapiens]
8874	GM_144_A2_G10_MR	g3097320	BLASTN	1208	1e-47	81	Glycine max gene for Bd 30K, complete cds
8875	GM_144_A2_H03_MR	g4049345	BLASTX	248	1e-31	54	(AL034567) putative protein [Arabidopsis thaliana]
8876	GM_144_A2_H08_MR	g3777527	BLASTX	694	2e-66	98	(AF053008) gag-pol polyprotein [Glycine max]
8877	GM_144_A2_H09_MR	g2924730	BLASTN	371	1e-09	77	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence [Arabidopsis thaliana]
8878	GM_144_A2_H10_MR	g3426062	BLASTX	225	2e-17	39	(AJ007587) monooxygenase [Arabidopsis thaliana]
8879	GM_144_B1_A02_T7	g100484	BLASTX	184	2e-12	39	hypothetical protein - garden snapdragon
8880	GM_144_B1_A03_T7	g421955	BLASTX	166	1e-19	61	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
8881	GM_144_B1_A04_T7	g2792208	BLASTX	286	2e-24	39	(AF032682) NBS-LRR type resistance protein [Hordeum vulgare]
8882	GM_144_B1_A05_MR	g2244915	BLASTX	250	2e-19	49	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
8883	GM_144_B1_A09_MR	g507910	BLASTN	371	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
8884	GM_144_B1_A09_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8885	GM_144_B1_B03_T7	g296873	BLASTN	358	3e-09	61	W.mrakii mitochondrial DNA
8886	GM_144_B1_B04_T7	g3426334	BLASTN	570	8e-19	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
8887	GM_144_B1_B08_T7	g3645899	BLASTX	153	6e-09	38	(U68408) 5' end not determined experimentally [Zea mays]
8888	GM_144_B1_B09_T7	g3928116	BLASTN	361	3e-09	59	, complete sequence [Homo sapiens]
8889	GM_144_B1_B10_MR	g18559	BLASTN	642	4e-22	68	G.max gene for catalase
8890	GM_144_B1_B12_T7	g1363528	BLASTX	146	6e-09	27	gag protein - maize gi 507845 (U11059) gag gene product [Zea mays]
8891	GM_144_B1_C03_T7	g4063760	BLASTX	229	6e-17	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8892	GM_144_B1_C07_MR	g2462134	BLASTX	163	2e-10	49	(Y13368) reverse transcriptase [Beta vulgaris]
8893	GM_144_B1_C08_MR	g4160362	BLASTN	346	2e-09	60	Saccharomyces cerevisiae complete mitochondrial genome
8894	GM_144_B1_C08_T7	g100484	BLASTX	470	2e-43	52	hypothetical protein - garden snapdragon
8895	GM_144_B1_C12_T7	g507910	BLASTN	582	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
8896	GM_144_B1_D06_T7	g2864621	BLASTX	150	2e-18	52	hypothetical protein [Arabidopsis thaliana]
8897	GM_144_B1_E02_T7	g2801681	BLASTN	1016	1e-39	83	Glycine max telomere-associated sequence STAS10
8898	GM_144_B1_E12_T7	g507910	BLASTN	522	6e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
8899	GM_144_B1_F03_T7	g507910	BLASTN	520	7e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
8900	GM_144_B1_F05_T7	g3810596	BLASTX	238	5e-18	31	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8901	GM_144_B1_F09_MR	g3142328	BLASTN	636	8e-22	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8902	GM_144_B1_G02_T7	g4063760	BLASTX	202	2e-26	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8903	GM_144_B1_G03_T7	g3097320	BLASTN	1005	2e-38	73	Glycine max gene for Bd 30K, complete cds
8904	GM_144_B1_G05_T7	g2583130	BLASTX	216	2e-15	36	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
8905	GM_144_B1_G07_T7	g3059060	BLASTN	358	4e-09	58	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
8906	GM_144_B1_G10_MR	g3452140	BLASTX	124	1e-09	43	(AJ004901) resistance protein [Glycine max]
8907	GM_144_B1_H03_T7	g4063760	BLASTX	238	6e-18	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8908	GM_144_B2_A05_MR	g3097320	BLASTN	480	1e-14	68	Glycine max gene for Bd 30K, complete cds
8909	GM_144_B2_A06_MR	g3142328	BLASTN	380	3e-10	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8910	GM_144_B2_A09_MR	g3367570	BLASTX	131	3e-14	86	putative protein [Arabidopsis thaliana]
8911	GM_144_B2_A09_T7	g2262178	BLASTX	185	9e-13	56	(AC002329) putative Mlo-like protein [Arabidopsis thaliana]
8912	GM_144_B2_B04_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
8913	GM_144_B2_B04_T7	g507910	BLASTN	543	6e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
8914	GM_144_B2_B05_T7	g3249086	BLASTX	194	1e-14	70	(AC004473) Contains similarity to 21 KD subunit of the Arp2/3 protein complex (ARC21) gb AF006086 from Homo sapiens. EST gb Z37222 comes [Arabidopsis thaliana]
8915	GM_144_B2_B10_T7	g4038056	BLASTX	325	2e-27	56	(AC005897) putative transposon [Arabidopsis thaliana]
8916	GM_144_B2_C03_MR	g2129618	BLASTX	215	1e-15	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
8917	GM_144_B2_C03_T7	g905361	BLASTX	654	2e-63	95	(U22103) gag-protease polyprotein [Glycine max]
8918	GM_144_B2_C06_T7	g18563	BLASTN	362	2e-09	73	G.max intergenic region DNA (between Gmachs1 and Gmachs3)
8919	GM_144_B2_C10_T7	g1142699	BLASTN	287	6e-15	68	Glycine max satellite STR120-A.1.
8920	GM_144_B2_C12_MR	g1142701	BLASTN	263	1e-19	76	Glycine max satellite STR120-A.3.
8921	GM_144_B2_D04_MR	g2245104	BLASTX	327	3e-27	44	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
8922	GM_144_B2_D04_T7	g130582	BLASTX	363	3e-31	47	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
8923	GM_144_B2_D05_T7	g2522228	BLASTX	285	2e-31	55	(AB007466) reverse transcriptase-like protein [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8924	GM_144_B2_D07_MR	g507910	BLASTN	695	8e-25	86	Glycine max BSR-101 satellite SB92 genomic sequence.
8925	GM_144_B2_E03_MR	g99922	BLASTX	182	6e-13	55	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
8926	GM_144_B2_E04_T7	g3645899	BLASTX	197	1e-13	36	(U68408) 5' end not determined experimentally [Zea mays]
8927	GM_144_B2_E05_T7	g3650039	BLASTX	288	1e-23	45	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
8928	GM_144_B2_E07_MR	g2522227	BLASTX	208	3e-16	53	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
8929	GM_144_B2_E08_T7	g2262177	BLASTX	121	8e-17	50	(AC002329) hypothetical protein similar to T18A10.3 [Arabidopsis thaliana]
8930	GM_144_B2_E10_MR	g3142328	BLASTN	1094	1e-42	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8931	GM_144_B2_E10_T7	g905361	BLASTX	648	9e-63	92	(U22103) gag-protease polyprotein [Glycine max]
8932	GM_144_B2_F04_MR	g3142303	BLASTX	195	6e-16	45	(AC002411) Strong similarity to MRP-like ABC transporter gb U92650 from A. thaliana and canalicular multi-drug resistance protein gb L49379 from Rattus norvegicus. [Arabidopsis thaliana]
8933	GM_144_B2_F04_T7	g20854	BLASTN	386	1e-10	67	Pea rbcS-3A gene for ribulose 1.5-bisphosphate carboxylase (RBC) small subunit
8934	GM_144_B2_F07_MR	g3461839	BLASTX	142	4e-14	52	(AC005315) putative receptor protein kinase [Arabidopsis thaliana]
8935	GM_144_B2_F08_MR	g4063760	BLASTX	585	5e-55	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8936	GM_144_B2_F08_T7	g125889	BLASTX	156	8e-10	36	PROBABLE PECTATE LYASE P59 PRECURSOR gi 280400 pir S27098 pectate lyase (EC 4.2.2.2) LAT59 - tomato gi 19271 (X15499) P59 protein [Lycopersicon esculentum]
8937	GM_144_B2_F09_T7	g178823	BLASTN	337	4e-09	62	Human apolipoprotein B gene hypervariable region, 3' flank.
8938	GM_144_B2_G03_MR	g507910	BLASTN	362	9e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8939	GM_144_B2_G03_T7	g507910	BLASTN	341	8e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
8940	GM_144_B2_G04_T7	g3142328	BLASTN	700	1e-24	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8941	GM_144_B2_G06_MR	g3097320	BLASTN	444	5e-13	68	Glycine max gene for Bd 30K, complete cds
8942	GM_144_B2_G07_MR	g507910	BLASTN	666	2e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8943	GM_144_B2_G10_T7	g1717949	BLASTX	404	7e-37	86	UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT 1 PRECURSOR (RIESKE IRON-SULFUR PROTEIN 1) (RISP1) gi 100375 pir B41607 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) iron-sulfur protein precursor - common tobacco (fragment) gi 170322 (M77225) Rieske Fe-S protein [Nicotiana tabacum]
8944	GM_144_B2_H02_T7	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8945	GM_144_B2_H05_MR	g4056496	BLASTX	181	1e-12	62	(AC005896) unknown protein [Arabidopsis thaliana]
8946	GM_144_B2_H07_MR	g2995405	BLASTX	237	5e-18	45	(Y12432) polyprotein [Ananas comosus]
8947	GM_144_B2_H08_T7	g3702323	BLASTX	358	8e-32	76	(AC005397) unknown protein [Arabidopsis thaliana]
8948	GM_144_B2_H10_MR	g18559	BLASTN	378	4e-10	65	G.max gene for catalase
8949	GM_144_B2_H12_T7	g4063760	BLASTX	250	3e-19	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8950	GM_145_A1_A09_MR	g3097320	BLASTN	653	1e-22	75	Glycine max gene for Bd 30K, complete cds
8951	GM_145_A1_A10_T7	g3550435	BLASTN	553	6e-18	64	Hordeum vulgare Hotr1 gene
8952	GM_145_A1_A11_T7	g4063760	BLASTX	175	7e-13	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8953	GM_145_A1_B01_T7	g1172495	BLASTX	582	8e-55	93	PHYTOCHROME A gi 515749 (L34842) phytochrome A [Glycine max] gi 515751 (L34844) phytochrome A [Glycine max]
8954	GM_145_A1_B02_T7	g4063760	BLASTX	437	4e-39	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8955	GM_145_A1_B03_MR	g3142328	BLASTN	2065	4e-87	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8956	GM_145_A1_B03_T7	g4063760	BLASTX	298	2e-24	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8957	GM_145_A1_B05_MR	g3097320	BLASTN	426	3e-12	73	Glycine max gene for Bd 30K, complete cds
8958	GM_145_A1_B05_T7	g3142328	BLASTN	837	6e-31	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
8959	GM_145_A1_B06_MR	g3046854	BLASTN	654	2e-22	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]
8960	GM_145_A1_B06_T7	g1769897	BLASTX	224	5e-17	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
8961	GM_145_A1_B09_MR	g181904	BLASTN	483	7e-16	63	Homo sapiens DZY2 satellite sequence HinfA fragment.
8962	GM_145_A1_B11_MR	g3779030	BLASTX	160	4e-11	34	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
8963	GM_145_A1_B12_T7	g3097320	BLASTN	972	5e-37	81	Glycine max gene for Bd 30K, complete cds
8964	GM_145_A1_C01_MR	g2522230	BLASTX	176	9e-13	35	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
8965	GM_145_A1_C03_MR	g2522228	BLASTX	248	3e-28	50	(AB007466) reverse transcriptase-like protein [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8966	GM_145_A1_C04_MR	g114268	BLASTX	269	5e-40	65	L-ASCORBATE OXIDASE HOMOLOG PRECURSOR (ASCORBASE) gi 541907 pir S23763 gene Bp10 protein - rape gi 17789 (X64257) protein homologous to ascorbate oxidase [Brassica napus]
8967	GM_145_A1_C06_MR	g4063760	BLASTX	148	3e-13	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8968	GM_145_A1_C08_T7	g100484	BLASTX	302	4e-25	49	hypothetical protein - garden snapdragon
8969	GM_145_A1_C10_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
8970	GM_145_A1_C10_T7	g4063760	BLASTX	484	3e-44	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8971	GM_145_A1_D07_T7	g3786007	BLASTX	159	6e-10	38	(AC005499) hypothetical protein [Arabidopsis thaliana]
8972	GM_145_A1_D08_T7	g3426334	BLASTN	453	2e-13	63	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
8973	GM_145_A1_D11_T7	g3777527	BLASTX	285	9e-23	73	(AF053008) gag-pol polyprotein [Glycine max]
8974	GM_145_A1_E02_MR	g2443320	BLASTX	296	5e-24	39	(D85597) polyprotein [Oryza australiensis]
8975	GM_145_A1_E10_MR	g4063760	BLASTX	581	1e-54	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8976	GM_145_A1_E10_T7	g3930515	BLASTX	122	2e-12	38	(AF059674) putative gag protein [Nicotiana tabacum]
8977	GM_145_A1_E11_MR	g3097320	BLASTN	739	2e-26	78	Glycine max gene for Bd 30K, complete cds
8978	GM_145_A1_F01_T7	g19642	BLASTN	380	4e-10	69	Medicago sativa nodulin-25 gene
8979	GM_145_A1_F02_MR	g522302	BLASTX	206	1e-14	34	(L35053) endonuclease [Magnaporthe grisea]
8980	GM_145_A1_F05_MR	g3421413	BLASTX	195	7e-14	81	(AF081922) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa] gi 3421415 (AF081923) protein phosphatase 2A 55 kDa B regulatory subunit [Oryza sativa]
8981	GM_145_A1_F06_T7	g3142379	BLASTX	310	5e-27	65	(AF053008) envelope-like [Glycine max]
8982	GM_145_A1_F07_T7	g1707642	BLASTX	205	1e-14	33	(Y07748) TMK [Oryza sativa]
8983	GM_145_A1_F09_T7	g3820757	BLASTN	545	5e-18	67	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
8984	GM_145_A1_F10_MR	g421955	BLASTX	206	2e-15	42	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
8985	GM_145_A1_F11_T7	g3859610	BLASTN	414	1e-11	65	Arabidopsis thaliana BAC T9E19
8986	GM_145_A1_F12_MR	g322663	BLASTX	223	9e-18	68	S-receptor kinase-related protein - Chinese kale gi 17917 (Z18884) S-receptor kinase related protein [Brassica oleracea]
8987	GM_145_A1_G01_MR	g507910	BLASTN	420	2e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
8988	GM_145_A1_G01_T7	g507910	BLASTN	375	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
8989	GM_145_A1_G02_MR	g507910	BLASTN	550	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
8990	GM_145_A1_G03_T7	g3777527	BLASTX	226	1e-20	57	(AF053008) gag-pol polyprotein [Glycine max]
8991	GM_145_A1_G08_T7	g3176711	BLASTX	256	5e-20	51	(AC002392) bZIP-like protein [Arabidopsis thaliana]
8992	GM_145_A1_G10_MR	g1663551	BLASTX	367	5e-33	66	(U55810) disease resistance protein homolog [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
8993	GM_145_A1_G10_T7	g1314277	BLASTX	154	3e-09	55	(U34919) white homolog [Homo sapiens]
8994	GM_145_A1_H01_T7	g2443320	BLASTX	433	1e-38	58	(D85597) polyprotein [Oryza australiensis]
8995	GM_145_A1_H02_MR	g1084606	BLASTX	157	5e-11	35	TyB protein - yeast (Saccharomyces cerevisiae) retrotransposon Ty3-2
8996	GM_145_A1_H04_MR	g2244915	BLASTX	261	1e-20	41	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
8997	GM_145_A1_H05_T7	g18559	BLASTN	1307	3e-52	90	G.max gene for catalase
8998	GM_145_A1_H08_MR	g4063760	BLASTX	443	8e-40	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
8999	GM_145_A1_H10_MR	g507910	BLASTN	505	3e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9000	GM_145_A1_H10_T7	g507910	BLASTN	415	4e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
9001	GM_145_A2_A08_T7	g507910	BLASTN	601	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
9002	GM_145_A2_A09_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9003	GM_145_A2_A10_T7	g3080448	BLASTX	217	4e-16	64	(AL022605) putative protein [Arabidopsis thaliana]
9004	GM_145_A2_B02_MR	g3116020	BLASTX	329	5e-29	80	(Y15383) FtsZ protein [Pisum sativum]
9005	GM_145_A2_B03_MR	g3097320	BLASTN	365	2e-09	73	Glycine max gene for Bd 30K, complete cds
9006	GM_145_A2_B03_T7	g3142328	BLASTN	984	1e-37	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9007	GM_145_A2_B05_MR	g2522228	BLASTX	161	2e-10	78	(AB007466) reverse transcriptase-like protein [Vicia faba]
9008	GM_145_A2_B08_MR	g18559	BLASTN	874	1e-32	74	G.max gene for catalase
9009	GM_145_A2_B09_MR	g3513747	BLASTX	310	2e-25	51	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
9010	GM_145_A2_B12_MR	g3845264	BLASTN	366	2e-09	63	Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence
9011	GM_145_A2_C05_T7	g2995279	BLASTX	141	3e-12	46	hypothetical protein [Lycopersicon esculentum]
9012	GM_145_A2_C09_MR	g1666236	BLASTX	229	2e-18	35	(U76261) unknown [Hordeum vulgare]
9013	GM_145_A2_C09_T7	g21479	BLASTX	226	4e-18	81	(Z11985) 70-Kd heat shock protein [Solanum tuberosum]
9014	GM_145_A2_C11_T7	g3650039	BLASTX	248	2e-19	43	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
9015	GM_145_A2_D01_T7	g18695	BLASTN	353	5e-09	62	Soybean nodulin 22 gene
9016	GM_145_A2_D02_MR	g3097320	BLASTN	352	7e-09	73	Glycine max gene for Bd 30K, complete cds
9017	GM_145_A2_D02_T7	g2443320	BLASTX	215	2e-15	35	(D85597) polyprotein [Oryza australiensis]
9018	GM_145_A2_D03_MR	g2864621	BLASTX	185	6e-13	41	hypothetical protein [Arabidopsis thaliana]
9019	GM_145_A2_D07_T7	g343022	BLASTN	454	1e-13	85	Pea chloroplast photosystem II gene encoding the D2 and 44kd chlorophyll a-binding proteins, complete cds.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9020	GM_145_A2_D09_MR	g3142328	BLASTN	1033	7e-40	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9021	GM_145_A2_D10_MR	g4063760	BLASTX	355	2e-30	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9022	GM_145_A2_D10_T7	g3930515	BLASTX	122	1e-11	38	(AF059674) putative gag protein [Nicotiana tabacum]
9023	GM_145_A2_D12_MR	g507910	BLASTN	421	2e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9024	GM_145_A2_E03_MR	g422418	BLASTX	207	1e-14	37	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
9025	GM_145_A2_E05_T7	g2947063	BLASTX	165	2e-10	42	(AC002521) putative Ser/Thr protein kinase [Arabidopsis thaliana]
9026	GM_145_A2_E09_MR	g3810596	BLASTX	192	4e-13	52	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
9027	GM_145_A2_E12_T7	g1169013	BLASTX	148	8e-10	81	COP9 PROTEIN (FUSCA PROTEIN FUS7) gi 625971 pir A54842 COP9 protein - Arabidopsis thaliana gi 530870 (L32874) COP9 [Arabidopsis thaliana] gi 2244767 gnl PID e326869 (Z97335) COP9 protein [Arabidopsis thaliana]
9028	GM_145_A2_F01_MR	g2764526	BLASTN	541	2e-17	66	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
9029	GM_145_A2_F02_T7	g3142328	BLASTN	1151	3e-45	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9030	GM_145_A2_F07_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9031	GM_145_A2_F07_T7	g507910	BLASTN	356	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9032	GM_145_A2_F09_MR	g507910	BLASTN	601	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
9033	GM_145_A2_F09_T7	g507910	BLASTN	547	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9034	GM_145_A2_F10_MR	g421955	BLASTX	194	4e-14	44	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
9035	GM_145_A2_F12_MR	g18559	BLASTN	1616	2e-69	90	G.max gene for catalase
9036	GM_145_A2_F12_T7	g1769897	BLASTX	343	1e-31	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9037	GM_145_A2_G05_T7	g3319682	BLASTX	156	2e-09	64	(Y17720) SPINDLY protein [Petunia x hybrida]
9038	GM_145_A2_G09_T7	g421955	BLASTX	216	9e-20	50	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
9039	GM_145_A2_G11_MR	g3777527	BLASTX	204	1e-19	39	(AF053008) gag-pol polyprotein [Glycine max]
9040	GM_145_A2_H01_MR	g4063760	BLASTX	272	1e-21	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9041	GM_145_A2_H02_T7	g18768	BLASTN	557	8e-19	73	Soybean Tgm6 transposable element 3' end
9042	GM_145_A2_H03_T7	g3142379	BLASTX	311	4e-27	68	(AF053008) envelope-like [Glycine max]
9043	GM_145_A2_H05_T7	g3777527	BLASTX	215	2e-15	36	(AF053008) gag-pol polyprotein [Glycine max]
9044	GM_145_A2_H07_MR	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9045	GM_145_A2_H07_T7	g507910	BLASTN	547	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9046	GM_145_A2_H09_MR	g294042	BLASTN	416	9e-12	63	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
9047	GM_145_B1_A04_T7	g2911075	BLASTX	184	5e-14	76	(AL021960) putative protein [Arabidopsis thaliana]
9048	GM_145_B1_B03_T7	g3142328	BLASTN	1067	2e-41	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9049	GM_145_B1_D02_T7	g507910	BLASTN	456	5e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9050	GM_145_B1_D04_T7	g505129	BLASTN	323	1e-10	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9051	GM_145_B1_E02_T7	g507910	BLASTN	358	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9052	GM_145_B1_E05_T7	g3924609	BLASTX	189	1e-12	39	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
9053	GM_145_B1_E06_T7	g2970554	BLASTN	407	2e-11	69	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
9054	GM_145_B2_A03_MR	g507910	BLASTN	526	4e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
9055	GM_145_B2_A03_T7	g507910	BLASTN	588	6e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9056	GM_145_B2_A04_MR	g507910	BLASTN	679	4e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
9057	GM_145_B2_A04_T7	g507910	BLASTN	558	1e-18	85	Glycine max BSR-101 satellite SB92 genomic sequence.
9058	GM_145_B2_A05_MR	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
9059	GM_145_B2_A05_T7	g4063756	BLASTN	359	3e-09	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9060	GM_145_B2_A06_MR	g4115365	BLASTX	293	1e-23	44	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
9061	GM_145_B2_A07_T7	g2522226	BLASTN	829	1e-30	68	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
9062	GM_145_B2_A08_T7	g505129	BLASTN	315	8e-10	68	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9063	GM_145_B2_A09_T7	g4115365	BLASTX	253	2e-19	41	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
9064	GM_145_B2_A12_T7	g2129618	BLASTX	239	3e-18	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9065	GM_145_B2_B04_T7	g1204057	BLASTN	442	6e-13	61	Caenorhabditis elegans cosmid C04B4, complete sequence [Caenorhabditis elegans]
9066	GM_145_B2_B05_MR	g559261	BLASTN	291	1e-09	66	Saccharomyces cerevisiae mitochondrion 21S R2 ribosomal RNA, 3' end.
9067	GM_145_B2_B09_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9068	GM_145_B2_B11_MR	g2522228	BLASTX	247	5e-20	55	(AB007466) reverse transcriptase-like protein [Vicia faba]
9069	GM_145_B2_B12_MR	g3599418	BLASTN	370	1e-09	67	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9070	GM_145_B2_B12_T7	g3097320	BLASTN	786	2e-28	74	Glycine max gene for Bd 30K, complete cds
9071	GM_145_B2_C03_MR	g4038056	BLASTX	337	1e-28	54	(AC005897) putative transposon [Arabidopsis thaliana]
9072	GM_145_B2_C03_T7	g4098966	BLASTN	344	6e-09	70	Glycine max putative reistance gene analog genomic sequence
9073	GM_145_B2_C04_T7	g3600044	BLASTX	116	4e-21	48	(AF080119) contains similarity to proteases [Arabidopsis thaliana]
9074	GM_145_B2_C06_T7	g2738248	BLASTX	420	7e-38	81	(U97200) cobalamin-independent methionine synthase [Arabidopsis thaliana]
9075	GM_145_B2_C07_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
9076	GM_145_B2_C09_T7	g18559	BLASTN	604	2e-20	71	G.max gene for catalase
9077	GM_145_B2_C11_T7	g505129	BLASTN	356	2e-11	69	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9078	GM_145_B2_D02_MR	g2494132	BLASTX	415	4e-38	64	(AC002376) Contains similarity to human dimethylaniline monooxygenase (gb M64082). [Arabidopsis thaliana]
9079	GM_145_B2_D06_T7	g18559	BLASTN	949	5e-36	77	G.max gene for catalase
9080	GM_145_B2_D08_T7	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
9081	GM_145_B2_D09_T7	g4038056	BLASTX	367	6e-32	49	(AC005897) putative transposon [Arabidopsis thaliana]
9082	GM_145_B2_E04_MR	g2462134	BLASTX	299	2e-25	40	(Y13368) reverse transcriptase [Beta vulgaris]
9083	GM_145_B2_E04_T7	g2129618	BLASTX	182	4e-12	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9084	GM_145_B2_E05_T7	g4063760	BLASTX	207	1e-14	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9085	GM_145_B2_E09_MR	g2462134	BLASTX	192	7e-18	36	(Y13368) reverse transcriptase [Beta vulgaris]
9086	GM_145_B2_F01_MR	g3097320	BLASTN	1063	4e-41	77	Glycine max gene for Bd 30K, complete cds
9087	GM_145_B2_F03_MR	g3746069	BLASTX	182	6e-14	39	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
9088	GM_145_B2_F06_MR	g507910	BLASTN	384	9e-11	77	Glycine max BSR-101 satellite SB92 genomic sequence.
9089	GM_145_B2_F06_T7	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9090	GM_145_B2_F08_T7	g3123745	BLASTX	203	4e-31	92	(AB013447) aluminum-induced [Brassica napus]
9091	GM_145_B2_F09_T7	g3097320	BLASTN	487	5e-15	73	Glycine max gene for Bd 30K, complete cds
9092	GM_145_B2_G02_T7	g18559	BLASTN	1136	2e-44	75	G.max gene for catalase
9093	GM_145_B2_G05_T7	g1840106	BLASTN	375	2e-10	61	Human fragile site locus (FRA16B) minisatellite repeat
9094	GM_145_B2_G06_MR	g99922	BLASTX	263	4e-26	53	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
9095	GM_145_B2_G08_T7	g507910	BLASTN	374	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9096	GM_145_B2_G11_MR	g3142328	BLASTN	1104	4e-43	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9097	GM_145_B2_H04_MR	g3894211	BLASTN	456	1e-13	62	Homo sapiens PAC clone DJ0888A21 from 7q31, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9098	GM_145_B2_H06_MR	g507910	BLASTN	481	4e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9099	GM_145_B2_H07_T7	g3142328	BLASTN	1008	1e-38	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9100	GM_145_B2_H11_MR	g1369852	BLASTX	324	5e-27	81	(L46702) kinesin heavy chain-like protein [Solanum tuberosum]
9101	GM_145_B2_H12_MR	g4063760	BLASTX	252	2e-19	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9102	GM_146_A1_A01_MR	g2129618	BLASTX	190	6e-13	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9103	GM_146_A1_A02_MR	g3779021	BLASTX	397	9e-35	53	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]
9104	GM_146_A1_A08_MR	g2129618	BLASTX	187	1e-12	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9105	GM_146_A1_A09_MR	g3599418	BLASTN	673	2e-23	73	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
9106	GM_146_A1_A09_T7	g3935200	BLASTN	386	2e-10	65	Homo sapiens Chromosome 22q11.2 PAC Clone p201m18 In DGCR Region, complete sequence [Homo sapiens]
9107	GM_146_A1_B06_MR	g226407	BLASTX	158	3e-09	42	retrotransposon del1-46 [Lilium henryi]
9108	GM_146_A1_B08_T7	g2895633	BLASTN	462	3e-14	63	Zerene cesonia large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
9109	GM_146_A1_B11_T7	g2129618	BLASTX	213	2e-15	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9110	GM_146_A1_C01_T7	g18559	BLASTN	839	5e-31	78	G.max gene for catalase
9111	GM_146_A1_C03_MR	g2522230	BLASTX	241	5e-22	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
9112	GM_146_A1_C06_MR	g3599418	BLASTN	351	7e-09	65	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
9113	GM_146_A1_C09_MR	g3914056	BLASTX	140	2e-12	82	DNA MISMATCH REPAIR PROTEIN MSH2 >gi 2522362 (AF002706) MutS homolog 2 [Arabidopsis thaliana] >gi 2522364 (AF003005) MutS homolog 2 [Arabidopsis thaliana] >gi 2547236 (AF026549) DNA mismatch repair protein MSH2 [Arabidopsis thaliana]
9114	GM_146_A1_C10_T7	g294042	BLASTN	372	8e-10	64	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
9115	GM_146_A1_C11_MR	g18559	BLASTN	781	2e-28	78	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9116	GM_146_A1_D02_MR	g3142295	BLASTX	417	4e-37	56	(AC002411) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. [Arabidopsis thaliana]
9117	GM_146_A1_D03_MR	g3319351	BLASTX	215	3e-25	51	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
9118	GM_146_A1_D04_T7	g3193290	BLASTX	383	5e-34	56	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabido...
9119	GM_146_A1_D06_T7	g1091678	BLASTX	186	1e-12	36	activator-like transposable element [Pennisetum glaucum]
9120	GM_146_A1_D07_T7	g3894208	BLASTN	365	2e-09	61	Homo sapiens BAC clone GS180J15 from 7q31, complete sequence [Homo sapiens]
9121	GM_146_A1_D08_MR	g4063760	BLASTX	465	4e-42	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9122	GM_146_A1_D08_T7	g4063760	BLASTX	408	5e-36	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9123	GM_146_A1_D11_MR	g3777527	BLASTX	673	4e-64	95	(AF053008) gag-pol polyprotein [Glycine max]
9124	GM_146_A1_E01_T7	g1435023	BLASTX	280	4e-28	77	(D26578) DNA-binding protein [Daucus carota]
9125	GM_146_A1_E07_T7	g2995405	BLASTX	367	6e-35	64	(Y12432) polyprotein [Ananas comosus]
9126	GM_146_A1_E10_MR	g2995405	BLASTX	214	1e-39	56	(Y12432) polyprotein [Ananas comosus]
9127	GM_146_A1_E11_T7	g3777527	BLASTX	207	4e-15	38	(AF053008) gag-pol polyprotein [Glycine max]
9128	GM_146_A1_F01_MR	g3810596	BLASTX	282	9e-23	41	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
9129	GM_146_A1_F01_T7	g4063760	BLASTX	210	6e-15	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9130	GM_146_A1_F06_T7	g3777527	BLASTX	773	7e-75	96	(AF053008) gag-pol polyprotein [Glycine max]
9131	GM_146_A1_F07_MR	g507910	BLASTN	373	3e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
9132	GM_146_A1_F07_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
9133	GM_146_A1_F08_MR	g905361	BLASTX	226	5e-17	41	(U22103) gag-protease polyprotein [Glycine max]
9134	GM_146_A1_F11_MR	g18559	BLASTN	676	1e-23	72	G.max gene for catalase
9135	GM_146_A1_G02_T7	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9136	GM_146_A1_G05_MR	g1480927	BLASTN	843	2e-31	92	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
9137	GM_146_A1_G05_T7	g2129618	BLASTX	206	1e-14	48	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9138	GM_146_A1_G07_T7	g3142328	BLASTN	1117	1e-43	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9139	GM_146_A1_G09_MR	g2924341	BLASTN	356	3e-09	64	Saccharomyces cerevisiae mitochondrial Tyr-tRNA, Asn-tRNA and Met-tRNA genes

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9140	GM_146_A1_G09_T7	g927574	BLASTN	377	3e-10	74	Glycine max williams alpha galactosidase mRNA, complete cds. >gi 2086979 gb I36466 I36466 Sequence 8 from patent US 5606042
9141	GM_146_A1_G11_MR	g2264320	BLASTN	563	2e-18	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
9142	GM_146_A1_G12_MR	g3319345	BLASTX	233	1e-17	43	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
9143	GM_146_A1_G12_T7	g3142328	BLASTN	993	5e-38	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9144	GM_146_A1_H05_MR	g4063760	BLASTX	261	2e-20	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9145	GM_146_A1_H08_T7	g18559	BLASTN	997	3e-38	74	G.max gene for catalase
9146	GM_146_A2_A01_MR	g1666236	BLASTX	207	7e-16	31	(U76261) unknown [Hordeum vulgare]
9147	GM_146_A2_A03_T7	g3449333	BLASTN	388	2e-10	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXF12, complete sequence [Arabidopsis thaliana]
9148	GM_146_A2_A07_T7	g507910	BLASTN	376	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
9149	GM_146_A2_A08_MR	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9150	GM_146_A2_A11_MR	g170606	BLASTN	752	2e-27	67	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
9151	GM_146_A2_A11_T7	g1666236	BLASTX	181	7e-13	31	(U76261) unknown [Hordeum vulgare]
9152	GM_146_A2_B03_MR	g2708743	BLASTX	116	6e-15	41	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
9153	GM_146_A2_B12_MR	g3142328	BLASTN	818	4e-30	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9154	GM_146_A2_C03_T7	g3687234	BLASTX	186	2e-14	43	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
9155	GM_146_A2_C04_MR	g1931654	BLASTX	266	1e-21	45	(U95973) BRCA1-associated RING domain protein isolog [Arabidopsis thaliana]
9156	GM_146_A2_C06_MR	g18702	BLASTN	347	2e-09	60	Soybean nodulin-24 gene 5' end
9157	GM_146_A2_C10_MR	g2316016	BLASTX	286	6e-23	60	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
9158	GM_146_A2_C11_MR	g861155	BLASTX	203	1e-14	83	(Z35162) beta-fructofuranosidase; cell wall invertase I; fructosidase [Vicia faba]
9159	GM_146_A2_D05_MR	g1709930	BLASTX	171	3e-11	94	PHOSPHORIBOSYLAMINOIMIDAZOLE CARBOXYLASE PRECURSOR (AIR CARBOXYLASE) (AIRC) gi 629656 pir S43322 phosphoribosylaminoimidazole carboxylase (EC 4.1.1.21) - moth bean gi 349159 (L22584) 5-aminoimidazole ribonucleotide carboxylase [Vigna aconitifolia]
9160	GM_146_A2_D08_MR	g4006831	BLASTX	267	6e-23	42	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9161	GM_146_A2_D09_MR	g507910	BLASTN	359	1e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
9162	GM_146_A2_E02_MR	g18695	BLASTN	487	3e-15	83	Soybean nodulin 22 gene
9163	GM_146_A2_E03_T7	g100484	BLASTX	374	6e-33	61	hypothetical protein - garden snapdragon
9164	GM_146_A2_E08_T7	g100484	BLASTX	187	6e-14	47	hypothetical protein - garden snapdragon
9165	GM_146_A2_E10_MR	g3746069	BLASTX	156	2e-22	50	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
9166	GM_146_A2_E11_T7	g509768	BLASTN	417	6e-12	67	Glycine max seed-specific low molecular weight sulfur-rich protein.
9167	GM_146_A2_E12_T7	g2497538	BLASTX	147	9e-09	55	PYRUVATE KINASE, CYTOSOLIC ISOZYME gi 466350 (L08632) pyruvate kinase [Glycine max]
9168	GM_146_A2_F04_MR	g2815075	BLASTN	390	1e-10	60	Caenorhabditis elegans cosmid Y38H8A, complete sequence [Caenorhabditis elegans]
9169	GM_146_A2_F05_T7	g4063756	BLASTN	514	4e-16	70	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9170	GM_146_A2_F08_MR	g3319362	BLASTX	210	7e-30	57	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
9171	GM_146_A2_F11_MR	g170606	BLASTN	787	4e-29	68	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
9172	GM_146_A2_F12_T7	g3810596	BLASTX	152	7e-09	62	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
9173	GM_146_A2_G08_MR	g507910	BLASTN	545	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
9174	GM_146_A2_G10_MR	g4159709	BLASTN	593	9e-20	67	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MLN21, complete sequence [Arabidopsis thaliana]
9175	GM_146_A2_H04_T7	g4063770	BLASTX	167	1e-10	49	(AB004906) transposase [Ipomoea purpurea]
9176	GM_146_A2_H06_T7	g3142379	BLASTX	319	6e-28	82	(AF053008) envelope-like [Glycine max]
9177	GM_146_A2_H07_T7	g2443899	BLASTN	402	4e-11	62	A. thaliana BAC T3F12 from chromsome IV, likely from the long arm, complete sequence [Arabidopsis thaliana]
9178	GM_146_A2_H08_MR	g507910	BLASTN	659	4e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
9179	GM_146_A2_H11_T7	g1174779	BLASTX	195	6e-14	84	TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR gi 166894 (M81620) tryptophan synthase beta-subunit [Arabidopsis thaliana]
9180	GM_146_B1_A01_T7	g1769897	BLASTX	425	7e-45	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9181	GM_146_B1_A02_MR	g3645899	BLASTX	140	7e-16	35	(U68408) 5' end not determined experimentally [Zea mays]
9182	GM_146_B1_A02_T7	g4063760	BLASTX	236	1e-17	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9183	GM_146_B1_A03_MR	g4006838	BLASTN	380	4e-10	62	Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence [Homo sapiens]
9184	GM_146_B1_A03_T7	g3402755	BLASTX	189	3e-19	38	(AL031187) putative transposable element [Arabidopsis thaliana]
9185	GM_146_B1_A04_T7	g1142702	BLASTN	354	2e-09	78	Glycine max satellite STR120-A.4.
9186	GM_146_B1_A05_T7	g3142330	BLASTX	732	1e-71	85	(U96295) envelope-like [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9187	GM_146_B1_A06_T7	g2062167	BLASTX	247	8e-42	79	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]
9188	GM_146_B1_A07_T7	g294042	BLASTN	350	8e-09	61	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
9189	GM_146_B1_A08_MR	g4049647	BLASTN	349	1e-08	61	Melanoplus sanguinipes entomopoxvirus, complete genome
9190	GM_146_B1_A09_T7	g1142702	BLASTN	338	9e-09	78	Glycine max satellite STR120-A.4.
9191	GM_146_B1_B05_T7	g170080	BLASTN	441	3e-15	74	Soybean seed lectin gene transposable element tgm1.
9192	GM_146_B1_B06_MR	g507910	BLASTN	405	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9193	GM_146_B1_B06_T7	g507910	BLASTN	396	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9194	GM_146_B1_B07_T7	g1666236	BLASTX	287	1e-24	36	(U76261) unknown [Hordeum vulgare]
9195	GM_146_B1_B12_MR	g13096	BLASTN	359	3e-09	59	Leishmania tarentolae maxicircle DNA fragment
9196	GM_146_B1_C04_MR	g2213599	BLASTX	251	2e-22	37	(AC000348) T7N9.19 [Arabidopsis thaliana]
9197	GM_146_B1_C05_MR	g3142328	BLASTN	2400	4e-103	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9198	GM_146_B1_C08_T7	g3859592	BLASTX	338	2e-55	74	(AF104919) contains similarity to expansins [Arabidopsis thaliana]
9199	GM_146_B1_C09_MR	g18559	BLASTN	556	3e-18	72	G.max gene for catalase
9200	GM_146_B1_D02_T7	g100484	BLASTX	356	4e-43	60	hypothetical protein - garden snapdragon
9201	GM_146_B1_D06_MR	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
9202	GM_146_B1_D08_MR	g507910	BLASTN	372	3e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
9203	GM_146_B1_D11_T7	g2281092	BLASTX	144	2e-09	72	(AC002333) hypothetical protein [Arabidopsis thaliana]
9204	GM_146_B1_E01_T7	g2281092	BLASTX	206	6e-16	64	(AC002333) hypothetical protein [Arabidopsis thaliana]
9205	GM_146_B1_E02_T7	g3217506	BLASTN	389	1e-10	62	Caenorhabditis elegans cosmid F55C9, complete sequence [Caenorhabditis elegans]
9206	GM_146_B1_E03_MR	g4063760	BLASTX	264	1e-20	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9207	GM_146_B1_E05_T7	g18559	BLASTN	631	1e-21	76	G.max gene for catalase
9208	GM_146_B1_E06_T7	g3845307	BLASTN	379	4e-10	58	Plasmodium falciparum chromosome 2, section 61 of 73 of the complete sequence
9209	GM_146_B1_E08_MR	g3746069	BLASTX	163	3e-27	51	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
9210	GM_146_B1_E09_MR	g1142701	BLASTN	1083	1e-42	83	Glycine max satellite STR120-A.3.
9211	GM_146_B1_E11_MR	g1666236	BLASTX	144	9e-09	35	(U76261) unknown [Hordeum vulgare]
9212	GM_146_B1_F06_T7	g3097320	BLASTN	1114	2e-43	79	Glycine max gene for Bd 30K, complete cds
9213	GM_146_B1_G01_MR	g507910	BLASTN	407	9e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9214	GM_146_B1_G01_T7	g507910	BLASTN	394	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9215	GM_146_B1_G03_T7	g1871192	BLASTX	143	7e-10	37	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]
9216	GM_146_B1_G06_T7	g2245120	BLASTX	208	1e-14	39	(Z97343) hypothetical protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9217	GM_146_B1_G07_T7	g543905	BLASTX	176	1e-12	69	BRASSINOSTEROID-REGULATED PROTEIN BRU1 gi 347459 (L22162) brassinosteroid-regulated protein [Glycine max]
9218	GM_146_B1_H01_T7	g905361	BLASTX	362	7e-32	85	(U22103) gag-protease polyprotein [Glycine max]
9219	GM_146_B1_H02_MR	g4063760	BLASTX	279	3e-22	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9220	GM_146_B1_H03_T7	g3845197	BLASTN	594	8e-20	63	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
9221	GM_146_B1_H07_MR	g1769897	BLASTX	364	2e-32	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9222	GM_146_B1_H11_MR	g1769897	BLASTX	282	3e-23	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9223	GM_146_B1_H12_T7	g3142379	BLASTX	262	2e-21	85	(AF053008) envelope-like [Glycine max]
9224	GM_146_B2_A05_MR	g3777527	BLASTX	726	8e-70	97	(AF053008) gag-pol polyprotein [Glycine max]
9225	GM_146_B2_A11_MR	g507910	BLASTN	396	3e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
9226	GM_146_B2_B03_MR	g3142328	BLASTN	662	5e-23	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9227	GM_146_B2_C11_MR	g3142379	BLASTX	291	8e-25	68	(AF053008) envelope-like [Glycine max]
9228	GM_146_B2_C12_MR	g4063760	BLASTX	189	1e-12	31	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9229	GM_146_B2_D01_MR	g3777527	BLASTX	260	5e-21	46	(AF053008) gag-pol polyprotein [Glycine max]
9230	GM_146_B2_D04_MR	g3873182	BLASTN	385	2e-10	63	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
9231	GM_146_B2_D08_MR	g18559	BLASTN	363	2e-09	62	G.max gene for catalase
9232	GM_146_B2_D11_MR	g2130096	BLASTX	353	4e-31	55	cytochrome P450tyr - sorghum gi 984543 (U32624) cytochrome P-450 [Sorghum bicolor]
9233	GM_146_B2_E01_MR	g905361	BLASTX	709	3e-69	95	(U22103) gag-protease polyprotein [Glycine max]
9234	GM_146_B2_E10_MR	g505129	BLASTN	315	3e-10	67	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9235	GM_146_B2_E11_MR	g4063760	BLASTX	401	3e-35	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9236	GM_146_B2_F05_MR	g320565	BLASTX	219	3e-17	48	transposon TA1-1 KAS-1 - Arabidopsis thaliana (fragment)
9237	GM_146_B2_G01_MR	g3097320	BLASTN	416	8e-12	73	Glycine max gene for Bd 30K, complete cds
9238	GM_146_B2_G05_MR	g1142701	BLASTN	1383	4e-56	86	Glycine max satellite STR120-A.3.
9239	GM_146_B2_G12_MR	g4063760	BLASTX	339	1e-28	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9240	GM_146_B2_H03_MR	g505129	BLASTN	356	4e-09	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9241	GM_147_A1_A01_MR	g100728	BLASTX	156	8e-10	87	aspartate transaminase (EC 2.6.1.1) AAT3 precursor - proso millet gi 1084464 pir S53304 aspartate aminotransferase - proso millet gi 20601 (X63430) aspartate aminotransferase [Panicum miliaceum] gi 435459 gnl PID d1005534 (D25323) aspartate aminotransferase [Panicum miliaceum]
9242	GM_147_A1_A04_MR	g18559	BLASTN	906	5e-34	77	G.max gene for catalase
9243	GM_147_A1_A06_MR	g905361	BLASTX	206	6e-15	36	(U22103) gag-protease polyprotein [Glycine max]
9244	GM_147_A1_A06_T7	g100484	BLASTX	359	3e-31	61	hypothetical protein - garden snapdragon
9245	GM_147_A1_A07_MR	g507910	BLASTN	517	9e-17	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9246	GM_147_A1_A07_T7	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9247	GM_147_A1_A08_MR	g1236949	BLASTX	303	4e-25	98	(U50075) lipoxygenase L-5 [Glycine max]
9248	GM_147_A1_A09_T7	g4050011	BLASTN	398	6e-11	64	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
9249	GM_147_A1_A12_MR	g3097320	BLASTN	1037	6e-40	81	Glycine max gene for Bd 30K, complete cds
9250	GM_147_A1_B02_T7	g2129473	BLASTX	234	6e-19	38	arabinogalactan-like protein - loblolly pine gi 607774 (U09556) arabinogalactan-like protein [Pinus taeda]
9251	GM_147_A1_B05_T7	g8540	BLASTN	383	4e-11	70	Drosophila satellite DNA fragment 1.672-614 >gi 158379 gb M29744 DROSAT02 Drosophila satellite DNA fragment 1.672-614.
9252	GM_147_A1_B11_T7	g4063760	BLASTX	255	9e-20	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9253	GM_147_A1_C01_T7	g4063760	BLASTX	155	6e-11	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9254	GM_147_A1_C02_T7	g1769897	BLASTX	326	7e-30	67	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9255	GM_147_A1_C07_MR	g3142328	BLASTN	691	3e-24	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9256	GM_147_A1_C10_MR	g3599418	BLASTN	533	4e-17	69	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
9257	GM_147_A1_C11_MR	g421954	BLASTX	339	3e-29	55	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
9258	GM_147_A1_D01_MR	g2764526	BLASTN	372	9e-10	60	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
9259	GM_147_A1_D03_T7	g2522228	BLASTX	210	8e-16	35	(AB007466) reverse transcriptase-like protein [Vicia faba]
9260	GM_147_A1_D04_MR	g507910	BLASTN	560	1e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9261	GM_147_A1_E03_T7	g507910	BLASTN	401	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9262	GM_147_A1_E05_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9263	GM_147_A1_E11_T7	g13596	BLASTN	398	8e-12	62	Yeast mit DNA for promoter upstream of tRNA-Leu gene 3 *Source:
9264	GM_147_A1_E12_MR	g507910	BLASTN	394	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9265	GM_147_A1_E12_T7	g507910	BLASTN	377	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9266	GM_147_A1_F01_MR	g3777527	BLASTX	512	6e-47	97	(AF053008) gag-pol polyprotein [Glycine max]
9267	GM_147_A1_F01_T7	g1666236	BLASTX	193	3e-14	30	(U76261) unknown [Hordeum vulgare]
9268	GM_147_A1_G01_T7	g3097320	BLASTN	891	3e-33	73	Glycine max gene for Bd 30K, complete cds
9269	GM_147_A1_G02_MR	g1335862	BLASTX	204	5e-30	90	(U42608) clathrin heavy chain [Glycine max]
9270	GM_147_A1_G06_T7	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9271	GM_147_A1_G07_MR	g2522226	BLASTN	623	3e-21	70	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
9272	GM_147_A1_G08_MR	g3599418	BLASTN	523	1e-16	73	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
9273	GM_147_A1_G12_T7	g3097320	BLASTN	446	4e-13	70	Glycine max gene for Bd 30K, complete cds
9274	GM_147_A1_H03_MR	g2244965	BLASTX	166	1e-10	38	(Z97340) unnamed protein product [Arabidopsis thaliana]
9275	GM_147_A1_H05_T7	g99755	BLASTX	248	1e-19	59	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
9276	GM_147_A1_H08_MR	g3281868	BLASTX	319	5e-27	55	(AL031004) putative protein [Arabidopsis thaliana]
9277	GM_147_A1_H09_T7	g3599418	BLASTN	354	5e-09	86	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
9278	GM_147_A2_A06_T7	g3645899	BLASTX	193	3e-13	57	(U68408) 5' end not determined experimentally [Zea mays]
9279	GM_147_A2_A07_T7	g3142328	BLASTN	603	3e-20	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9280	GM_147_A2_A08_MR	g3650039	BLASTX	159	8e-10	40	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
9281	GM_147_A2_A11_T7	g2462745	BLASTX	216	6e-16	58	(AC002292) Hypothetical protein [Arabidopsis thaliana]
9282	GM_147_A2_B07_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9283	GM_147_A2_B07_T7	g4063760	BLASTX	270	2e-21	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9284	GM_147_A2_B09_T7	g507910	BLASTN	570	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9285	GM_147_A2_B11_MR	g3645899	BLASTX	337	1e-28	51	(U68408) 5' end not determined experimentally [Zea mays]
9286	GM_147_A2_C05_MR	g4063760	BLASTX	172	5e-16	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9287	GM_147_A2_C06_MR	g4063760	BLASTX	312	8e-26	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9288	GM_147_A2_C09_MR	g2522227	BLASTX	150	1e-09	36	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
9289	GM_147_A2_C09_T7	g507910	BLASTN	380	1e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
9290	GM_147_A2_C11_T7	g3097320	BLASTN	429	2e-12	71	Glycine max gene for Bd 30K, complete cds
9291	GM_147_A2_C12_T7	g3894385	BLASTX	187	1e-12	36	(AF053994) Hcr2-0A [Lycopersicon esculentum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9292	GM_147_A2_D01_MR	g2982444	BLASTX	158	1e-13	37	(AL022224) CLV1 receptor kinase like protein [Arabidopsis thaliana]
9293	GM_147_A2_D01_T7	g3779021	BLASTX	233	2e-17	43	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]
9294	GM_147_A2_D03_T7	g18559	BLASTN	922	9e-35	77	G.max gene for catalase
9295	GM_147_A2_D05_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9296	GM_147_A2_D07_MR	g507910	BLASTN	391	5e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9297	GM_147_A2_D12_T7	g3645899	BLASTX	146	7e-11	46	(U68408) 5' end not determined experimentally [Zea mays]
9298	GM_147_A2_E01_T7	g507910	BLASTN	408	8e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9299	GM_147_A2_E02_T7	g4092471	BLASTN	483	9e-15	67	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
9300	GM_147_A2_E04_MR	g507910	BLASTN	566	6e-19	83	Glycine max BSR-101 satellite SB92 genomic sequence.
9301	GM_147_A2_E05_MR	g130582	BLASTX	208	1e-15	44	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
9302	GM_147_A2_E06_T7	g507910	BLASTN	584	9e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9303	GM_147_A2_E07_T7	g2996647	BLASTN	357	4e-09	62	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
9304	GM_147_A2_E08_T7	g3860272	BLASTX	100	2e-11	68	(AC005824) putative suppressor protein [Arabidopsis thaliana]
9305	GM_147_A2_E10_T7	g2764526	BLASTN	467	4e-14	68	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
9306	GM_147_A2_F05_MR	g4160362	BLASTN	401	4e-11	61	Saccharomyces cerevisiae complete mitochondrial genome
9307	GM_147_A2_F08_MR	g3402703	BLASTX	201	8e-15	70	(AC004261) hypothetical protein [Arabidopsis thaliana]
9308	GM_147_A2_F11_T7	g3142379	BLASTX	215	3e-16	78	(AF053008) envelope-like [Glycine max]
9309	GM_147_A2_G02_T7	g4063760	BLASTX	152	3e-12	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9310	GM_147_A2_G08_T7	g99922	BLASTX	240	1e-19	78	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
9311	GM_147_A2_G10_T7	g3810595	BLASTX	367	1e-31	55	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
9312	GM_147_A2_H02_T7	g2244802	BLASTX	142	5e-10	45	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
9313	GM_147_A2_H04_T7	g18695	BLASTN	792	3e-29	91	Soybean nodulin 22 gene
9314	GM_147_A2_H05_T7	g99755	BLASTX	302	2e-25	51	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9315	GM_147_A2_H11_T7	g507910	BLASTN	382	1e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
9316	GM_147_A2_H12_MR	g4063756	BLASTN	430	2e-12	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9317	GM_147_A2_H12_T7	g3930515	BLASTX	126	2e-11	50	(AF059674) putative gag protein [Nicotiana tabacum]
9318	GM_147_B1_A02_MR	g507910	BLASTN	747	4e-27	90	Glycine max BSR-101 satellite SB92 genomic sequence.
9319	GM_147_B1_A02_T7	g4063760	BLASTX	252	2e-19	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9320	GM_147_B1_A04_MR	g2996576	BLASTN	371	1e-09	60	Homo sapiens DNA sequence from PAC 29C18 on chromosome 22
9321	GM_147_B1_A05_T7	g13557	BLASTN	380	3e-10	72	Yeast mitochondrial genes for 15S rRNA and tRNA-Trp
9322	GM_147_B1_A06_T7	g99922	BLASTX	579	4e-62	72	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
9323	GM_147_B1_A07_T7	g4003350	BLASTN	344	9e-10	68	Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q25.1, complete sequence [Homo sapiens]
9324	GM_147_B1_A08_T7	g2708743	BLASTX	314	6e-26	42	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
9325	GM_147_B1_B02_MR	g2914707	BLASTX	155	1e-10	34	(AC003974) putative disease resistance protein (Cf-2.2) [Arabidopsis thaliana] gi 3298554 (AC004681) putative disease resistance protein [Arabidopsis thaliana]
9326	GM_147_B1_B05_T7	g1769897	BLASTX	213	3e-17	36	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9327	GM_147_B1_B08_MR	g507910	BLASTN	387	7e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9328	GM_147_B1_B08_T7	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
9329	GM_147_B1_B10_T7	g507910	BLASTN	429	9e-13	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9330	GM_147_B1_C04_MR	g3097320	BLASTN	474	2e-14	71	Glycine max gene for Bd 30K, complete cds
9331	GM_147_B1_C09_T7	g18559	BLASTN	1692	8e-70	90	G.max gene for catalase
9332	GM_147_B1_C10_T7	g4092470	BLASTN	695	2e-24	67	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
9333	GM_147_B1_C11_MR	g507910	BLASTN	346	5e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9334	GM_147_B1_D04_MR	g3152629	BLASTN	384	3e-10	65	Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence [Homo sapiens]
9335	GM_147_B1_D05_T7	g3820757	BLASTN	374	4e-10	62	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
9336	GM_147_B1_D06_MR	g4063760	BLASTX	277	5e-22	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9337	GM_147_B1_E03_T7	g3319362	BLASTX	183	3e-12	31	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
9338	GM_147_B1_E04_MR	g18559	BLASTN	1043	3e-40	75	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9339	GM_147_B1_E05_MR	g422418	BLASTX	139	2e-09	41	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
9340	GM_147_B1_E07_T7	g3036785	BLASTN	465	6e-14	60	Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains histone genes H2A/l,H2B.1A,H4,H2A.1b,H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG island
9341	GM_147_B1_F01_T7	g4115365	BLASTX	367	1e-31	47	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
9342	GM_147_B1_F04_MR	g3097320	BLASTN	476	2e-14	72	Glycine max gene for Bd 30K, complete cds
9343	GM_147_B1_F04_T7	g3097320	BLASTN	693	2e-24	76	Glycine max gene for Bd 30K, complete cds
9344	GM_147_B1_F05_MR	g3319362	BLASTX	430	1e-38	61	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
9345	GM_147_B1_F08_MR	g1658457	BLASTX	137	1e-12	61	(U75248) reverse transcriptase [Gossypium barbadense]
9346	GM_147_B1_F09_T7	g2522227	BLASTX	218	3e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
9347	GM_147_B1_F10_MR	g421954	BLASTX	163	1e-14	37	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
9348	GM_147_B1_G02_MR	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
9349	GM_147_B1_G02_T7	g507910	BLASTN	414	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
9350	GM_147_B1_G03_T7	g1171591	BLASTN	371	1e-09	62	P.falciparum complete gene map of plastid-like DNA (IR-B)
9351	GM_147_B1_G05_T7	g469153	BLASTN	402	4e-11	65	P.sativum (Birte) Lox1:Ps:2 gene.
9352	GM_147_B1_G06_MR	g507910	BLASTN	535	1e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
9353	GM_147_B1_G06_T7	g4063760	BLASTX	290	2e-23	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9354	GM_147_B1_G07_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9355	GM_147_B1_G07_T7	g507910	BLASTN	597	2e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9356	GM_147_B1_G08_T7	g4038056	BLASTX	256	5e-20	52	(AC005897) putative transposon [Arabidopsis thaliana]
9357	GM_147_B1_H05_MR	g4063756	BLASTN	421	6e-12	69	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9358	GM_147_B1_H07_MR	g505129	BLASTN	441	5e-13	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9359	GM_147_B1_H08_MR	g3645899	BLASTX	342	4e-29	47	(U68408) 5' end not determined experimentally [Zea mays]
9360	GM_147_B1_H09_MR	g4063760	BLASTX	650	5e-62	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9361	GM_147_B1_H10_T7	g100484	BLASTX	320	4e-27	58	hypothetical protein - garden snapdragon
9362	GM_147_B1_H12_T7	g3142328	BLASTN	433	1e-12	69	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9363	GM_147_B2_A04_MR	g4063760	BLASTX	559	3e-52	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9364	GM_147_B2_A08_T7	g3097320	BLASTN	403	3e-11	70	Glycine max gene for Bd 30K, complete cds
9365	GM_147_B2_A09_T7	g1431738	BLASTN	630	1e-21	74	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
9366	GM_147_B2_B01_MR	g2995405	BLASTX	291	7e-46	64	(Y12432) polyprotein [Ananas comosus]
9367	GM_147_B2_B04_MR	g1769897	BLASTX	209	2e-15	35	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9368	GM_147_B2_B12_MR	g2894575	BLASTX	157	1e-10	67	(AL021890) putative protein [Arabidopsis thaliana]
9369	GM_147_B2_C04_T7	g4038056	BLASTX	296	3e-24	48	(AC005897) putative transposon [Arabidopsis thaliana]
9370	GM_147_B2_C06_T7	g1142702	BLASTN	605	8e-21	79	Glycine max satellite STR120-A.4.
9371	GM_147_B2_C11_T7	g2995405	BLASTX	260	2e-20	46	(Y12432) polyprotein [Ananas comosus]
9372	GM_147_B2_D02_MR	g507910	BLASTN	559	1e-18	86	Glycine max BSR-101 satellite SB92 genomic sequence.
9373	GM_147_B2_D02_T7	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9374	GM_147_B2_D03_MR	g507910	BLASTN	588	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9375	GM_147_B2_D04_MR	g2997694	BLASTX	232	1e-18	42	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
9376	GM_147_B2_D11_MR	g3746062	BLASTX	140	7e-14	60	(AC005311) hypothetical protein [Arabidopsis thaliana]
9377	GM_147_B2_E06_MR	g3924609	BLASTX	260	7e-24	50	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
9378	GM_147_B2_E09_MR	g905361	BLASTX	141	4e-20	69	(U22103) gag-protease polyprotein [Glycine max]
9379	GM_147_B2_E11_T7	g2522227	BLASTX	170	3e-14	57	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
9380	GM_147_B2_F02_MR	g3097320	BLASTN	474	2e-14	69	Glycine max gene for Bd 30K, complete cds
9381	GM_147_B2_F05_MR	g2894575	BLASTX	172	2e-12	71	(AL021890) putative protein [Arabidopsis thaliana]
9382	GM_147_B2_F07_MR	g505129	BLASTN	347	1e-08	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9383	GM_147_B2_F08_MR	g1666236	BLASTX	155	6e-10	29	(U76261) unknown [Hordeum vulgare]
9384	GM_147_B2_G10_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9385	GM_147_B2_G11_MR	g4063760	BLASTX	216	1e-15	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9386	GM_147_B2_G12_T7	g3097320	BLASTN	682	8e-24	75	Glycine max gene for Bd 30K, complete cds
9387	GM_147_B2_H05_MR	g4038056	BLASTX	394	8e-35	55	(AC005897) putative transposon [Arabidopsis thaliana]
9388	GM_147_B2_H06_MR	g3777527	BLASTX	241	4e-18	38	(AF053008) gag-pol polyprotein [Glycine max]
9389	GM_147_B2_H07_MR	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9390	GM_147_B2_H07_T7	g507910	BLASTN	476	7e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
9391	GM_148_A1_A02_MR	g2459422	BLASTX	115	2e-09	42	(AC002332) unknown protein [Arabidopsis thaliana]
9392	GM_148_A1_A05_MR	g1488266	BLASTN	370	5e-10	60	Arabidopsis thaliana low affinity calcium antiporter CAX2 mRNA, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9393	GM_148_A1_A08_T7	g3668091	BLASTX	181	3e-12	29	(AC004667) hypothetical protein [Arabidopsis thaliana]
9394	GM_148_A1_A11_MR	g3142328	BLASTN	974	4e-37	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9395	GM_148_A1_B09_MR	g3777527	BLASTX	310	2e-25	52	(AF053008) gag-pol polyprotein [Glycine max]
9396	GM_148_A1_B11_T7	g2258317	BLASTX	114	2e-12	33	(AF004879) resistance complex protein I2C-2 [Lycopersicon esculentum]
9397	GM_148_A1_C03_MR	g3695387	BLASTX	259	3e-20	68	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
9398	GM_148_A1_C06_MR	g4063770	BLASTX	186	1e-12	39	(AB004906) transposase [Ipomoea purpurea]
9399	GM_148_A1_D10_MR	g3695395	BLASTX	217	4e-16	37	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
9400	GM_148_A1_E02_MR	g3142328	BLASTN	1045	2e-40	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9401	GM_148_A1_E02_T7	g1666236	BLASTX	157	3e-10	30	(U76261) unknown [Hordeum vulgare]
9402	GM_148_A1_F03_MR	g2213608	BLASTX	177	1e-12	38	(AC000103) F21J9.2 [Arabidopsis thaliana]
9403	GM_148_A1_F04_MR	g3142328	BLASTN	847	5e-61	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9404	GM_148_A1_F07_T7	g3426334	BLASTN	354	5e-09	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
9405	GM_148_A1_F12_MR	g13768	BLASTN	276	1e-09	69	Torulopsis glabrata mitochondrial DNA for tRNA-Thr,-His and -Glu upstream of cytochrome b gene >gi 343951 gb M11856 YSLMTIG01 Yeast (T.glabrata) mitochondrial DNA between L rRNA and cytochrome b genes.
9406	GM_148_A1_G04_T7	g4063760	BLASTX	270	2e-21	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9407	GM_148_A1_G05_T7	g905361	BLASTX	587	3e-56	94	(U22103) gag-protease polyprotein [Glycine max]
9408	GM_148_A1_G08_MR	g8543	BLASTN	372	1e-10	67	Drosophila satellite DNA fragment 1.672-573
9409	GM_148_A1_H07_MR	g18559	BLASTN	992	6e-38	73	G.max gene for catalase
9410	GM_148_A1_H07_T7	g4063770	BLASTX	186	3e-16	53	(AB004906) transposase [Ipomoea purpurea]
9411	GM_148_A1_H11_T7	g1666236	BLASTX	139	9e-13	44	(U76261) unknown [Hordeum vulgare]
9412	GM_148_A1_H12_T7	g3004564	BLASTX	134	5e-17	75	(AC003673) putative receptor Ser/Thr protein kinase [Arabidopsis thaliana]
9413	GM_148_A2_A02_MR	g507910	BLASTN	531	2e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
9414	GM_148_A2_A02_T7	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9415	GM_148_A2_A03_T7	g1000971	BLASTN	382	3e-10	62	Hansenula wingei mitochondrial DNA, complete sequence
9416	GM_148_A2_A05_MR	g507910	BLASTN	598	2e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9417	GM_148_A2_A05_T7	g3777527	BLASTX	728	5e-70	97	(AF053008) gag-pol polyprotein [Glycine max]
9418	GM_148_A2_A08_MR	g905361	BLASTX	181	3e-12	29	(U22103) gag-protease polyprotein [Glycine max]
9419	GM_148_A2_B07_T7	g2347190	BLASTX	274	5e-22	38	(AC002338) Na/H antiporter isolog [Arabidopsis thaliana] gi 3150398 (AC004165) putative Na/H antiporter [Arabidopsis thaliana]
9420	GM_148_A2_B09_MR	g3510337	BLASTN	359	3e-09	69	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19E20, complete sequence [Arabidopsis thaliana]
9421	GM_148_A2_B11_T7	g4063760	BLASTX	557	5e-52	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9422	GM_148_A2_B12_MR	g3777527	BLASTX	191	9e-13	34	(AF053008) gag-pol polyprotein [Glycine max]
9423	GM_148_A2_C05_T7	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
9424	GM_148_A2_C06_MR	g505129	BLASTN	371	5e-12	71	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9425	GM_148_A2_C06_T7	g507910	BLASTN	607	8e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
9426	GM_148_A2_C07_T7	g1666236	BLASTX	136	4e-15	34	(U76261) unknown [Hordeum vulgare]
9427	GM_148_A2_C10_MR	g100484	BLASTX	363	9e-32	60	hypothetical protein - garden snapdragon
9428	GM_148_A2_D04_T7	g3650039	BLASTX	272	6e-22	43	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
9429	GM_148_A2_D09_MR	g3426334	BLASTN	503	9e-16	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
9430	GM_148_A2_D10_MR	g3873182	BLASTN	427	3e-12	62	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
9431	GM_148_A2_D10_T7	g18768	BLASTN	507	1e-16	67	Soybean Tgm6 transposable element 3' end
9432	GM_148_A2_E06_T7	g2522228	BLASTX	281	1e-36	63	(AB007466) reverse transcriptase-like protein [Vicia faba]
9433	GM_148_A2_E08_T7	g3273120	BLASTN	352	7e-09	63	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-57, complete sequence [Plasmodium falciparum]
9434	GM_148_A2_E10_MR	g3645899	BLASTX	263	1e-20	45	(U68408) 5' end not determined experimentally [Zea mays]
9435	GM_148_A2_E12_T7	g3097320	BLASTN	416	8e-12	73	Glycine max gene for Bd 30K, complete cds
9436	GM_148_A2_F01_T7	g100484	BLASTX	284	4e-23	60	hypothetical protein - garden snapdragon
9437	GM_148_A2_F04_MR	g4063760	BLASTX	539	5e-50	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9438	GM_148_A2_F04_T7	g2264312	BLASTN	420	6e-12	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]
9439	GM_148_A2_F10_T7	g3096945	BLASTX	244	6e-20	67	(AL023094) putative auxin-regulated protein [Arabidopsis thaliana]
9440	GM_148_A2_G01_MR	g3097320	BLASTN	463	6e-14	72	Glycine max gene for Bd 30K, complete cds
9441	GM_148_A2_G04_T7	g2791289	BLASTX	193	4e-13	41	(AJ000387) protease [Drosophila melanogaster]
9442	GM_148_A2_G05_T7	g4063760	BLASTX	252	2e-19	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9443	GM_148_A2_G08_MR	g4063760	BLASTX	212	4e-15	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9444	GM_148_A2_H03_MR	g507910	BLASTN	576	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9445	GM_148_A2_H03_T7	g507910	BLASTN	492	1e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
9446	GM_148_A2_H04_MR	g4063760	BLASTX	473	5e-43	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9447	GM_148_A2_H04_T7	g3645899	BLASTX	188	3e-17	46	(U68408) 5' end not determined experimentally [Zea mays]
9448	GM_148_A2_H06_MR	g507910	BLASTN	371	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9449	GM_148_A2_H06_T7	g507910	BLASTN	422	2e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9450	GM_148_A2_H10_MR	g18559	BLASTN	544	1e-17	81	G.max gene for catalase
9451	GM_148_A2_H10_T7	g3777527	BLASTX	726	8e-70	97	(AF053008) gag-pol polyprotein [Glycine max]
9452	GM_148_A2_H11_MR	g4150933	BLASTN	390	1e-10	63	Homo sapiens BAC clone NH0520M18 from 7q31.1-q31.2, complete sequence [Homo sapiens]
9453	GM_148_A2_H12_MR	g2443320	BLASTX	235	1e-17	37	(D85597) polyprotein [Oryza australiensis]
9454	GM_148_B1_A02_MR	g3777527	BLASTX	628	2e-59	93	(AF053008) gag-pol polyprotein [Glycine max]
9455	GM_148_B1_A05_MR	g4092470	BLASTN	632	2e-21	66	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
9456	GM_148_B1_A05_T7	g2443320	BLASTX	246	1e-18	39	(D85597) polyprotein [Oryza australiensis]
9457	GM_148_B1_A06_MR	g840618	BLASTN	375	4e-10	60	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
9458	GM_148_B1_A07_MR	g4063760	BLASTX	574	8e-54	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9459	GM_148_B1_A07_T7	g3645899	BLASTX	188	1e-19	46	(U68408) 5' end not determined experimentally [Zea mays]
9460	GM_148_B1_A08_T7	g4063760	BLASTX	213	3e-15	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9461	GM_148_B1_A10_MR	g3142328	BLASTN	597	2e-27	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9462	GM_148_B1_B05_MR	g18559	BLASTN	907	4e-34	79	G.max gene for catalase
9463	GM_148_B1_B08_T7	g166421	BLASTN	375	2e-10	66	Medicago sativa ubiquitin carrier protein mRNA, complete cds.
9464	GM_148_B1_B10_T7	g18559	BLASTN	584	5e-31	78	G.max gene for catalase
9465	GM_148_B1_B12_T7	g1769897	BLASTX	308	3e-26	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9466	GM_148_B1_C01_MR	g1899158	BLASTN	555	2e-18	64	Saccharomyces cerevisiae synthetic green fluorescent protein (cox3::GFPm) gene, mitochondrial gene construct, complete cds
9467	GM_148_B1_C04_MR	g2443320	BLASTX	238	4e-30	46	(D85597) polyprotein [Oryza australiensis]
9468	GM_148_B1_C07_T7	g4138265	BLASTX	197	2e-14	91	(AJ006228) Avr9 elicitor response protein [Nicotiana tabacum]
9469	GM_148_B1_C08_MR	g2583130	BLASTX	178	1e-12	37	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
9470	GM_148_B1_C08_T7	g4038056	BLASTX	275	5e-25	52	(AC005897) putative transposon [Arabidopsis thaliana]
9471	GM_148_B1_C12_MR	g3036806	BLASTX	108	3e-09	30	(AL022373) glycine-rich protein [Arabidopsis thaliana]
9472	GM_148_B1_C12_T7	g3096945	BLASTX	219	2e-17	59	(AL023094) putative auxin-regulated protein [Arabidopsis thaliana]
9473	GM_148_B1_D03_MR	g3777527	BLASTX	335	4e-28	45	(AF053008) gag-pol polyprotein [Glycine max]
9474	GM_148_B1_D04_MR	g3645899	BLASTX	234	1e-17	45	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9475	GM_148_B1_D10_MR	g3097320	BLASTN	1016	6e-39	80	Glycine max gene for Bd 30K, complete cds
9476	GM_148_B1_D10_T7	g4050011	BLASTN	499	1e-15	67	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
9477	GM_148_B1_D12_MR	g1769897	BLASTX	127	1e-17	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9478	GM_148_B1_E01_MR	g2828293	BLASTX	201	4e-14	49	(AL021687) putative protein [Arabidopsis thaliana]
9479	GM_148_B1_E03_T7	g3777527	BLASTX	702	3e-67	97	(AF053008) gag-pol polyprotein [Glycine max]
9480	GM_148_B1_E04_T7	g100484	BLASTX	321	3e-27	50	hypothetical protein - garden snapdragon
9481	GM_148_B1_E06_MR	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
9482	GM_148_B1_E06_T7	g507910	BLASTN	407	9e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9483	GM_148_B1_E07_MR	g130582	BLASTX	468	2e-42	57	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
9484	GM_148_B1_E12_T7	g2522230	BLASTX	189	1e-17	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
9485	GM_148_B1_F03_T7	g1769898	BLASTX	146	3e-17	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9486	GM_148_B1_F06_MR	g342964	BLASTN	383	3e-11	61	paramecium species 5,311 mt dna dimer: replication init. region.
9487	GM_148_B1_F06_T7	g1144553	BLASTN	365	2e-10	65	Anopheles melas 12S ribosomal RNA, D-loop, and tRNA-Ile mitochondrial genes, partial sequence.
9488	GM_148_B1_F07_MR	g4160362	BLASTN	349	1e-08	61	Saccharomyces cerevisiae complete mitochondrial genome
9489	GM_148_B1_F07_T7	g3097320	BLASTN	1168	7e-46	80	Glycine max gene for Bd 30K, complete cds
9490	GM_148_B1_F08_T7	g507910	BLASTN	419	3e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
9491	GM_148_B1_F09_MR	g4063756	BLASTN	438	9e-13	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9492	GM_148_B1_F09_T7	g507910	BLASTN	719	7e-26	88	Glycine max BSR-101 satellite SB92 genomic sequence.
9493	GM_148_B1_F10_MR	g1142702	BLASTN	362	7e-10	74	Glycine max satellite STR120-A.4.
9494	GM_148_B1_F12_T7	g2995405	BLASTX	312	5e-26	61	(Y12432) polyprotein [Ananas comosus]
9495	GM_148_B1_G02_T7	g2522227	BLASTX	237	1e-21	41	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
9496	GM_148_B1_G03_T7	g3763998	BLASTN	449	3e-13	60	Plasmodium falciparum MAL3P4, complete sequence [Plasmodium falciparum]
9497	GM_148_B1_G04_MR	g99922	BLASTX	315	2e-27	57	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9498	GM_148_B1_G05_T7	g2656029	BLASTN	429	2e-12	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQB2
9499	GM_148_B1_G07_MR	g18559	BLASTN	1143	8e-45	74	G.max gene for catalase
9500	GM_148_B1_G07_T7	g4063770	BLASTX	159	2e-23	48	(AB004906) transposase [Ipomoea purpurea]
9501	GM_148_B1_G09_MR	g507910	BLASTN	527	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
9502	GM_148_B1_G12_MR	g4063756	BLASTN	474	2e-14	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9503	GM_148_B1_G12_T7	g507910	BLASTN	579	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9504	GM_148_B1_H01_MR	g3777527	BLASTX	569	5e-53	87	(AF053008) gag-pol polyprotein [Glycine max]
9505	GM_148_B1_H03_T7	g1173624	BLASTX	477	1e-44	75	(U34744) cytochrome P-450 [Phalaenopsis sp. 'hybrid SM9108']
9506	GM_148_B1_H06_T7	g100484	BLASTX	401	7e-36	56	hypothetical protein - garden snapdragon
9507	GM_148_B1_H11_MR	g905361	BLASTX	200	3e-14	32	(U22103) gag-protease polyprotein [Glycine max]
9508	GM_148_B2_A02_MR	g130582	BLASTX	394	2e-34	60	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
9509	GM_148_B2_A05_MR	g3777527	BLASTX	687	1e-65	95	(AF053008) gag-pol polyprotein [Glycine max]
9510	GM_148_B2_A07_MR	g1167523	BLASTX	195	3e-13	47	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
9511	GM_148_B2_A08_MR	g507910	BLASTN	434	5e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9512	GM_148_B2_B06_MR	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9513	GM_148_B2_B11_MR	g507910	BLASTN	579	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9514	GM_148_B2_C03_MR	g3142328	BLASTN	460	8e-14	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9515	GM_148_B2_C11_MR	g3097320	BLASTN	846	3e-31	80	Glycine max gene for Bd 30K, complete cds
9516	GM_148_B2_D06_MR	g100484	BLASTX	220	1e-18	51	hypothetical protein - garden snapdragon
9517	GM_148_B2_E03_MR	g3777527	BLASTX	683	3e-65	94	(AF053008) gag-pol polyprotein [Glycine max]
9518	GM_148_B2_E06_MR	g4063756	BLASTN	495	2e-15	69	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9519	GM_148_B2_E10_MR	g100484	BLASTX	261	1e-20	46	hypothetical protein - garden snapdragon
9520	GM_148_B2_F02_MR	g2443320	BLASTX	228	9e-17	46	(D85597) polyprotein [Oryza australiensis]
9521	GM_148_B2_F10_MR	g3776013	BLASTX	298	1e-25	70	(AJ010470) RNA helicase [Arabidopsis thaliana]
9522	GM_148_B2_G03_MR	g2828293	BLASTX	172	6e-11	66	(AL021687) putative protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9523	GM_148_B2_G04_MR	g2769655	BLASTN	476	2e-14	65	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
9524	GM_149_A1_A01_MR	g3645899	BLASTX	142	6e-22	57	(U68408) 5' end not determined experimentally [Zea mays]
9525	GM_149_A1_A05_T7	g130582	BLASTX	393	2e-34	68	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
9526	GM_149_A1_A09_T7	g3869075	BLASTN	406	3e-11	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]
9527	GM_149_A1_B03_T7	g3021268	BLASTX	134	4e-15	50	(AL022347) putative protein [Arabidopsis thaliana]
9528	GM_149_A1_B04_MR	g4063760	BLASTX	191	7e-13	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9529	GM_149_A1_B06_T7	g3142379	BLASTX	262	2e-21	80	(AF053008) envelope-like [Glycine max]
9530	GM_149_A1_B11_MR	g3599418	BLASTN	441	6e-13	78	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
9531	GM_149_A1_B11_T7	g2522227	BLASTX	157	2e-10	39	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
9532	GM_149_A1_C03_MR	g100484	BLASTX	352	1e-30	52	hypothetical protein - garden snapdragon
9533	GM_149_A1_C05_MR	g18559	BLASTN	757	2e-44	75	G.max gene for catalase
9534	GM_149_A1_C09_MR	g2880051	BLASTX	161	3e-22	78	(AC002340) putative protein kinase [Arabidopsis thaliana]
9535	GM_149_A1_C09_T7	g2462058	BLASTX	298	1e-25	56	(Y13389) reverse transcriptase [Antirrhinum majus]
9536	GM_149_A1_D02_MR	g3695395	BLASTX	151	5e-12	42	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
9537	GM_149_A1_D04_MR	g3930515	BLASTX	115	7e-12	46	(AF059674) putative gag protein [Nicotiana tabacum]
9538	GM_149_A1_D12_MR	g3142328	BLASTN	836	7e-31	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9539	GM_149_A1_E12_MR	g3810596	BLASTX	142	2e-11	52	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
9540	GM_149_A1_F02_T7	g507910	BLASTN	541	8e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
9541	GM_149_A1_F07_MR	g3695395	BLASTX	200	3e-14	38	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
9542	GM_149_A1_F09_T7	g896244	BLASTX	206	6e-16	39	(S75260) pol [Drosophila buzzatii, BU-24, Peptide Transposon, 263 aa] [Drosophila buzzatii]
9543	GM_149_A1_G01_T7	g3785980	BLASTX	151	5e-09	35	(AC005560) hypothetical protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9544	GM_149_A1_G03_MR	g507910	BLASTN	371	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
9545	GM_149_A1_G03_T7	g3142328	BLASTN	764	1e-27	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9546	GM_149_A1_G09_T7	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9547	GM_149_A1_G10_T7	g639722	BLASTX	292	9e-25	81	(L27484) calcium-dependent protein kinase [Zea mays]
9548	GM_149_A1_G12_T7	g2244915	BLASTX	169	1e-10	37	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
9549	GM_149_A1_H02_MR	g3377856	BLASTX	164	4e-15	43	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 19.54) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 12.35) [Arabidopsis thaliana]
9550	GM_149_A1_H03_MR	g2522230	BLASTX	226	5e-18	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
9551	GM_149_A2_A01_MR	g3426334	BLASTN	355	5e-09	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
9552	GM_149_A2_A02_T7	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9553	GM_149_A2_A03_MR	g3377834	BLASTX	219	3e-16	35	(AF075598) No definition line found [Arabidopsis thaliana]
9554	GM_149_A2_A03_T7	g3004564	BLASTX	198	1e-14	87	(AC003673) putative receptor Ser/Thr protein kinase [Arabidopsis thaliana]
9555	GM_149_A2_A04_T7	g550118	BLASTN	335	5e-09	63	L.tarentolae mRNA encoding putative NADH subunit (G rich region 4)
9556	GM_149_A2_A11_T7	g2262177	BLASTX	102	2e-11	51	(AC002329) hypothetical protein similar to T18A10.3 [Arabidopsis thaliana]
9557	GM_149_A2_B03_MR	g1167523	BLASTX	475	4e-43	68	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
9558	GM_149_A2_B05_MR	g3820757	BLASTN	380	2e-10	61	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
9559	GM_149_A2_B06_MR	g3834322	BLASTX	146	5e-09	46	(AC005679) EST gb R30300 comes from this gene. [Arabidopsis thaliana]
9560	GM_149_A2_B08_MR	g3786414	BLASTN	473	2e-14	64	Caenorhabditis elegans cosmid H28G03
9561	GM_149_A2_B11_MR	g3142379	BLASTX	282	9e-24	84	(AF053008) envelope-like [Glycine max]
9562	GM_149_A2_C01_MR	g505129	BLASTN	353	2e-11	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9563	GM_149_A2_C02_MR	g4038056	BLASTX	237	5e-18	50	(AC005897) putative transposon [Arabidopsis thaliana]
9564	GM_149_A2_C02_T7	g2104945	BLASTN	626	2e-21	66	Glycine max copia-like retrotransposon Tgmr, complete sequence
9565	GM_149_A2_C04_MR	g18559	BLASTN	351	7e-09	71	G.max gene for catalase
9566	GM_149_A2_C07_T7	g3142328	BLASTN	810	1e-29	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9567	GM_149_A2_C08_MR	g2244859	BLASTX	137	2e-17	41	(Z97337) hypothetical protein [Arabidopsis thaliana]
9568	GM_149_A2_C08_T7	g3785980	BLASTX	149	5e-14	44	(AC005560) hypothetical protein [Arabidopsis thaliana]
9569	GM_149_A2_C09_MR	g3845310	BLASTN	353	6e-09	61	Plasmodium falciparum chromosome 2, section 62 of 73 of the complete sequence
9570	GM_149_A2_D03_MR	g414665	BLASTN	391	1e-10	66	G.max gene for coproporphyrinogen oxidase
9571	GM_149_A2_D04_MR	g12212	BLASTN	998	2e-43	91	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
9572	GM_149_A2_D07_MR	g3645899	BLASTX	291	1e-24	51	(U68408) 5' end not determined experimentally [Zea mays]
9573	GM_149_A2_D08_T7	g4063756	BLASTN	383	3e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9574	GM_149_A2_D10_MR	g2462134	BLASTX	252	4e-20	33	(Y13368) reverse transcriptase [Beta vulgaris]
9575	GM_149_A2_D11_T7	g3097320	BLASTN	741	2e-26	77	Glycine max gene for Bd 30K, complete cds
9576	GM_149_A2_E01_T7	g3097320	BLASTN	777	4e-28	77	Glycine max gene for Bd 30K, complete cds
9577	GM_149_A2_E02_T7	g2522230	BLASTX	241	1e-19	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
9578	GM_149_A2_E03_MR	g100484	BLASTX	321	3e-27	49	hypothetical protein - garden snapdragon
9579	GM_149_A2_E04_MR	g4063760	BLASTX	268	4e-21	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9580	GM_149_A2_E06_MR	g3777526	BLASTN	502	1e-15	73	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
9581	GM_149_A2_E07_MR	g2522227	BLASTX	200	3e-15	52	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
9582	GM_149_A2_E11_MR	g2335061	BLASTN	503	1e-15	65	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence [Homo sapiens]
9583	GM_149_A2_E11_T7	g2121303	BLASTN	356	5e-09	66	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
9584	GM_149_A2_F02_MR	g2326363	BLASTX	171	2e-23	82	(AJ001037) DNA-directed RNA polymerase [Arabidopsis thaliana]
9585	GM_149_A2_F03_T7	g3080423	BLASTX	312	6e-26	51	(AL022604) putative protein [Arabidopsis thaliana]
9586	GM_149_A2_F06_T7	g3142379	BLASTX	298	1e-25	67	(AF053008) envelope-like [Glycine max]
9587	GM_149_A2_F12_MR	g2443320	BLASTX	463	7e-42	59	(D85597) polyprotein [Oryza australiensis]
9588	GM_149_A2_G01_MR	g396249	BLASTN	399	3e-11	63	S.douglasii mitochondrial ATP subunit 9 gene, complete CDS

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9589	GM_149_A2_G01_T7	g130582	BLASTX	326	3e-27	49	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
9590	GM_149_A2_G02_MR	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
9591	GM_149_A2_G05_MR	g18559	BLASTN	948	6e-36	75	G.max gene for catalase
9592	GM_149_A2_G05_T7	g905361	BLASTX	636	2e-61	98	(U22103) gag-protease polyprotein [Glycine max]
9593	GM_149_A2_G06_T7	g3645899	BLASTX	312	6e-26	51	(U68408) 5' end not determined experimentally [Zea mays]
9594	GM_149_A2_G07_MR	g2444271	BLASTX	206	4e-15	66	(AF019637) putative amino acid or GABA permease [Arabidopsis thaliana]
9595	GM_149_A2_G08_MR	g3242708	BLASTX	235	6e-18	52	(AC003040) putative serine/threonine protein kinase [Arabidopsis thaliana]
9596	GM_149_A2_G09_T7	g18559	BLASTN	699	1e-24	72	G.max gene for catalase
9597	GM_149_A2_G11_MR	g3810596	BLASTX	285	4e-23	41	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
9598	GM_149_A2_G12_T7	g3702964	BLASTX	117	9e-10	95	(AF079485) rac GTP binding protein Arac10 [Arabidopsis thaliana]
9599	GM_149_A2_H05_T7	g3097320	BLASTN	597	5e-20	85	Glycine max gene for Bd 30K, complete cds
9600	GM_149_A2_H09_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
9601	GM_149_A2_H10_T7	g3135263	BLASTX	152	1e-09	80	(AC003058) hypothetical protein [Arabidopsis thaliana]
9602	GM_149_A2_H11_T7	g3097320	BLASTN	896	2e-33	77	Glycine max gene for Bd 30K, complete cds
9603	GM_149_B1_A02_MR	g1335695	BLASTX	257	2e-21	45	(X02600) unidentified open reading frame II (146 aa) [Drosophila melanogaster]
9604	GM_149_B1_A04_MR	g3171159	BLASTN	615	1e-20	66	Homo sapiens chromosome 21q22.3 PAC 21L13, complete sequence [Homo sapiens]
9605	GM_149_B1_A08_MR	g2801682	BLASTN	676	5e-24	81	Glycine max telomere-associated sequence STAS11
9606	GM_149_B1_A09_MR	g3600062	BLASTN	398	6e-11	68	Arabidopsis thaliana BAC T25C13
9607	GM_149_B1_B02_MR	g3645899	BLASTX	455	3e-41	61	(U68408) 5' end not determined experimentally [Zea mays]
9608	GM_149_B1_B08_MR	g1666236	BLASTX	149	2e-11	31	(U76261) unknown [Hordeum vulgare]
9609	GM_149_B1_C06_MR	g1944188	BLASTN	388	9e-11	72	Soybean DNA for nodulin 35, partial cds
9610	GM_149_B1_C11_MR	g2160165	BLASTX	246	6e-19	45	(AC000132) F21M12.11 gene product [Arabidopsis thaliana]
9611	GM_149_B1_E06_MR	g3695401	BLASTX	170	1e-11	43	(AF096373) No definition line found [Arabidopsis thaliana]
9612	GM_149_B1_E09_MR	g18559	BLASTN	968	7e-37	73	G.max gene for catalase
9613	GM_149_B1_E10_MR	g3142303	BLASTX	498	1e-45	68	(AC002411) Strong similarity to MRP-like ABC transporter gb U92650 from A. thaliana and canalicular multi-drug resistance protein gb L49379 from Rattus norvegicus. [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9614	GM_149_B1_E11_MR	g1769898	BLASTX	388	9e-35	71	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9615	GM_149_B1_E12_MR	g1769898	BLASTX	425	5e-39	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9616	GM_149_B1_F02_MR	g507910	BLASTN	553	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9617	GM_149_B1_F03_MR	g1769898	BLASTX	408	5e-37	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9618	GM_149_B1_F12_MR	g3845197	BLASTN	445	4e-13	64	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
9619	GM_149_B1_G02_MR	g18559	BLASTN	406	2e-11	72	G.max gene for catalase
9620	GM_149_B1_G03_MR	g2129618	BLASTX	254	8e-20	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9621	GM_149_B1_G05_MR	g3777527	BLASTX	156	1e-14	44	(AF053008) gag-pol polyprotein [Glycine max]
9622	GM_149_B1_H02_MR	g280492	BLASTX	199	7e-14	44	pol polyprotein homolog - fungus (Cladosporium fulvum) transposon CfT-1 (fragment) gi 2564 (Z11866) Reverse Transcriptase [Cladosporium fulvum]
9623	GM_149_B1_H03_MR	g2055374	BLASTX	136	1e-19	60	(U29095) serine-threonine protein kinase [Triticum aestivum]
9624	GM_149_B1_H09_MR	g3687234	BLASTX	172	6e-11	47	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
9625	GM_153_A2_A05_MR	g507910	BLASTN	377	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
9626	GM_153_A2_A05_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9627	GM_153_A2_A06_T7	g507910	BLASTN	579	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9628	GM_153_A2_A08_T7	g1769898	BLASTX	313	2e-26	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9629	GM_153_A2_A11_MR	g4140712	BLASTX	148	8e-10	52	(AF110183) putative integrase [Oryza sativa]
9630	GM_153_A2_A12_MR	g2921625	BLASTN	498	2e-15	75	Lupinus luteus leghemoglobin (LbI) gene, complete cds
9631	GM_153_A2_B01_MR	g3645899	BLASTX	253	3e-24	63	(U68408) 5' end not determined experimentally [Zea mays]
9632	GM_153_A2_B03_T7	g3645899	BLASTX	174	1e-15	37	(U68408) 5' end not determined experimentally [Zea mays]
9633	GM_153_A2_B04_MR	g3142328	BLASTN	1791	2e-74	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9634	GM_153_A2_B04_T7	g3097320	BLASTN	437	9e-13	67	Glycine max gene for Bd 30K, complete cds
9635	GM_153_A2_B06_T7	g2982550	BLASTN	370	1e-09	63	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-65, complete sequence [Plasmodium falciparum]
9636	GM_153_A2_B10_T7	g3097320	BLASTN	1170	6e-46	81	Glycine max gene for Bd 30K, complete cds
9637	GM_153_A2_C01_MR	g3142328	BLASTN	1847	5e-77	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9638	GM_153_A2_C04_MR	g18737	BLASTN	411	1e-11	73	Glycine max RPRP3 gene for repetitive proline-rich protein 3
9639	GM_153_A2_D02_MR	g3142328	BLASTN	1029	1e-39	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9640	GM_153_A2_D03_MR	g2656024	BLASTN	360	3e-09	63	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6
9641	GM_153_A2_D03_T7	g3777527	BLASTX	152	3e-18	57	(AF053008) gag-pol polyprotein [Glycine max]
9642	GM_153_A2_D05_MR	g4063760	BLASTX	208	1e-14	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9643	GM_153_A2_E02_MR	g2492782	BLASTX	102	2e-09	78	ALPHA-GALACTOSIDASE PRECURSOR (MELIBIASE) (ALPHA-D-GALACTOSIDE GALACTOHYDROLASE) gi 504489 (L27992) alpha-galactosidase [Coffea arabica]
9644	GM_153_A2_E03_MR	g2654095	BLASTX	106	5e-09	80	(AF034210) aspartate aminotransferase cytosolic isozyme AAT2 [Glycine max]
9645	GM_153_A2_E05_T7	g1480927	BLASTN	721	7e-26	82	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
9646	GM_153_A2_E07_T7	g3645899	BLASTX	292	9e-24	53	(U68408) 5' end not determined experimentally [Zea mays]
9647	GM_153_A2_E10_MR	g3097320	BLASTN	560	3e-18	70	Glycine max gene for Bd 30K, complete cds
9648	GM_153_A2_F01_T7	g2522226	BLASTN	507	5e-16	64	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
9649	GM_153_A2_F04_T7	g166884	BLASTN	466	8e-15	77	A.thaliana telomeric DNA. >gi 589934 gb I07744 Sequence 1 from Patent EP 0338266
9650	GM_153_A2_F05_MR	g1769898	BLASTX	331	2e-28	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9651	GM_153_A2_F05_T7	g1167523	BLASTX	308	3e-25	48	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
9652	GM_153_A2_F06_T7	g2245104	BLASTX	311	1e-25	47	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
9653	GM_153_A2_F07_T7	g2129618	BLASTX	180	7e-12	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9654	GM_153_A2_F12_T7	g507910	BLASTN	385	9e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
9655	GM_153_A2_G05_MR	g2522228	BLASTX	362	8e-42	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
9656	GM_153_A2_G08_T7	g3645899	BLASTX	170	9e-11	42	(U68408) 5' end not determined experimentally [Zea mays]
9657	GM_153_A2_G12_T7	g1040717	BLASTN	498	2e-16	65	D.polychroa microsatellite sequence (clone Dp ch1 F3)
9658	GM_153_B1_A06_T7	g2129618	BLASTX	180	7e-12	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9659	GM_153_B1_A08_MR	g3097320	BLASTN	416	8e-12	72	Glycine max gene for Bd 30K, complete cds
9660	GM_153_B1_A08_T7	g3894099	BLASTX	187	7e-24	90	(AJ012750) MCM3 protein [Pisum sativum]
9661	GM_153_B1_B02_MR	g3777527	BLASTX	571	3e-53	94	(AF053008) gag-pol polyprotein [Glycine max]
9662	GM_153_B1_B02_T7	g507910	BLASTN	386	8e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9663	GM_153_B1_B04_MR	g4038056	BLASTX	378	4e-33	50	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9664	GM_153_B1_B05_MR	g3193290	BLASTX	208	2e-16	55	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabido...
9665	GM_153_B1_C01_T7	g3097320	BLASTN	393	9e-11	68	Glycine max gene for Bd 30K, complete cds
9666	GM_153_B1_C04_MR	g3645899	BLASTX	251	2e-22	52	(U68408) 5' end not determined experimentally [Zea mays]
9667	GM_153_B1_C06_MR	g1550814	BLASTX	163	7e-13	96	(Y07959) 60S acidic ribosomal protein P0 [Zea mays]
9668	GM_153_B1_C09_MR	g4063760	BLASTX	184	3e-13	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9669	GM_153_B1_D01_T7	g2129618	BLASTX	257	4e-20	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9670	GM_153_B1_D04_MR	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
9671	GM_153_B1_D04_T7	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
9672	GM_153_B1_D09_T7	g1707938	BLASTX	202	4e-30	95	GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE SMALL SUBUNIT (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE B) (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) gi 312721 (X73365) glucose-1-phosphate adenylyltransferase [Arabidopsis thaliana]
9673	GM_153_B1_D11_T7	g18559	BLASTN	618	6e-21	75	G.max gene for catalase
9674	GM_153_B1_E04_MR	g99730	BLASTX	148	7e-09	44	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
9675	GM_153_B1_E06_T7	g2980795	BLASTX	94	5e-10	78	(AL022197) putative protein [Arabidopsis thaliana]
9676	GM_153_B1_E07_T7	g3097320	BLASTN	471	3e-14	76	Glycine max gene for Bd 30K, complete cds
9677	GM_153_B1_E09_MR	g18559	BLASTN	795	5e-29	72	G.max gene for catalase
9678	GM_153_B1_E11_MR	g541825	BLASTX	136	4e-18	86	protein kinase - spinach gi 457711 (Z30332) protein kinase [Spinacia oleracea]
9679	GM_153_B1_F01_T7	g507910	BLASTN	444	2e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
9680	GM_153_B1_F10_MR	g100484	BLASTX	336	8e-29	58	hypothetical protein - garden snapdragon
9681	GM_153_B1_G06_T7	g2522230	BLASTX	263	6e-22	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
9682	GM_153_B1_G12_T7	g2443320	BLASTX	342	6e-29	57	(D85597) polyprotein [Oryza australiensis]
9683	GM_153_B1_H02_T7	g2443320	BLASTX	301	1e-24	50	(D85597) polyprotein [Oryza australiensis]
9684	GM_153_B1_H03_T7	g507910	BLASTN	593	3e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9685	GM_153_B1_H09_MR	g2982540	BLASTN	375	7e-10	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-30, complete sequence [Plasmodium falciparum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9686	GM_153_B1_H11_T7	g1370140	BLASTX	215	6e-17	67	(X98308) myb-related transcription factor [Lycopersicon esculentum]
9687	GM_153_B1_H12_T7	g100484	BLASTX	341	2e-29	56	hypothetical protein - garden snapdragon
9688	GM_153_B2_A01_T7	g3738114	BLASTN	377	5e-10	60	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
9689	GM_153_B2_A02_T7	g3386534	BLASTX	498	6e-62	59	(AF078934) mariner transposase [Glycine max]
9690	GM_153_B2_A03_MR	g1769897	BLASTX	373	1e-33	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9691	GM_153_B2_A03_T7	g2522227	BLASTX	205	7e-16	47	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
9692	GM_153_B2_A04_MR	g4063756	BLASTN	630	2e-21	67	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9693	GM_153_B2_A05_T7	g3367515	BLASTX	299	8e-26	78	(AC004392) Similar to glucose-6-phosphate/phosphate-translocator (GPT) gb AF020814 from Pisum sativum. [Arabidopsis thaliana]
9694	GM_153_B2_A06_T7	g2443320	BLASTX	317	1e-37	48	(D85597) polyprotein [Oryza australiensis]
9695	GM_153_B2_A07_MR	g2522227	BLASTX	192	2e-14	42	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
9696	GM_153_B2_A08_MR	g18559	BLASTN	394	8e-11	71	G.max gene for catalase
9697	GM_153_B2_A09_T7	g3142379	BLASTX	268	4e-22	48	(AF053008) envelope-like [Glycine max]
9698	GM_153_B2_B01_MR	g2316016	BLASTX	550	5e-51	60	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
9699	GM_153_B2_B03_MR	g3845197	BLASTN	544	2e-17	63	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
9700	GM_153_B2_B11_T7	g3097320	BLASTN	376	5e-10	74	Glycine max gene for Bd 30K, complete cds
9701	GM_153_B2_C01_T7	g3599418	BLASTN	533	4e-17	67	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
9702	GM_153_B2_C04_MR	g1769899	BLASTX	248	2e-20	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9703	GM_153_B2_C06_MR	g3281870	BLASTX	297	3e-25	59	(AL031004) putative protein [Arabidopsis thaliana]
9704	GM_153_B2_C08_MR	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
9705	GM_153_B2_C08_T7	g507910	BLASTN	396	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9706	GM_153_B2_C09_MR	g1769899	BLASTX	333	2e-29	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9707	GM_153_B2_C09_T7	g4063760	BLASTX	186	4e-19	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9708	GM_153_B2_C10_T7	g3273127	BLASTN	385	2e-10	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-54, complete sequence [Plasmodium falciparum]
9709	GM_153_B2_C12_MR	g3097320	BLASTN	645	4e-22	81	Glycine max gene for Bd 30K, complete cds
9710	GM_153_B2_D01_T7	g99922	BLASTX	876	6e-87	87	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
9711	GM_153_B2_D03_MR	g4063760	BLASTX	158	2e-09	31	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9712	GM_153_B2_D03_T7	g2791289	BLASTX	254	1e-19	35	(AJ000387) protease [Drosophila melanogaster]
9713	GM_153_B2_D04_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9714	GM_153_B2_D05_MR	g3283026	BLASTX	260	1e-20	38	putative transposase [Arabidopsis thaliana]
9715	GM_153_B2_D07_T7	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9716	GM_153_B2_E02_T7	g3201682	BLASTX	451	2e-44	64	(AF060942) extra-large G-protein [Arabidopsis thaliana]
9717	GM_153_B2_E05_MR	g1666236	BLASTX	209	4e-16	32	(U76261) unknown [Hordeum vulgare]
9718	GM_153_B2_E05_T7	g3142328	BLASTN	2544	1e-109	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9719	GM_153_B2_E11_MR	g2522228	BLASTX	655	2e-63	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
9720	GM_153_B2_E12_MR	g3892045	BLASTX	123	2e-09	80	(AC002330) putative zinc finger protein [Arabidopsis thaliana]
9721	GM_153_B2_F01_MR	g2522228	BLASTX	224	2e-17	64	(AB007466) reverse transcriptase-like protein [Vicia faba]
9722	GM_153_B2_F02_T7	g507910	BLASTN	570	4e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9723	GM_153_B2_F06_T7	g507910	BLASTN	419	3e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
9724	GM_153_B2_F07_MR	g99721	BLASTX	153	1e-21	45	retrovirus-related polyprotein - Arabidopsis thaliana retrotransposon Ta1-3 gi 16534 (X13291) polyprotein [Arabidopsis thaliana]
9725	GM_153_B2_F08_MR	g2072628	BLASTX	126	1e-14	65	(Y12641) superoxide dismutase [Arabidopsis thaliana]
9726	GM_153_B2_F09_T7	g1480927	BLASTN	352	5e-09	85	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
9727	GM_153_B2_F11_MR	g3152600	BLASTX	320	5e-28	59	(AC002986) Contains similarity to S. cerevisiae hypothetical protein YOR197w, gb Z75105. ESTs gb H37409, gb AA395290, and gb T43907 come from this gene. [Arabidopsis thaliana]
9728	GM_153_B2_F11_T7	g4038056	BLASTX	208	9e-27	47	(AC005897) putative transposon [Arabidopsis thaliana]
9729	GM_153_B2_F12_T7	g100484	BLASTX	377	3e-33	62	hypothetical protein - garden snapdragon
9730	GM_153_B2_G02_MR	g3142328	BLASTN	1516	7e-62	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9731	GM_153_B2_G03_MR	g3810596	BLASTX	299	1e-24	43	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
9732	GM_153_B2_G03_T7	g3097320	BLASTN	437	9e-13	70	Glycine max gene for Bd 30K, complete cds
9733	GM_153_B2_G05_MR	g505129	BLASTN	378	4e-10	60	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9734	GM_153_B2_G07_MR	g3142328	BLASTN	2124	8e-90	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9735	GM_153_B2_G09_T7	g3135962	BLASTN	353	7e-09	59	Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence [Homo sapiens]
9736	GM_153_B2_G10_T7	g4038057	BLASTX	174	2e-11	36	(AC005897) hypothetical protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9737	GM_153_B2_G11_MR	g3142328	BLASTN	608	1e-20	68	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9738	GM_153_B2_G12_MR	g13774	BLASTN	302	3e-10	61	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
9739	GM_153_B2_G12_T7	g3283026	BLASTX	207	6e-15	41	putative transposase [Arabidopsis thaliana]
9740	GM_153_B2_H02_T7	g3097320	BLASTN	1010	1e-38	81	Glycine max gene for Bd 30K, complete cds
9741	GM_153_B2_H06_T7	g3097320	BLASTN	490	4e-15	71	Glycine max gene for Bd 30K, complete cds
9742	GM_153_B2_H11_T7	g3777527	BLASTX	842	3e-82	94	(AF053008) gag-pol polyprotein [Glycine max]
9743	GM_153_B2_H12_MR	g4038056	BLASTX	303	4e-27	46	(AC005897) putative transposon [Arabidopsis thaliana]
9744	GM_154_A1_A02_MR	g3914006	BLASTX	146	3e-15	70	MITOCHONDRIAL LON PROTEASE HOMOLOG 2 PRECURSOR >gi 1816588 (U85495) LON2 [Zea mays]
9745	GM_154_A1_A02_T7	g4049647	BLASTN	386	2e-10	62	Melanoplus sanguinipes entomopoxvirus, complete genome
9746	GM_154_A1_A05_T7	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9747	GM_154_A1_A09_T7	g13619	BLASTN	339	6e-09	63	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
9748	GM_154_A1_A12_T7	g3319372	BLASTX	189	1e-12	37	(AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]
9749	GM_154_A1_B03_MR	g507910	BLASTN	621	2e-21	86	Glycine max BSR-101 satellite SB92 genomic sequence.
9750	GM_154_A1_B03_T7	g507910	BLASTN	559	1e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9751	GM_154_A1_B04_T7	g100484	BLASTX	359	3e-31	61	hypothetical protein - garden snapdragon
9752	GM_154_A1_B10_T7	g3097320	BLASTN	480	1e-14	71	Glycine max gene for Bd 30K, complete cds
9753	GM_154_A1_B12_T7	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9754	GM_154_A1_C01_MR	g3777527	BLASTX	576	2e-54	96	(AF053008) gag-pol polyprotein [Glycine max]
9755	GM_154_A1_C01_T7	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
9756	GM_154_A1_C03_T7	g507910	BLASTN	520	7e-17	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9757	GM_154_A1_C05_MR	g18559	BLASTN	1055	8e-41	77	G.max gene for catalase
9758	GM_154_A1_C08_MR	g905361	BLASTX	428	3e-39	95	(U22103) gag-protease polyprotein [Glycine max]
9759	GM_154_A1_C10_T7	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9760	GM_154_A1_C11_MR	g100484	BLASTX	196	2e-18	57	hypothetical protein - garden snapdragon
9761	GM_154_A1_D06_T7	g2522228	BLASTX	274	1e-28	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
9762	GM_154_A1_D09_MR	g3426334	BLASTN	398	5e-11	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
9763	GM_154_A1_D11_T7	g3660471	BLASTX	213	1e-15	88	(AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9764	GM_154_A1_E07_T7	g505129	BLASTN	364	2e-09	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9765	GM_154_A1_E09_T7	g1778843	BLASTN	424	3e-12	66	Dictyostelium discoideum LimA (limA) mRNA, partial cds
9766	GM_154_A1_E11_MR	g18559	BLASTN	767	9e-28	78	G.max gene for catalase
9767	GM_154_A1_E11_T7	g2497540	BLASTX	194	1e-19	57	PYRUVATE KINASE, CHLOROPLAST ISOZYME G
9768	GM_154_A1_F02_T7	g3097320	BLASTN	514	3e-16	79	Glycine max gene for Bd 30K, complete cds
9769	GM_154_A1_F05_T7	g2244960	BLASTX	337	8e-30	44	(Z97340) similarity to copia-like retrotransposon [Arabidopsis thaliana]
9770	GM_154_A1_F07_T7	g3097320	BLASTN	614	9e-21	80	Glycine max gene for Bd 30K, complete cds
9771	GM_154_A1_F09_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9772	GM_154_A1_F09_T7	g507910	BLASTN	388	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9773	GM_154_A1_F12_T7	g170080	BLASTN	655	1e-22	90	Soybean seed lectin gene transposable element tgm1.
9774	GM_154_A1_G01_MR	g2414681	BLASTX	156	9e-10	90	(Z99174) cysteine proteinase precursor [Vicia narbonensis]
9775	GM_154_A1_G02_T7	g3777527	BLASTX	630	1e-61	96	(AF053008) gag-pol polyprotein [Glycine max]
9776	GM_154_A1_G04_MR	g2129618	BLASTX	153	5e-09	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9777	GM_154_A1_G06_MR	g3694834	BLASTN	448	3e-13	69	Glycine max alcohol dehydrogenase Adh-1 gene, partial cds
9778	GM_154_A1_G07_T7	g1488267	BLASTX	151	2e-21	66	(U57412) low affinity calcium antiporter CAX2 [Arabidopsis thaliana]
9779	GM_154_A1_G09_MR	g2688828	BLASTX	151	1e-09	72	(U97530) ethylene-forming-enzyme-like dioxygenase [Prunus armeniaca]
9780	GM_154_A1_G12_MR	g507910	BLASTN	509	2e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
9781	GM_154_A1_G12_T7	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9782	GM_154_A1_H02_T7	g3461846	BLASTX	381	4e-33	55	(AC005315) putative zinc-finger protein [Arabidopsis thaliana]
9783	GM_154_A1_H04_T7	g507910	BLASTN	594	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9784	GM_154_A1_H05_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9785	GM_154_A1_H08_MR	g3142328	BLASTN	1120	8e-44	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9786	GM_154_A1_H09_MR	g2429543	BLASTX	200	7e-14	42	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]
9787	GM_154_A1_H10_T7	g2443320	BLASTX	156	4e-09	35	(D85597) polyprotein [Oryza australiensis]
9788	GM_154_A1_H12_T7	g1272349	BLASTX	188	3e-13	53	(U51740) secreted glycoprotein 3 [Ipomoea trifida]
9789	GM_154_B2_A02_MR	g3142379	BLASTX	258	5e-21	61	(AF053008) envelope-like [Glycine max]
9790	GM_154_B2_A04_MR	g4063760	BLASTX	358	2e-33	77	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9791	GM_154_B2_A06_MR	g2522228	BLASTX	151	2e-09	30	(AB007466) reverse transcriptase-like protein [Vicia faba]
9792	GM_154_B2_A09_MR	g1749831	BLASTX	153	4e-09	60	(Z56279) beta-xylo-glucosidase [Thermoanaerobacter brockii]
9793	GM_154_B2_A09_T7	g2656031	BLASTN	345	8e-10	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20
9794	GM_154_B2_B03_T7	g629693	BLASTX	155	8e-10	43	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
9795	GM_154_B2_B04_T7	g4160362	BLASTN	275	9e-16	68	Saccharomyces cerevisiae complete mitochondrial genome
9796	GM_154_B2_B06_MR	g3777527	BLASTX	562	3e-52	88	(AF053008) gag-pol polyprotein [Glycine max]
9797	GM_154_B2_B12_MR	g2522228	BLASTX	329	6e-29	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
9798	GM_154_B2_C04_MR	g3650039	BLASTX	200	3e-14	39	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
9799	GM_154_B2_C04_T7	g3874213	BLASTX	154	8e-11	37	(Z83217) Similarity to Drosophila White protein (SW:WHIT_DROME); cDNA EST EMBL:T01609 comes from this gene; cDNA EST EMBL:D67987 comes from this gene; cDNA EST EMBL:D34570 comes from this gene; cDNA EST EMBL:D32839 comes fro...
9800	GM_154_B2_C06_T7	g2995405	BLASTX	367	6e-32	56	(Y12432) polyprotein [Ananas comosus]
9801	GM_154_B2_D02_MR	g507910	BLASTN	584	9e-20	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9802	GM_154_B2_D04_T7	g3097320	BLASTN	437	9e-13	78	Glycine max gene for Bd 30K, complete cds
9803	GM_154_B2_D06_MR	g2995405	BLASTX	362	2e-31	48	(Y12432) polyprotein [Ananas comosus]
9804	GM_154_B2_D12_T7	g18559	BLASTN	719	1e-25	74	G.max gene for catalase
9805	GM_154_B2_E01_MR	g3097320	BLASTN	376	5e-10	74	Glycine max gene for Bd 30K, complete cds
9806	GM_154_B2_E02_T7	g3097320	BLASTN	416	8e-12	77	Glycine max gene for Bd 30K, complete cds
9807	GM_154_B2_E03_T7	g4063770	BLASTX	226	7e-17	39	(AB004906) transposase [Ipomoea purpurea]
9808	GM_154_B2_E04_MR	g4063760	BLASTX	253	2e-19	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9809	GM_154_B2_E07_MR	g18559	BLASTN	358	3e-09	63	G.max gene for catalase
9810	GM_154_B2_F01_MR	g1666236	BLASTX	186	2e-13	31	(U76261) unknown [Hordeum vulgare]
9811	GM_154_B2_F04_T7	g3645899	BLASTX	310	1e-25	51	(U68408) 5' end not determined experimentally [Zea mays]
9812	GM_154_B2_F10_MR	g18559	BLASTN	355	5e-09	65	G.max gene for catalase
9813	GM_154_B2_F12_MR	g4063760	BLASTX	211	4e-15	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9814	GM_154_B2_G01_T7	g1142701	BLASTN	433	1e-30	75	Glycine max satellite STR120-A.3.
9815	GM_154_B2_G07_T7	g3426334	BLASTN	541	2e-17	60	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
9816	GM_154_B2_G11_T7	g3142328	BLASTN	610	1e-20	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9817	GM_154_B2_H04_T7	g505129	BLASTN	381	3e-10	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9818	GM_154_B2_H05_T7	g18559	BLASTN	612	1e-20	69	G.max gene for catalase
9819	GM_154_B2_H06_T7	g3645899	BLASTX	418	3e-37	55	(U68408) 5' end not determined experimentally [Zea mays]
9820	GM_154_B2_H07_MR	g507910	BLASTN	344	6e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
9821	GM_154_B2_H09_T7	g1785744	BLASTX	143	9e-16	44	(Y08502) orf158 [Arabidopsis thaliana]
9822	GM_154_B2_H10_MR	g4063760	BLASTX	298	3e-24	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9823	GM_154_B2_H10_T7	g3319345	BLASTX	189	6e-15	36	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
9824	GM_154_B2_H11_T7	g3777526	BLASTN	414	1e-11	83	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
9825	GM_155_A1_A03_T7	g2129618	BLASTX	200	5e-14	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
9826	GM_155_A1_A05_MR	g3650035	BLASTX	221	4e-16	40	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
9827	GM_155_A1_A05_T7	g2443320	BLASTX	248	6e-19	40	(D85597) polyprotein [Oryza australiensis]
9828	GM_155_A1_A07_MR	g507910	BLASTN	590	5e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
9829	GM_155_A1_A07_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
9830	GM_155_A1_A08_T7	g3033389	BLASTX	157	2e-09	30	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
9831	GM_155_A1_A11_MR	g4006838	BLASTN	409	2e-11	65	Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence [Homo sapiens]
9832	GM_155_A1_B03_T7	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
9833	GM_155_A1_B09_MR	g1769898	BLASTX	152	2e-20	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9834	GM_155_A1_B11_MR	g1666236	BLASTX	182	6e-13	30	(U76261) unknown [Hordeum vulgare]
9835	GM_155_A1_B12_MR	g3777527	BLASTX	249	6e-19	47	(AF053008) gag-pol polyprotein [Glycine max]
9836	GM_155_A1_C01_T7	g3142328	BLASTN	1258	4e-50	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9837	GM_155_A1_C03_T7	g905361	BLASTX	203	1e-14	35	(U22103) gag-protease polyprotein [Glycine max]
9838	GM_155_A1_C06_MR	g507910	BLASTN	410	6e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9839	GM_155_A1_C06_T7	g507910	BLASTN	380	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
9840	GM_155_A1_D01_T7	g439231	BLASTN	357	7e-10	60	Human DNA-unwinding elements sequence
9841	GM_155_A1_D08_MR	g2961349	BLASTX	162	1e-18	39	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
9842	GM_155_A1_D08_T7	g4115365	BLASTX	227	1e-16	47	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
9843	GM_155_A1_D10_T7	g1226168	BLASTX	108	1e-10	32	(M32662) ORF B (bases 1850-5560) first start codon at 2306 [Autographa californica nucleopolyhedrovirus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9844	GM_155_A1_E01_MR	g3097320	BLASTN	476	2e-14	75	Glycine max gene for Bd 30K, complete cds
9845	GM_155_A1_E09_T7	g4063760	BLASTX	303	7e-25	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9846	GM_155_A1_F01_MR	g3746069	BLASTX	178	1e-16	29	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
9847	GM_155_A1_F03_MR	g18559	BLASTN	406	2e-11	69	G.max gene for catalase
9848	GM_155_A1_F04_MR	g1769898	BLASTX	400	4e-36	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9849	GM_155_A1_F07_MR	g3097320	BLASTN	464	6e-14	73	Glycine max gene for Bd 30K, complete cds
9850	GM_155_A1_F12_MR	g2262135	BLASTN	432	6e-13	74	Arabidopsis thaliana BAC T10P11, complete sequence [Arabidopsis thaliana]
9851	GM_155_A1_G04_T7	g1055224	BLASTX	152	3e-10	42	(U20977) cellular nucleic acid binding protein [Xenopus laevis]
9852	GM_155_A1_G05_T7	g3142328	BLASTN	842	4e-31	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9853	GM_155_A1_G07_MR	g18683	BLASTN	486	4e-15	86	G.max N-20t gene
9854	GM_155_A1_G09_MR	g2564044	BLASTN	355	5e-09	75	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19P17, complete sequence [Arabidopsis thaliana]
9855	GM_155_A1_G09_T7	g1431738	BLASTN	637	5e-22	93	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
9856	GM_155_A1_G12_MR	g3142328	BLASTN	1612	3e-66	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9857	GM_155_A1_H02_MR	g3252807	BLASTX	485	2e-45	67	(AC004705) hypothetical protein [Arabidopsis thaliana]
9858	GM_155_A1_H03_MR	g507910	BLASTN	340	9e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
9859	GM_155_A1_H03_T7	g507910	BLASTN	416	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9860	GM_155_A1_H04_MR	g4038056	BLASTX	272	9e-22	43	(AC005897) putative transposon [Arabidopsis thaliana]
9861	GM_155_A1_H04_T7	g1935006	BLASTX	152	5e-15	46	(Y12320) starch branching enzyme I [Triticum aestivum]
9862	GM_155_A1_H05_MR	g130582	BLASTX	98	1e-09	37	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
9863	GM_155_A1_H06_MR	g3695387	BLASTX	138	4e-09	42	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
9864	GM_155_A1_H09_MR	g3645899	BLASTX	271	1e-21	60	(U68408) 5' end not determined experimentally [Zea mays]
9865	GM_155_A2_A03_MR	g507910	BLASTN	423	2e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
9866	GM_155_A2_A03_T7	g507910	BLASTN	564	7e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
9867	GM_155_A2_A04_T7	g3549639	BLASTX	127	2e-16	78	(AJ005194) receiver-like protein 3 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9868	GM_155_A2_A12_T7	g3142328	BLASTN	409	2e-11	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9869	GM_155_A2_B01_T7	g497835	BLASTN	375	3e-13	69	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
9870	GM_155_A2_B02_T7	g4063760	BLASTX	460	1e-41	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9871	GM_155_A2_B06_MR	g4092470	BLASTN	719	2e-25	67	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
9872	GM_155_A2_B07_T7	g1167523	BLASTX	351	6e-30	58	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
9873	GM_155_A2_B09_T7	g3947433	BLASTN	352	7e-09	65	Homo sapiens BAC clone RG060P12 from 7q21, complete sequence [Homo sapiens]
9874	GM_155_A2_B10_MR	g2335097	BLASTX	281	1e-22	47	(AC002339) putative receptor-like protein kinase [Arabidopsis thaliana]
9875	GM_155_A2_B11_T7	g2244802	BLASTX	223	7e-18	47	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
9876	GM_155_A2_C01_MR	g1142702	BLASTN	256	1e-12	72	Glycine max satellite STR120-A.4.
9877	GM_155_A2_C01_T7	g4063770	BLASTX	219	4e-16	40	(AB004906) transposase [Ipomoea purpurea]
9878	GM_155_A2_C06_MR	g507910	BLASTN	422	2e-12	78	Glycine max BSR-101 satellite SB92 genomic sequence.
9879	GM_155_A2_C06_T7	g4063760	BLASTX	236	1e-17	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9880	GM_155_A2_D01_MR	g507910	BLASTN	435	5e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
9881	GM_155_A2_D01_T7	g4063760	BLASTX	422	1e-37	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9882	GM_155_A2_D04_MR	g3097320	BLASTN	368	1e-09	74	Glycine max gene for Bd 30K, complete cds
9883	GM_155_A2_D07_MR	g3097320	BLASTN	613	1e-20	78	Glycine max gene for Bd 30K, complete cds
9884	GM_155_A2_D09_MR	g99922	BLASTX	364	1e-32	69	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
9885	GM_155_A2_D10_MR	g1865677	BLASTX	255	7e-20	77	(Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]
9886	GM_155_A2_D11_T7	g2808683	BLASTX	249	2e-19	46	(AJ002235) Cf-4 [Lycopersicon hirsutum]
9887	GM_155_A2_D12_MR	g3599418	BLASTN	706	5e-25	83	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
9888	GM_155_A2_E06_MR	g905361	BLASTX	675	1e-65	93	(U22103) gag-protease polyprotein [Glycine max]
9889	GM_155_A2_E07_T7	g4050011	BLASTN	411	1e-11	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
9890	GM_155_A2_E09_MR	g905361	BLASTX	235	5e-18	42	(U22103) gag-protease polyprotein [Glycine max]
9891	GM_155_A2_E10_T7	g3702732	BLASTN	687	5e-24	68	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MGF10, complete sequence [Arabidopsis thaliana]
9892	GM_155_A2_E11_MR	g1769899	BLASTX	190	3e-14	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9893	GM_155_A2_F03_MR	g3063708	BLASTX	254	2e-19	48	(AL022537) putative protein [Arabidopsis thaliana]
9894	GM_155_A2_F05_MR	g3777527	BLASTX	634	5e-60	90	(AF053008) gag-pol polyprotein [Glycine max]
9895	GM_155_A2_F07_MR	g3695395	BLASTX	256	2e-20	45	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
9896	GM_155_A2_F08_MR	g2995405	BLASTX	406	4e-36	57	(Y12432) polyprotein [Ananas comosus]
9897	GM_155_A2_F11_MR	g4100321	BLASTX	207	4e-16	41	(U96642) A sunflower resistance gene homolog, partial cds [Helianthus annuus]
9898	GM_155_A2_F12_MR	g507910	BLASTN	495	9e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
9899	GM_155_A2_F12_T7	g507910	BLASTN	417	3e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
9900	GM_155_A2_G06_MR	g421954	BLASTX	225	6e-17	44	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
9901	GM_155_A2_G07_MR	g3377855	BLASTX	248	2e-20	81	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
9902	GM_155_A2_G08_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9903	GM_155_A2_G08_T7	g507910	BLASTN	394	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
9904	GM_155_A2_G11_T7	g3142330	BLASTX	491	4e-46	93	(U96295) envelope-like [Glycine max]
9905	GM_155_A2_H02_MR	g2522227	BLASTX	211	2e-16	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
9906	GM_155_A2_H03_T7	g3395443	BLASTX	207	2e-15	41	(AC004683) putative ammonium transporter, 3' partial [Arabidopsis thaliana]
9907	GM_155_A2_H05_T7	g4115357	BLASTX	293	9e-25	45	(AC005957) hypothetical protein [Arabidopsis thaliana]
9908	GM_155_A2_H06_T7	g4063760	BLASTX	305	4e-25	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9909	GM_155_A2_H07_MR	g282881	BLASTX	412	7e-37	67	receptor-like protein kinase precursor - Arabidopsis thaliana gi 166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]
9910	GM_155_A2_H08_MR	g507910	BLASTN	405	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9911	GM_155_A2_H09_MR	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9912	GM_155_B1_A02_T7	g18559	BLASTN	403	3e-11	70	G.max gene for catalase
9913	GM_155_B1_A04_T7	g1666236	BLASTX	171	9e-12	30	(U76261) unknown [Hordeum vulgare]
9914	GM_155_B1_A06_MR	g1769898	BLASTX	395	2e-35	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9915	GM_155_B1_A08_T7	g4140712	BLASTX	188	2e-22	42	(AF110183) putative integrase [Oryza sativa]
9916	GM_155_B1_A12_MR	g1769898	BLASTX	358	2e-31	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9917	GM_155_B1_B01_T7	g3869063	BLASTN	393	1e-10	64	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17O22, complete sequence [Arabidopsis thaliana]
9918	GM_155_B1_B03_MR	g4063760	BLASTX	349	9e-30	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9919	GM_155_B1_B04_T7	g1666236	BLASTX	169	1e-11	28	(U76261) unknown [Hordeum vulgare]
9920	GM_155_B1_B05_MR	g3142328	BLASTN	1124	5e-44	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9921	GM_155_B1_B09_T7	g1514643	BLASTX	167	3e-10	62	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
9922	GM_155_B1_C04_MR	g4063760	BLASTX	188	1e-12	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9923	GM_155_B1_C04_T7	g3777527	BLASTX	579	4e-54	95	(AF053008) gag-pol polyprotein [Glycine max]
9924	GM_155_B1_C05_MR	g2522228	BLASTX	409	2e-37	76	(AB007466) reverse transcriptase-like protein [Vicia faba]
9925	GM_155_B1_C07_MR	g905361	BLASTX	250	1e-19	41	(U22103) gag-protease polyprotein [Glycine max]
9926	GM_155_B1_C11_MR	g1666236	BLASTX	168	2e-11	28	(U76261) unknown [Hordeum vulgare]
9927	GM_155_B1_C12_T7	g3097320	BLASTN	462	7e-14	74	Glycine max gene for Bd 30K, complete cds
9928	GM_155_B1_D02_MR	g1142701	BLASTN	245	5e-19	75	Glycine max satellite STR120-A.3.
9929	GM_155_B1_D03_MR	g2275090	BLASTN	548	2e-18	77	Swietenia humilis DNA for simple tandem repeat (341bp)
9930	GM_155_B1_D04_MR	g629693	BLASTX	199	1e-14	34	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
9931	GM_155_B1_D07_MR	g2708743	BLASTX	255	1e-19	36	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
9932	GM_155_B1_D08_T7	g3142328	BLASTN	869	2e-32	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9933	GM_155_B1_E01_T7	g4063756	BLASTN	562	2e-18	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9934	GM_155_B1_E02_MR	g100484	BLASTX	268	2e-21	39	hypothetical protein - garden snapdragon
9935	GM_155_B1_E02_T7	g3645899	BLASTX	192	7e-29	54	(U68408) 5' end not determined experimentally [Zea mays]
9936	GM_155_B1_E05_MR	g100484	BLASTX	333	2e-28	53	hypothetical protein - garden snapdragon
9937	GM_155_B1_E06_MR	g629693	BLASTX	160	2e-10	44	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
9938	GM_155_B1_E07_T7	g507910	BLASTN	738	1e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
9939	GM_155_B1_E10_T7	g170605	BLASTN	485	3e-15	64	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
9940	GM_155_B1_F02_MR	g1658435	BLASTX	143	3e-09	78	(U75225) reverse transcriptase [Gossypium barbadense]
9941	GM_155_B1_F04_MR	g2809251	BLASTX	129	1e-16	53	(AC002560) F21B7.20 [Arabidopsis thaliana]
9942	GM_155_B1_F06_MR	g170029	BLASTN	389	1e-10	80	Glycine max cv. Dare nodulin 26 gene fragment.
9943	GM_155_B1_F06_T7	g3142328	BLASTN	1923	2e-80	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9944	GM_155_B1_F07_T7	g4063760	BLASTX	414	1e-36	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9945	GM_155_B1_F09_T7	g421955	BLASTX	270	9e-23	48	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9946	GM_155_B1_F11_T7	g905361	BLASTX	185	1e-12	30	(U22103) gag-protease polyprotein [Glycine max]
9947	GM_155_B1_G01_T7	g3914056	BLASTX	111	6e-10	71	DNA MISMATCH REPAIR PROTEIN MSH2 >gi 2522362 (AF002706) MutS homolog 2 [Arabidopsis thaliana] >gi 2522364 (AF003005) MutS homolog 2 [Arabidopsis thaliana] >gi 2547236 (AF026549) DNA mismatch repair protein MSH2 [Arabidopsis thaliana]
9948	GM_155_B1_G06_MR	g507910	BLASTN	494	1e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
9949	GM_155_B1_G06_T7	g507910	BLASTN	569	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
9950	GM_155_B1_G12_MR	g342959	BLASTN	452	2e-14	62	paramecium species 4.51er mt dna dimer: replication init. region, clone 3.
9951	GM_155_B1_H02_T7	g905361	BLASTX	202	2e-14	33	(U22103) gag-protease polyprotein [Glycine max]
9952	GM_155_B1_H07_MR	g3549672	BLASTX	155	9e-10	88	(AL031394) putative protein [Arabidopsis thaliana]
9953	GM_155_B2_A04_MR	g3097320	BLASTN	1159	2e-45	75	Glycine max gene for Bd 30K, complete cds
9954	GM_155_B2_A06_MR	g3510347	BLASTN	460	1e-13	67	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]
9955	GM_155_B2_A08_MR	g4063760	BLASTX	551	2e-51	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9956	GM_155_B2_A11_MR	g3645899	BLASTX	301	5e-30	49	(U68408) 5' end not determined experimentally [Zea mays]
9957	GM_155_B2_A11_T7	g1165321	BLASTN	452	2e-13	68	Glycine max extensin (SbHRGP3) gene, complete cds
9958	GM_155_B2_B02_T7	g3269288	BLASTX	419	2e-38	59	(AL030978) putative protein [Arabidopsis thaliana]
9959	GM_155_B2_B03_MR	g507910	BLASTN	539	1e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
9960	GM_155_B2_B05_T7	g4063756	BLASTN	589	1e-19	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9961	GM_155_B2_B07_MR	g1666236	BLASTX	179	1e-12	27	(U76261) unknown [Hordeum vulgare]
9962	GM_155_B2_B08_T7	g1370140	BLASTX	215	6e-17	66	(X98308) myb-related transcription factor [Lycopersicon esculentum]
9963	GM_155_B2_B09_MR	g4063760	BLASTX	242	1e-21	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9964	GM_155_B2_B11_T7	g3777527	BLASTX	614	8e-58	95	(AF053008) gag-pol polyprotein [Glycine max]
9965	GM_155_B2_C02_MR	g507910	BLASTN	603	1e-20	85	Glycine max BSR-101 satellite SB92 genomic sequence.
9966	GM_155_B2_C02_T7	g4063756	BLASTN	437	1e-12	70	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
9967	GM_155_B2_C03_MR	g3097320	BLASTN	1217	4e-48	76	Glycine max gene for Bd 30K, complete cds
9968	GM_155_B2_C05_MR	g3097320	BLASTN	625	3e-21	72	Glycine max gene for Bd 30K, complete cds
9969	GM_155_B2_C07_T7	g2522228	BLASTX	244	1e-19	46	(AB007466) reverse transcriptase-like protein [Vicia faba]
9970	GM_155_B2_C09_MR	g4063760	BLASTX	280	2e-22	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9971	GM_155_B2_C10_MR	g3142328	BLASTN	783	7e-57	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
9972	GM_155_B2_C11_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
9973	GM_155_B2_C11_T7	g4063760	BLASTX	321	9e-27	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9974	GM_155_B2_D01_MR	g2522230	BLASTX	335	1e-29	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
9975	GM_155_B2_D01_T7	g2522228	BLASTX	371	2e-33	57	(AB007466) reverse transcriptase-like protein [Vicia faba]
9976	GM_155_B2_D02_T7	g3777527	BLASTX	394	2e-34	93	(AF053008) gag-pol polyprotein [Glycine max]
9977	GM_155_B2_D04_MR	g3777527	BLASTX	307	4e-25	93	(AF053008) gag-pol polyprotein [Glycine max]
9978	GM_155_B2_D04_T7	g2194136	BLASTX	321	1e-26	61	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
9979	GM_155_B2_D06_T7	g3850630	BLASTX	235	4e-21	73	(AJ012581) cytochrome P450 [Cicer arietinum]
9980	GM_155_B2_E01_MR	g507910	BLASTN	347	4e-09	68	Glycine max BSR-101 satellite SB92 genomic sequence.
9981	GM_155_B2_E01_T7	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
9982	GM_155_B2_E06_MR	g2114242	BLASTN	358	4e-09	61	Human (lambda) DNA for immunoglobulin light chain
9983	GM_155_B2_E07_MR	g4063760	BLASTX	171	8e-11	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9984	GM_155_B2_E09_T7	g2191197	BLASTX	232	2e-18	67	(AF007271) contains similarity to Synechococcus PCC7942 chromosomal region used as basis of neutral siteII recombinational cloning vector (PID:g1174192) [Arabidopsis thaliana]
9985	GM_155_B2_E12_T7	g905361	BLASTX	534	1e-50	98	(U22103) gag-protease polyprotein [Glycine max]
9986	GM_155_B2_F01_MR	g905361	BLASTX	216	6e-16	32	(U22103) gag-protease polyprotein [Glycine max]
9987	GM_155_B2_F02_T7	g1326016	BLASTX	344	3e-29	50	TY3-2 orfB
9988	GM_155_B2_F03_T7	g507910	BLASTN	626	1e-21	85	Glycine max BSR-101 satellite SB92 genomic sequence.
9989	GM_155_B2_F04_MR	g3142328	BLASTN	821	3e-30	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9990	GM_155_B2_F05_T7	g1514643	BLASTX	167	3e-10	62	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
9991	GM_155_B2_F08_T7	g4063760	BLASTX	274	8e-22	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
9992	GM_155_B2_F09_MR	g3142328	BLASTN	723	9e-26	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
9993	GM_155_B2_F09_T7	g3645899	BLASTX	231	3e-17	51	(U68408) 5' end not determined experimentally [Zea mays]
9994	GM_155_B2_G03_MR	g1769897	BLASTX	166	9e-22	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
9995	GM_155_B2_G08_MR	g3386606	BLASTX	198	5e-14	55	(AC004665) putative beta-amylase [Arabidopsis thaliana]
9996	GM_155_B2_G09_T7	g507910	BLASTN	566	6e-19	83	Glycine max BSR-101 satellite SB92 genomic sequence.
9997	GM_155_B2_G11_MR	g3979928	BLASTN	485	7e-15	65	Caenorhabditis elegans cosmid Y18D10A, complete sequence [Caenorhabditis elegans]
9998	GM_155_B2_G11_T7	g3777527	BLASTX	207	2e-14	48	(AF053008) gag-pol polyprotein [Glycine max]
9999	GM_155_B2_H06_T7	g2522228	BLASTX	440	2e-47	63	(AB007466) reverse transcriptase-like protein [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10000	GM_155_B2_H07_MR	g629693	BLASTX	260	1e-21	59	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10001	GM_155_B2_H07_T7	g99755	BLASTX	311	2e-26	50	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
10002	GM_155_B2_H10_MR	g3097320	BLASTN	940	2e-35	76	Glycine max gene for Bd 30K, complete cds
10003	GM_156_B1_A05_T7	g2522228	BLASTX	415	4e-38	77	(AB007466) reverse transcriptase-like protein [Vicia faba]
10004	GM_156_B1_A08_T7	g4063760	BLASTX	172	7e-11	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10005	GM_156_B1_B02_T7	g505129	BLASTN	363	2e-09	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10006	GM_156_B1_B04_T7	g340796	BLASTN	388	2e-11	62	Figure 6. DNA sequence of three 3' apoB VNTR alleles.
10007	GM_156_B1_B08_T7	g170080	BLASTN	454	1e-13	69	Soybean seed lectin gene transposable element tgm1.
10008	GM_156_B1_B11_MR	g4038056	BLASTX	168	2e-13	45	(AC005897) putative transposon [Arabidopsis thaliana]
10009	GM_156_B1_B12_MR	g2853076	BLASTX	159	1e-09	62	(AL021768) putative protein [Arabidopsis thaliana]
10010	GM_156_B1_B12_T7	g3283026	BLASTX	153	7e-11	35	putative transposase [Arabidopsis thaliana]
10011	GM_156_B1_C05_T7	g2244915	BLASTX	147	6e-17	35	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
10012	GM_156_B1_C06_T7	g1666236	BLASTX	205	1e-15	33	(U76261) unknown [Hordeum vulgare]
10013	GM_156_B1_C10_MR	g507910	BLASTN	343	7e-09	81	Glycine max BSR-101 satellite SB92 genomic sequence.
10014	GM_156_B1_C12_MR	g3334667	BLASTX	267	9e-22	45	(Y10493) putative cytochrome P450 [Glycine max]
10015	GM_156_B1_C12_T7	g3334667	BLASTX	453	4e-42	65	(Y10493) putative cytochrome P450 [Glycine max]
10016	GM_156_B1_D03_MR	g2827516	BLASTX	226	1e-16	73	(AL021633) DNA topoisomerase like- protein [Arabidopsis thaliana]
10017	GM_156_B1_D04_T7	g840618	BLASTN	357	3e-09	62	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
10018	GM_156_B1_D06_MR	g3377848	BLASTX	240	3e-19	51	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
10019	GM_156_B1_D06_T7	g2316016	BLASTX	122	3e-09	45	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
10020	GM_156_B1_D07_MR	g2244915	BLASTX	168	1e-10	34	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
10021	GM_156_B1_E02_T7	g3142328	BLASTN	908	4e-34	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10022	GM_156_B1_E03_T7	g3142328	BLASTN	1040	4e-40	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10023	GM_156_B1_E04_MR	g3135252	BLASTX	152	2e-09	28	(AC003058) hypothetical protein [Arabidopsis thaliana] gi 3176720 (AC002392) hypothetical protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10024	GM_156_B1_E05_MR	g3513745	BLASTX	235	2e-17	40	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
10025	GM_156_B1_E08_T7	g1707657	BLASTX	375	7e-34	52	(Z71640) DnaJ homologue [Pisum sativum]
10026	GM_156_B1_E12_MR	g3695395	BLASTX	268	1e-21	37	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
10027	GM_156_B1_F04_MR	g3810596	BLASTX	158	2e-09	30	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
10028	GM_156_B1_F04_T7	g1769898	BLASTX	359	1e-31	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10029	GM_156_B1_F06_T7	g421955	BLASTX	425	4e-39	61	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
10030	GM_156_B1_F07_T7	g507910	BLASTN	570	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
10031	GM_156_B1_F08_MR	g3810596	BLASTX	169	1e-10	32	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
10032	GM_156_B1_G02_T7	g3142328	BLASTN	1206	1e-47	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10033	GM_156_B1_G03_MR	g1363492	BLASTX	178	2e-24	87	outer envelope membrane protein OEP75 precursor - garden pea gi 576507 (L36858) outer membrane protein [Pisum sativum] gi 633607 (X83767) chloroplastic outer envelope membrane protein (OEP75) [Pisum sativum]
10034	GM_156_B1_G09_MR	g3482913	BLASTX	122	8e-16	48	(AC003970) Similar to MtN21, gi 2598575, Megicago truncatula nodulation induced gene [Arabidopsis thaliana]
10035	GM_156_B1_G11_T7	g2522228	BLASTX	157	8e-21	87	(AB007466) reverse transcriptase-like protein [Vicia faba]
10036	GM_156_B1_H01_MR	g3142328	BLASTN	938	2e-35	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10037	GM_156_B1_H03_T7	g2129618	BLASTX	215	1e-15	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10038	GM_156_B2_A03_MR	g1666236	BLASTX	294	3e-25	34	(U76261) unknown [Hordeum vulgare]
10039	GM_156_B2_A08_MR	g3097320	BLASTN	1809	6e-75	82	Glycine max gene for Bd 30K, complete cds
10040	GM_156_B2_A10_MR	g629693	BLASTX	322	2e-40	51	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10041	GM_156_B2_C03_MR	g507910	BLASTN	465	2e-14	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10042	GM_156_B2_C07_MR	g2244807	BLASTX	260	7e-23	56	(Z97336) hypothetical protein [Arabidopsis thaliana]
10043	GM_156_B2_C09_MR	g2462936	BLASTX	325	1e-31	48	(Y12321) open reading frame 2 [Brassica oleracea]
10044	GM_156_B2_C10_MR	g2576326	BLASTN	393	9e-11	65	Phaseolus vulgaris tRNA-Pro (AGG), tRNA-Pro (UGG) genes
10045	GM_156_B2_D11_MR	g1769897	BLASTX	189	3e-13	32	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10046	GM_156_B2_D12_MR	g2315153	BLASTX	244	6e-28	75	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10047	GM_156_B2_E05_MR	g881595	BLASTN	372	8e-10	64	Pisum sativum cytosolic glutamine synthetase (GS3B) gene, complete cds.
10048	GM_156_B2_E07_MR	g3097320	BLASTN	417	8e-12	72	Glycine max gene for Bd 30K, complete cds
10049	GM_156_B2_E08_MR	g4063760	BLASTX	265	4e-22	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10050	GM_156_B2_E10_MR	g2739003	BLASTN	681	3e-24	86	Glycine max cytochrome P450 monooxygenase CYP82C1p (CYP82C1) mRNA, complete cds
10051	GM_156_B2_E11_MR	g3097320	BLASTN	402	4e-11	64	Glycine max gene for Bd 30K, complete cds
10052	GM_156_B2_F01_MR	g4038056	BLASTX	262	3e-36	45	(AC005897) putative transposon [Arabidopsis thaliana]
10053	GM_156_B2_F09_MR	g629693	BLASTX	225	1e-17	52	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10054	GM_156_B2_G01_MR	g3599418	BLASTN	523	6e-31	79	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
10055	GM_156_B2_G06_MR	g905361	BLASTX	219	3e-16	29	(U22103) gag-protease polyprotein [Glycine max]
10056	GM_156_B2_G08_MR	g507910	BLASTN	444	2e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
10057	GM_156_B2_G09_MR	g3777527	BLASTX	231	2e-19	34	(AF053008) gag-pol polyprotein [Glycine max]
10058	GM_156_B2_H01_MR	g505129	BLASTN	425	3e-12	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10059	GM_156_B2_H06_MR	g505129	BLASTN	384	1e-15	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10060	GM_156_B2_H07_MR	g1142699	BLASTN	1339	3e-54	87	Glycine max satellite STR120-A.1.
10061	GM_157_A1_A02_MR	g3810595	BLASTX	292	1e-23	57	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
10062	GM_157_A1_A04_MR	g461987	BLASTX	583	6e-56	92	ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) gi 82042 pir JS0719 translation elongation factor eEF-1 alpha chain - carrot gi 217913 gnl PID d1002697 (D12709) elongation factor 1-alpha [Daucus carota]
10063	GM_157_A1_A06_T7	g3452273	BLASTX	230	2e-26	83	(AF043110) phosphatidylinositol 4-kinase alpha [Daucus carota]
10064	GM_157_A1_A08_MR	g3097320	BLASTN	1007	1e-38	84	Glycine max gene for Bd 30K, complete cds
10065	GM_157_A1_A08_T7	g3319345	BLASTX	204	2e-14	39	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
10066	GM_157_A1_A09_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10067	GM_157_A1_A09_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10068	GM_157_A1_B04_MR	g3738114	BLASTN	441	7e-13	66	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
10069	GM_157_A1_B04_T7	g18559	BLASTN	890	3e-33	75	G.max gene for catalase
10070	GM_157_A1_B10_MR	g2995405	BLASTX	313	4e-26	55	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10071	GM_157_A1_B10_T7	g507910	BLASTN	684	3e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
10072	GM_157_A1_B11_T7	g4050011	BLASTN	361	3e-09	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
10073	GM_157_A1_C07_MR	g4063760	BLASTX	267	5e-21	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10074	GM_157_A1_D01_T7	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10075	GM_157_A1_D02_MR	g342964	BLASTN	346	2e-09	66	paramecium species 5,311 mt dna dimer: replication init. region.
10076	GM_157_A1_D02_T7	g2209031	BLASTX	128	1e-11	53	(AB001569) ORF of 1.56 kb [Daucus carota]
10077	GM_157_A1_D03_T7	g505129	BLASTN	424	3e-12	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10078	GM_157_A1_D04_MR	g3097320	BLASTN	473	2e-14	70	Glycine max gene for Bd 30K, complete cds
10079	GM_157_A1_D06_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10080	GM_157_A1_D06_T7	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10081	GM_157_A1_D08_MR	g4063760	BLASTX	145	9e-18	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10082	GM_157_A1_D09_T7	g3941729	BLASTN	365	2e-09	68	Homo sapiens chromosome 7 BAC clone F5, complete sequence [Homo sapiens]
10083	GM_157_A1_E03_MR	g507910	BLASTN	653	7e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
10084	GM_157_A1_E03_T7	g507910	BLASTN	616	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10085	GM_157_A1_E04_T7	g905361	BLASTX	230	2e-17	39	(U22103) gag-protease polyprotein [Glycine max]
10086	GM_157_A1_E05_MR	g2443320	BLASTX	256	9e-20	50	(D85597) polyprotein [Oryza australiensis]
10087	GM_157_A1_E07_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10088	GM_157_A1_E10_T7	g1769899	BLASTX	299	8e-26	77	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10089	GM_157_A1_E12_T7	g1785744	BLASTX	218	1e-20	62	(Y08502) orf158 [Arabidopsis thaliana]
10090	GM_157_A1_F03_MR	g4063760	BLASTX	436	5e-39	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10091	GM_157_A1_F03_T7	g3097320	BLASTN	554	5e-18	73	Glycine max gene for Bd 30K, complete cds
10092	GM_157_A1_F04_MR	g507910	BLASTN	368	5e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10093	GM_157_A1_F04_T7	g507910	BLASTN	388	6e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
10094	GM_157_A1_F05_T7	g2443320	BLASTX	329	2e-27	46	(D85597) polyprotein [Oryza australiensis]
10095	GM_157_A1_F06_MR	g2443320	BLASTX	249	5e-19	39	(D85597) polyprotein [Oryza australiensis]
10096	GM_157_A1_G05_MR	g507910	BLASTN	501	5e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
10097	GM_157_A1_G05_T7	g507910	BLASTN	520	7e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
10098	GM_157_A1_G07_MR	g3097320	BLASTN	650	2e-22	77	Glycine max gene for Bd 30K, complete cds
10099	GM_157_A1_H01_T7	g3142379	BLASTX	259	4e-21	56	(AF053008) envelope-like [Glycine max]
10100	GM_157_A1_H03_MR	g1431738	BLASTN	590	7e-20	94	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10101	GM_157_A1_H10_T7	g422418	BLASTX	116	3e-14	36	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
10102	GM_157_A2_A03_MR	g21430	BLASTN	370	1e-09	63	Potato DNA for copia-like transposable element
10103	GM_157_A2_A05_T7	g507910	BLASTN	727	3e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
10104	GM_157_A2_A08_T7	g2827550	BLASTX	222	6e-23	60	(AL021635) leucine rich repeat receptor kinase-like protein [Arabidopsis thaliana]
10105	GM_157_A2_A12_T7	g4038056	BLASTX	225	4e-25	50	(AC005897) putative transposon [Arabidopsis thaliana]
10106	GM_157_A2_B07_MR	g4063756	BLASTN	595	8e-20	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
10107	GM_157_A2_B08_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10108	GM_157_A2_B08_T7	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
10109	GM_157_A2_B11_T7	g3142328	BLASTN	1465	2e-59	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10110	GM_157_A2_C03_T7	g18559	BLASTN	595	2e-30	73	G.max gene for catalase
10111	GM_157_A2_C07_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10112	GM_157_A2_C08_MR	g623589	BLASTN	352	5e-09	69	Nicotiana tabacum SR1 Nt-rab7b mRNA, complete cds.
10113	GM_157_A2_C12_MR	g2586087	BLASTX	249	2e-19	38	(U72724) receptor kinase-like protein [Oryza sativa]
10114	GM_157_A2_C12_T7	g3288442	BLASTN	351	8e-09	62	Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Ga...
10115	GM_157_A2_D01_MR	g4038056	BLASTX	287	2e-23	39	(AC005897) putative transposon [Arabidopsis thaliana]
10116	GM_157_A2_D04_MR	g507910	BLASTN	509	2e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
10117	GM_157_A2_D06_MR	g3097320	BLASTN	918	1e-34	72	Glycine max gene for Bd 30K, complete cds
10118	GM_157_A2_D09_T7	g3097320	BLASTN	455	1e-13	73	Glycine max gene for Bd 30K, complete cds
10119	GM_157_A2_E02_T7	g507910	BLASTN	704	3e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
10120	GM_157_A2_E08_MR	g13096	BLASTN	390	1e-10	61	Leishmania tarentolae maxicircle DNA fragment
10121	GM_157_A2_F04_MR	g4038056	BLASTX	266	4e-21	37	(AC005897) putative transposon [Arabidopsis thaliana]
10122	GM_157_A2_F08_MR	g2961349	BLASTX	286	4e-23	45	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
10123	GM_157_A2_F10_T7	g1419127	BLASTX	133	8e-11	59	(Z75516) reverse transcriptase [Oryza sativa]
10124	GM_157_A2_G01_T7	g170029	BLASTN	440	7e-13	68	Glycine max cv. Dare nodulin 26 gene fragment.
10125	GM_157_A2_G05_T7	g4140712	BLASTX	361	2e-32	57	(AF110183) putative integrase [Oryza sativa]
10126	GM_157_A2_G08_T7	g507910	BLASTN	628	9e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10127	GM_157_A2_H02_T7	g2995405	BLASTX	213	2e-15	64	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10128	GM_157_A2_H05_MR	g629693	BLASTX	185	4e-13	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10129	GM_157_A2_H07_MR	g4063760	BLASTX	211	4e-15	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10130	GM_157_A2_H09_MR	g18766	BLASTN	367	6e-10	78	Soybean Tgm5 transposable element
10131	GM_157_B1_A02_MR	g3337392	BLASTN	357	4e-09	66	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence [Homo sapiens]
10132	GM_157_B1_A03_MR	g4063760	BLASTX	498	1e-45	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10133	GM_157_B1_A03_T7	g507910	BLASTN	389	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10134	GM_157_B1_A06_MR	g120539	BLASTX	182	2e-13	91	NADH-PLASTOQUINONE OXIDOREDUCTASE SUBUNIT I (FRXB PROTEIN) gi 65733 pir FENTB ferredoxin 2[4Fe-4S] frxB - common tobacco chloroplast gi 100289 pir S11956 iron-sulfur protein frxB - tobacco chloroplast gi 1223671 (Z00044) NADH dehydrogenase 18kD subunit [Nicotiana tabacum] gi 225259 prf 1211235CU ORF 167 [Nicotiana tabacum]
10135	GM_157_B1_A07_T7	g507910	BLASTN	527	3e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
10136	GM_157_B1_A12_T7	g2583106	BLASTN	401	4e-11	64	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]
10137	GM_157_B1_B02_T7	g2522230	BLASTX	143	4e-09	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
10138	GM_157_B1_B03_MR	g1142703	BLASTN	286	2e-15	76	Glycine max satellite STR120-B.1.
10139	GM_157_B1_B07_MR	g2979597	BLASTN	446	4e-13	64	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
10140	GM_157_B1_B09_MR	g3097320	BLASTN	905	6e-34	77	Glycine max gene for Bd 30K, complete cds
10141	GM_157_B1_B09_T7	g1666236	BLASTX	215	9e-17	31	(U76261) unknown [Hordeum vulgare]
10142	GM_157_B1_B12_T7	g3645899	BLASTX	152	8e-09	38	(U68408) 5' end not determined experimentally [Zea mays]
10143	GM_157_B1_C08_MR	g18559	BLASTN	704	7e-25	72	G.max gene for catalase
10144	GM_157_B1_C09_MR	g421954	BLASTX	150	7e-12	39	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
10145	GM_157_B1_C10_MR	g2828780	BLASTN	349	1e-08	64	Homo sapiens chromosome 17, clone 289A8, complete sequence [Homo sapiens]
10146	GM_157_B1_D03_MR	g3687221	BLASTN	378	5e-10	61	Arabidopsis thaliana chromosome II BAC F6F22 genomic sequence, complete sequence [Arabidopsis thaliana]
10147	GM_157_B1_D06_T7	g537319	BLASTX	176	2e-12	84	(L36158) peroxidase [Medicago sativa]
10148	GM_157_B1_D07_T7	g3645899	BLASTX	235	2e-18	47	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10149	GM_157_B1_D09_MR	g2335061	BLASTN	446	4e-13	64	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence [Homo sapiens]
10150	GM_157_B1_E02_T7	g3212855	BLASTX	184	6e-13	41	(AC004005) hypothetical protein [Arabidopsis thaliana]
10151	GM_157_B1_E04_T7	g3789709	BLASTN	424	4e-12	64	Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence [Homo sapiens]
10152	GM_157_B1_E05_T7	g1142699	BLASTN	617	1e-21	84	Glycine max satellite STR120-A.1.
10153	GM_157_B1_E08_MR	g4063760	BLASTX	229	5e-17	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10154	GM_157_B1_E10_MR	g170029	BLASTN	380	4e-10	79	Glycine max cv. Dare nodulin 26 gene fragment.
10155	GM_157_B1_E11_MR	g2827711	BLASTX	236	8e-18	68	(AL021684) oxoglutarate dehydrogenase - like protein [Arabidopsis thaliana]
10156	GM_157_B1_F01_MR	g2914707	BLASTX	160	7e-10	34	(AC003974) putative disease resistance protein (Cf-2.2) [Arabidopsis thaliana] gi 3298554 (AC004681) putative disease resistance protein [Arabidopsis thaliana]
10157	GM_157_B1_F01_T7	g1272349	BLASTX	253	2e-20	47	(U51740) secreted glycoprotein 3 [Ipomoea trifida]
10158	GM_157_B1_F09_T7	g18559	BLASTN	801	3e-29	73	G.max gene for catalase
10159	GM_157_B1_F11_MR	g3695395	BLASTX	211	2e-15	42	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
10160	GM_157_B1_G05_T7	g2522227	BLASTX	272	6e-23	45	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
10161	GM_157_B1_G09_MR	g3746060	BLASTX	238	2e-19	70	(AC005311) unknown protein [Arabidopsis thaliana]
10162	GM_157_B1_G09_T7	g3063446	BLASTX	177	3e-11	89	(AC003981) F22O13.8 [Arabidopsis thaliana]
10163	GM_157_B1_G11_MR	g507910	BLASTN	362	9e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10164	GM_157_B1_H01_MR	g3047060	BLASTN	377	5e-10	63	Arabidopsis thaliana BAC F7N22
10165	GM_157_B1_H04_MR	g2160158	BLASTX	207	2e-15	81	(AC000132) Similar to elongation factor 1-gamma (gb EF1G_XENLA). ESTs gb T20564,gb T45940,gb T04527 come from this gene. [Arabidopsis thaliana]
10166	GM_157_B1_H05_MR	g3097320	BLASTN	762	2e-27	74	Glycine max gene for Bd 30K, complete cds
10167	GM_157_B1_H07_MR	g2864621	BLASTX	215	3e-16	46	hypothetical protein [Arabidopsis thaliana]
10168	GM_157_B1_H09_MR	g507910	BLASTN	361	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10169	GM_157_B1_H11_T7	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10170	GM_157_B1_H12_T7	g4063760	BLASTX	444	7e-40	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10171	GM_158_A1_A03_T7	g3695395	BLASTX	201	7e-18	40	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
10172	GM_158_A1_A04_T7	g3021270	BLASTX	266	2e-37	66	(AL022347) serine/threonine kinase -like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10173	GM_158_A1_A11_MR	g905361	BLASTX	565	6e-54	91	(U22103) gag-protease polyprotein [Glycine max]
10174	GM_158_A1_A12_MR	g4063760	BLASTX	219	7e-16	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10175	GM_158_A1_B06_MR	g2264320	BLASTN	649	3e-22	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
10176	GM_158_A1_B08_T7	g3873182	BLASTN	405	3e-11	65	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
10177	GM_158_A1_B12_MR	g3097320	BLASTN	655	1e-22	73	Glycine max gene for Bd 30K, complete cds
10178	GM_158_A1_C02_MR	g3645899	BLASTX	216	5e-23	51	(U68408) 5' end not determined experimentally [Zea mays]
10179	GM_158_A1_C12_T7	g507910	BLASTN	445	2e-13	79	Glycine max BSR-101 satellite SB92 genomic sequence.
10180	GM_158_A1_D03_T7	g18559	BLASTN	1072	1e-41	77	G.max gene for catalase
10181	GM_158_A1_D04_T7	g3097320	BLASTN	489	4e-15	77	Glycine max gene for Bd 30K, complete cds
10182	GM_158_A1_D05_MR	g100484	BLASTX	259	2e-20	54	hypothetical protein - garden snapdragon
10183	GM_158_A1_D05_T7	g3319363	BLASTX	203	2e-14	59	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 33.26) [Arabidopsis thaliana]
10184	GM_158_A1_E04_MR	g13767	BLASTN	336	5e-09	67	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
10185	GM_158_A1_E05_MR	g1769898	BLASTX	294	2e-24	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10186	GM_158_A1_E06_MR	g3063446	BLASTX	250	5e-19	90	(AC003981) F22O13.8 [Arabidopsis thaliana]
10187	GM_158_A1_E07_T7	g421955	BLASTX	282	2e-27	56	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
10188	GM_158_A1_E08_T7	g3150402	BLASTX	151	2e-09	90	(AC004165) putative malonyl-CoA:Acyl carrier protein transacylase [Arabidopsis thaliana]
10189	GM_158_A1_E09_T7	g507910	BLASTN	385	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10190	GM_158_A1_E12_MR	g131150	BLASTX	520	3e-49	79	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2 gi 81515 pir S00445 photosystem I protein A2 - spinach chloroplast gi 12271 (X04131) psaB gene product (aa 1-734) P700 chlorophyll a apoprotein [Spinacia oleracea] gi 225422 prf 1303218B gene psaB [Spinacia oleracea]
10191	GM_158_A1_F01_T7	g3142328	BLASTN	2008	2e-84	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10192	GM_158_A1_F02_T7	g4038056	BLASTX	289	2e-23	46	(AC005897) putative transposon [Arabidopsis thaliana]
10193	GM_158_A1_F03_MR	g507910	BLASTN	678	5e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
10194	GM_158_A1_F03_T7	g4098865	BLASTN	352	5e-09	62	Dictyostelium discoideum unknown protein gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10195	GM_158_A1_F04_MR	g3033389	BLASTX	164	3e-10	35	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
10196	GM_158_A1_F05_MR	g3142328	BLASTN	1189	6e-47	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10197	GM_158_A1_F06_T7	g507910	BLASTN	576	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
10198	GM_158_A1_F07_T7	g3600045	BLASTN	361	3e-10	74	Arabidopsis thaliana BAC F2P3
10199	GM_158_A1_F12_T7	g1813979	BLASTX	190	4e-23	70	(Y10860) hypothetical protein [Musa acuminata]
10200	GM_158_A1_G03_MR	g4063760	BLASTX	385	1e-33	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10201	GM_158_A1_G03_T7	g3645899	BLASTX	228	6e-17	52	(U68408) 5' end not determined experimentally [Zea mays]
10202	GM_158_A1_G04_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10203	GM_158_A1_G04_T7	g507910	BLASTN	397	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10204	GM_158_A1_G06_T7	g2351063	BLASTN	410	2e-11	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19
10205	GM_158_A1_H01_MR	g507910	BLASTN	601	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10206	GM_158_A1_H02_MR	g3241923	BLASTN	476	2e-14	72	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]
10207	GM_158_A1_H04_MR	g4056432	BLASTX	146	1e-08	43	(AC005990) Similar to gi 2245014 glucosyltransferase homolog from Arabidopsis thaliana chromosome 4 contig gb Z97341. ESTs gb T20778 and gb AA586281 come from this gene. [Arabidopsis thaliana]
10208	GM_158_A1_H06_MR	g507910	BLASTN	413	5e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10209	GM_158_A2_A01_T7	g14227	BLASTN	424	5e-13	67	Yeast cytochrome c oxidase transcription initiation region subunit 1 (COX1) from mitochondrial DNA
10210	GM_158_A2_A04_MR	g3777527	BLASTX	273	8e-24	52	(AF053008) gag-pol polyprotein [Glycine max]
10211	GM_158_A2_A05_MR	g4063760	BLASTX	212	4e-15	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10212	GM_158_A2_A06_T7	g3097320	BLASTN	431	2e-12	68	Glycine max gene for Bd 30K, complete cds
10213	GM_158_A2_A11_MR	g3845197	BLASTN	447	4e-13	63	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
10214	GM_158_A2_A12_T7	g3777527	BLASTX	559	6e-52	91	(AF053008) gag-pol polyprotein [Glycine max]
10215	GM_158_A2_B03_T7	g3142328	BLASTN	616	7e-21	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10216	GM_158_A2_B05_T7	g2760839	BLASTX	178	7e-12	36	(AC003105) putative receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10217	GM_158_A2_B12_T7	g130582	BLASTX	171	1e-10	34	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
10218	GM_158_A2_C02_T7	g4063760	BLASTX	214	2e-15	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10219	GM_158_A2_C03_T7	g3097320	BLASTN	464	6e-14	73	Glycine max gene for Bd 30K, complete cds
10220	GM_158_A2_C04_T7	g4063760	BLASTX	454	5e-41	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10221	GM_158_A2_C06_T7	g2129559	BLASTX	158	8e-10	62	cellulase homolog OR16pep - Arabidopsis thaliana gi 1022807 (U37702) cellulase [Arabidopsis thaliana] gi 3493633 (AF074092) cellulase [Arabidopsis thaliana] gi 3598956 (AF074375) cellulase [Arabidopsis thaliana]
10222	GM_158_A2_C08_T7	g3645899	BLASTX	308	2e-25	55	(U68408) 5' end not determined experimentally [Zea mays]
10223	GM_158_A2_C09_MR	g2995405	BLASTX	226	3e-18	41	(Y12432) polyprotein [Ananas comosus]
10224	GM_158_A2_C10_MR	g3763969	BLASTN	361	3e-09	66	Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE ...
10225	GM_158_A2_C12_MR	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10226	GM_158_A2_D02_MR	g133917	BLASTX	108	2e-11	80	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 gi 70856 pir R3NT2 ribosomal protein S2 - common tobacco chloroplast gi 11814 (Z00044) ribosomal protein S2 [Nicotiana tabacum] gi 225274 prf 1211235J ribosomal protein S2 [Nicotiana tabacum]
10227	GM_158_A2_D04_MR	g2129618	BLASTX	178	1e-11	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10228	GM_158_A2_D06_MR	g3930515	BLASTX	115	8e-12	46	(AF059674) putative gag protein [Nicotiana tabacum]
10229	GM_158_A2_E02_T7	g130582	BLASTX	207	3e-31	56	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
10230	GM_158_A2_E03_MR	g2522227	BLASTX	214	8e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10231	GM_158_A2_E06_T7	g1171046	BLASTX	144	2e-09	59	METALLOTHIONEIN-LIKE PROTEIN B gi 480753 pir S37240 metallothionein-like protein - white clover gi 403329 (Z26493) metallothionein-like protein [Trifolium repens]
10232	GM_158_A2_E07_T7	g507910	BLASTN	548	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
10233	GM_158_A2_E08_T7	g1136741	BLASTX	168	6e-11	50	(D42052) predicted protein of 548 amino acids [Homo sapiens]
10234	GM_158_A2_E12_MR	g2282576	BLASTX	133	3e-11	59	(U77700) HsGCN1 [Homo sapiens]
10235	GM_158_A2_F03_T7	g3426334	BLASTN	366	1e-09	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
10236	GM_158_A2_F04_T7	g4038056	BLASTX	333	3e-28	45	(AC005897) putative transposon [Arabidopsis thaliana]
10237	GM_158_A2_F12_T7	g2769655	BLASTN	492	3e-15	64	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
10238	GM_158_A2_G01_MR	g4063770	BLASTX	195	1e-13	39	(AB004906) transposase [Ipomoea purpurea]
10239	GM_158_A2_G01_T7	g1142703	BLASTN	248	2e-12	72	Glycine max satellite STR120-B.1.
10240	GM_158_A2_G05_MR	g2583130	BLASTX	187	2e-12	35	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
10241	GM_158_A2_H01_T7	g4063760	BLASTX	272	1e-21	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10242	GM_158_A2_H02_MR	g1524103	BLASTN	376	6e-10	65	Human DNA sequence from cosmid U223G7, between markers DXS6791 and DXS8038 on chromosome X
10243	GM_158_A2_H09_T7	g505129	BLASTN	403	3e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10244	GM_158_B1_A02_MR	g82166	BLASTX	174	7e-12	87	glyceraldehyde-3-phosphate dehydrogenase (NADP+) (phosphorylating) (EC 1.2.1.13) B, chloroplast - common tobacco (fragment)
10245	GM_158_B1_A02_T7	g1171583	BLASTN	539	2e-17	69	P.falciparum complete gene map of plastid-like DNA (IR-A)
10246	GM_158_B1_A09_MR	g3461840	BLASTX	349	1e-29	46	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
10247	GM_158_B1_A09_T7	g4098966	BLASTN	1562	1e-64	82	Glycine max putative reistance gene analog genomic sequence
10248	GM_158_B1_A10_T7	g3176795	BLASTN	346	5e-09	63	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
10249	GM_158_B1_A12_MR	g1708464	BLASTX	164	2e-10	58	PUTATIVE DIHYDROXY-ACID DEHYDRATASE PRECURSOR (DAD) (2,3-DIHYDROXY ACID HYDROLYASE) gi 1213255 (Z69795) unknown [Schizosaccharomyces pombe]
10250	GM_158_B1_B03_T7	g3650035	BLASTX	171	7e-11	42	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
10251	GM_158_B1_B07_T7	g2462058	BLASTX	211	2e-16	61	(Y13389) reverse transcriptase [Antirrhinum majus]
10252	GM_158_B1_B12_T7	g13597	BLASTN	373	5e-10	66	Yeast mitochondrial tRNA genes for tRNA-Ala, tRNA-Tyr and tRNA-Ile

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10253	GM_158_B1_C05_T7	g507910	BLASTN	596	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
10254	GM_158_B1_C08_MR	g1769898	BLASTX	507	7e-48	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10255	GM_158_B1_C11_T7	g1480927	BLASTN	872	8e-33	80	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
10256	GM_158_B1_C12_MR	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10257	GM_158_B1_C12_T7	g2769655	BLASTN	519	2e-16	71	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
10258	GM_158_B1_D03_T7	g507910	BLASTN	514	1e-16	79	Glycine max BSR-101 satellite SB92 genomic sequence.
10259	GM_158_B1_D08_T7	g1136228	BLASTX	210	5e-15	40	(U32986) UV-damaged DNA binding factor [Homo sapiens] gi 1588524 prf 2208446A xeroderma pigmentosum group E-binding factor [Homo sapiens]
10260	GM_158_B1_D12_T7	g2244840	BLASTX	173	2e-12	52	(Z97337) hypothetical protein [Arabidopsis thaliana]
10261	GM_158_B1_E03_T7	g2244840	BLASTX	235	4e-19	46	(Z97337) hypothetical protein [Arabidopsis thaliana]
10262	GM_158_B1_F03_MR	g4115365	BLASTX	244	2e-18	53	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
10263	GM_158_B1_F07_MR	g1171591	BLASTN	367	9e-12	65	P.falciparum complete gene map of plastid-like DNA (IR-B)
10264	GM_158_B1_F08_MR	g4115365	BLASTX	329	1e-27	56	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
10265	GM_158_B1_G04_T7	g2760830	BLASTX	506	1e-47	75	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]
10266	GM_158_B1_G08_T7	g2564048	BLASTN	395	8e-11	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD15, complete sequence [Arabidopsis thaliana]
10267	GM_158_B1_G11_T7	g3600044	BLASTX	189	1e-12	43	(AF080119) contains similarity to proteases [Arabidopsis thaliana]
10268	GM_158_B1_H07_T7	g3860242	BLASTN	501	1e-15	72	Arabidopsis thaliana chromosome I BAC T13M11 genomic sequence, complete sequence [Arabidopsis thaliana]
10269	GM_158_B1_H08_MR	g3549672	BLASTX	162	1e-10	38	(AL031394) putative protein [Arabidopsis thaliana]
10270	GM_158_B1_H09_MR	g2522227	BLASTX	186	9e-14	54	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
10271	GM_158_B1_H10_MR	g2522230	BLASTX	270	1e-22	41	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
10272	GM_158_B1_H10_T7	g18768	BLASTN	455	3e-14	81	Soybean Tgm6 transposable element 3' end
10273	GM_158_B2_B07_T7	g3777527	BLASTX	154	2e-11	49	(AF053008) gag-pol polyprotein [Glycine max]
10274	GM_158_B2_B08_T7	g2583130	BLASTX	172	8e-11	42	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
10275	GM_158_B2_C01_T7	g905361	BLASTX	429	3e-39	95	(U22103) gag-protease polyprotein [Glycine max]
10276	GM_158_B2_C06_T7	g18559	BLASTN	348	1e-08	69	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10277	GM_158_B2_C10_T7	g3941442	BLASTX	173	7e-12	57	(AF062875) putative transcription factor [Arabidopsis thaliana]
10278	GM_158_B2_D06_T7	g3142300	BLASTX	269	4e-21	56	(AC002411) Contains similarity to pre-mRNA processing protein PRP39 gb L29224 from S. cerevisiae. ESTs gb R64908 and gb T88158, gb N38703 and gb AA651043 come from this gene. [Arabidopsis thaliana]
10279	GM_158_B2_D09_T7	g2290780	BLASTX	231	1e-18	52	(AF002667) heat shock cognate protein [Solanum commersonii]
10280	GM_158_B2_E02_T7	g1370287	BLASTX	93	4e-11	100	(Z73553) core protein [Pisum sativum]
10281	GM_159_A1_A02_T7	g507910	BLASTN	501	5e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
10282	GM_159_A1_A03_MR	g2864621	BLASTX	150	4e-09	46	hypothetical protein [Arabidopsis thaliana]
10283	GM_159_A1_A04_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10284	GM_159_A1_A07_T7	g2129675	BLASTX	120	4e-16	75	probable chlorophyll synthetase G4 - Arabidopsis thaliana gi 972938 (U19382) putative chlorophyll synthetase [Arabidopsis thaliana] gi 3068709 (AF049236) putative chlorophyll synthetase [Arabidopsis thaliana]
10285	GM_159_A1_A10_T7	g4063760	BLASTX	105	1e-08	30	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10286	GM_159_A1_B03_T7	g18559	BLASTN	393	9e-11	71	G.max gene for catalase
10287	GM_159_A1_B05_T7	g507910	BLASTN	557	1e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
10288	GM_159_A1_B06_MR	g507910	BLASTN	426	1e-12	80	Glycine max BSR-101 satellite SB92 genomic sequence.
10289	GM_159_A1_B06_T7	g507910	BLASTN	561	1e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
10290	GM_159_A1_B07_MR	g905361	BLASTX	257	2e-20	87	(U22103) gag-protease polyprotein [Glycine max]
10291	GM_159_A1_B08_T7	g2832611	BLASTN	355	5e-09	61	Arabidopsis thaliana DNA chromosome 4, BAC clone F13C5 (ESSAII project)
10292	GM_159_A1_B09_MR	g3378224	BLASTX	197	5e-15	66	(AJ001213) reverse transcriptase [Lycopersicon chilense]
10293	GM_159_A1_B10_T7	g1769897	BLASTX	171	3e-11	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10294	GM_159_A1_C01_T7	g20035	BLASTN	440	7e-13	75	Tobacco anther-specific gene TA-29 and stem-specific gene TSJT1
10295	GM_159_A1_C04_MR	g4063756	BLASTN	476	2e-14	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
10296	GM_159_A1_D03_MR	g507910	BLASTN	374	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10297	GM_159_A1_D03_T7	g507910	BLASTN	560	1e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
10298	GM_159_A1_D05_T7	g3757543	BLASTN	360	3e-09	60	Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence [Homo sapiens]
10299	GM_159_A1_D06_T7	g2924777	BLASTX	170	1e-10	42	(AC002334) putative receptor protein kinase [Arabidopsis thaliana]
10300	GM_159_A1_D08_MR	g2832612	BLASTX	198	4e-15	38	(AL021711) putative protein (fragment) [Arabidopsis thaliana]
10301	GM_159_A1_D08_T7	g3080374	BLASTX	276	3e-22	40	(AL022580) putative protein [Arabidopsis thaliana]
10302	GM_159_A1_E02_T7	g3810596	BLASTX	371	3e-32	43	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10303	GM_159_A1_E04_MR	g130582	BLASTX	437	4e-39	66	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
10304	GM_159_A1_E07_T7	g507910	BLASTN	384	9e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10305	GM_159_A1_E10_T7	g3142379	BLASTX	430	1e-39	74	(AF053008) envelope-like [Glycine max]
10306	GM_159_A1_E11_T7	g3645899	BLASTX	203	3e-14	60	(U68408) 5' end not determined experimentally [Zea mays]
10307	GM_159_A1_F02_T7	g2129618	BLASTX	215	1e-15	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10308	GM_159_A1_F03_MR	g2501496	BLASTX	152	8e-10	58	FLAVONOL 3-O-GLUCOSYLTRANSFERASE 7 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 7) gi 542017 pir S41953 UTP-glucose glucosyltransferase - cassava gi 453253 (X77464) UTP-glucose glucosyltransferase [Manihot esculenta]
10309	GM_159_A1_F03_T7	g1906826	BLASTX	158	1e-09	84	(Y11827) heat shock protein [Arabidopsis thaliana]
10310	GM_159_A1_F04_T7	g2982459	BLASTX	225	6e-18	81	(AL022223) putative protein [Arabidopsis thaliana]
10311	GM_159_A1_F05_T7	g531389	BLASTX	290	2e-23	40	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
10312	GM_159_A1_F08_MR	g1076570	BLASTX	245	4e-20	81	homeotic protein CHB6 - carrot
10313	GM_159_A1_F11_T7	g2708743	BLASTX	209	1e-14	36	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
10314	GM_159_A1_G01_T7	g4063760	BLASTX	263	1e-20	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10315	GM_159_A1_G04_MR	g99755	BLASTX	283	3e-23	47	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
10316	GM_159_A1_G08_MR	g3142328	BLASTN	1062	4e-41	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10317	GM_159_A1_G08_T7	g505129	BLASTN	402	3e-11	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10318	GM_159_A1_G11_MR	g3142379	BLASTX	221	6e-17	72	(AF053008) envelope-like [Glycine max]
10319	GM_159_A1_G11_T7	g18559	BLASTN	367	1e-09	63	G.max gene for catalase
10320	GM_159_A1_H04_MR	g905361	BLASTX	168	7e-11	37	(U22103) gag-protease polyprotein [Glycine max]
10321	GM_159_A1_H04_T7	g414863	BLASTN	285	4e-10	61	A.longa plastid genes for ribosomal proteins and tRNAs
10322	GM_159_A1_H05_MR	g507910	BLASTN	350	3e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10323	GM_159_A1_H05_T7	g4063760	BLASTX	388	5e-34	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10324	GM_159_A1_H07_T7	g3777527	BLASTX	777	3e-75	97	(AF053008) gag-pol polyprotein [Glycine max]
10325	GM_159_A2_B01_MR	g3097320	BLASTN	448	3e-13	73	Glycine max gene for Bd 30K, complete cds
10326	GM_159_A2_B02_MR	g507910	BLASTN	349	4e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10327	GM_159_A2_B02_T7	g4063760	BLASTX	351	6e-30	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10328	GM_159_A2_B03_T7	g2244753	BLASTX	385	3e-34	52	(Z97335) hypothetical protein [Arabidopsis thaliana]
10329	GM_159_A2_B04_MR	g2129618	BLASTX	176	2e-11	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10330	GM_159_A2_B05_MR	g1142702	BLASTN	1147	3e-45	98	Glycine max satellite STR120-A.4.
10331	GM_159_A2_B07_T7	g905360	BLASTN	979	1e-37	87	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
10332	GM_159_A2_B11_MR	g2665890	BLASTX	195	6e-14	66	(AF035944) calcium-dependent protein kinase [Fragaria x ananassa]
10333	GM_159_A2_C09_MR	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10334	GM_159_A2_C09_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10335	GM_159_A2_D04_T7	g3142328	BLASTN	796	4e-29	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10336	GM_159_A2_D05_MR	g2995405	BLASTX	452	3e-42	62	(Y12432) polyprotein [Ananas comosus]
10337	GM_159_A2_D06_MR	g507910	BLASTN	397	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10338	GM_159_A2_D08_T7	g3097320	BLASTN	1393	4e-56	83	Glycine max gene for Bd 30K, complete cds
10339	GM_159_A2_D09_T7	g2982550	BLASTN	353	7e-09	66	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-65, complete sequence [Plasmodium falciparum]
10340	GM_159_A2_D10_MR	g3033400	BLASTX	155	7e-13	56	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]
10341	GM_159_A2_D10_T7	g3319353	BLASTX	162	4e-19	45	(AF077407) contains similarity to copper-binding proteins [Arabidopsis thaliana]
10342	GM_159_A2_E04_T7	g3097320	BLASTN	719	2e-25	74	Glycine max gene for Bd 30K, complete cds
10343	GM_159_A2_E11_MR	g3980264	BLASTX	215	6e-17	95	(AJ011383) 20S proteasome beta subunit [Cicer arietinum]
10344	GM_159_A2_E12_T7	g507910	BLASTN	625	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10345	GM_159_A2_F02_MR	g662924	BLASTX	173	2e-12	55	(Z46952) heat shock transcription factor 21 [Glycine max]
10346	GM_159_A2_F04_T7	g18559	BLASTN	985	1e-37	76	G.max gene for catalase
10347	GM_159_A2_F05_MR	g3142328	BLASTN	650	2e-22	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10348	GM_159_A2_G01_T7	g18559	BLASTN	373	7e-10	72	G.max gene for catalase
10349	GM_159_A2_G02_MR	g1666236	BLASTX	157	3e-10	31	(U76261) unknown [Hordeum vulgare]
10350	GM_159_A2_G03_T7	g1572819	BLASTX	150	3e-13	40	(U70855) similar to the RAS gene family [Caenorhabditis elegans]
10351	GM_159_A2_G08_T7	g4038056	BLASTX	354	1e-30	52	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10352	GM_159_A2_G09_MR	g4063760	BLASTX	518	8e-48	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10353	GM_159_A2_G12_T7	g2462134	BLASTX	252	4e-20	40	(Y13368) reverse transcriptase [Beta vulgaris]
10354	GM_159_A2_H01_MR	g4063760	BLASTX	182	6e-12	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10355	GM_159_A2_H01_T7	g507910	BLASTN	635	4e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10356	GM_159_A2_H03_MR	g905361	BLASTX	693	2e-67	96	(U22103) gag-protease polyprotein [Glycine max]
10357	GM_159_A2_H03_T7	g3142328	BLASTN	532	4e-17	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10358	GM_159_A2_H07_T7	g4063770	BLASTX	148	4e-20	45	(AB004906) transposase [Ipomoea purpurea]
10359	GM_159_B2_A02_T7	g507910	BLASTN	555	2e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
10360	GM_159_B2_A08_MR	g2392762	BLASTN	352	7e-09	69	Arabidopsis thaliana BAC T32N15 from chromsome V, complete sequence [Arabidopsis thaliana]
10361	GM_159_B2_A09_MR	g507910	BLASTN	346	5e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
10362	GM_159_B2_A09_T7	g507910	BLASTN	379	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10363	GM_159_B2_A11_T7	g2522230	BLASTX	267	2e-22	41	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
10364	GM_159_B2_B03_MR	g3097320	BLASTN	806	2e-29	78	Glycine max gene for Bd 30K, complete cds
10365	GM_159_B2_B03_T7	g3142328	BLASTN	689	3e-24	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10366	GM_159_B2_B08_MR	g2209031	BLASTX	258	9e-21	49	(AB001569) ORF of 1.56 kb [Daucus carota]
10367	GM_159_B2_B09_MR	g3142328	BLASTN	843	3e-31	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10368	GM_159_B2_B12_T7	g1666236	BLASTX	201	4e-15	39	(U76261) unknown [Hordeum vulgare]
10369	GM_159_B2_C02_MR	g3319362	BLASTX	189	9e-24	59	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
10370	GM_159_B2_C07_T7	g3319362	BLASTX	220	4e-16	49	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
10371	GM_159_B2_C11_MR	g4038056	BLASTX	326	2e-27	57	(AC005897) putative transposon [Arabidopsis thaliana]
10372	GM_159_B2_D02_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10373	GM_159_B2_D03_MR	g4092471	BLASTN	446	4e-13	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
10374	GM_159_B2_D04_MR	g3426334	BLASTN	384	2e-10	66	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
10375	GM_159_B2_D07_T7	g3097320	BLASTN	459	9e-14	78	Glycine max gene for Bd 30K, complete cds
10376	GM_159_B2_D08_MR	g18695	BLASTN	417	5e-12	72	Soybean nodulin 22 gene
10377	GM_159_B2_D09_MR	g507910	BLASTN	350	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10378	GM_159_B2_D09_T7	g507910	BLASTN	365	7e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10379	GM_159_B2_E01_MR	g2522228	BLASTX	245	1e-19	70	(AB007466) reverse transcriptase-like protein [Vicia faba]
10380	GM_159_B2_E04_MR	g1769898	BLASTX	338	3e-29	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10381	GM_159_B2_F04_MR	g18559	BLASTN	558	3e-18	75	G.max gene for catalase
10382	GM_159_B2_F08_MR	g905361	BLASTX	176	1e-11	40	(U22103) gag-protease polyprotein [Glycine max]
10383	GM_159_B2_F10_T7	g507910	BLASTN	574	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
10384	GM_159_B2_F11_MR	g3645899	BLASTX	344	2e-29	59	(U68408) 5' end not determined experimentally [Zea mays]
10385	GM_159_B2_G04_MR	g905360	BLASTN	1146	2e-45	91	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
10386	GM_159_B2_G06_MR	g3645899	BLASTX	327	2e-27	57	(U68408) 5' end not determined experimentally [Zea mays]
10387	GM_159_B2_G06_T7	g3097320	BLASTN	418	7e-12	69	Glycine max gene for Bd 30K, complete cds
10388	GM_159_B2_H01_MR	g3142330	BLASTX	548	4e-52	95	(U96295) envelope-like [Glycine max]
10389	GM_159_B2_H03_T7	g1524103	BLASTN	489	5e-15	64	Human DNA sequence from cosmid U223G7, between markers DXS6791 and DXS8038 on chromosome X
10390	GM_159_B2_H05_T7	g4063760	BLASTX	192	2e-27	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10391	GM_159_B2_H06_T7	g4050011	BLASTN	395	8e-11	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
10392	GM_159_B2_H07_MR	g3777527	BLASTX	390	6e-34	66	(AF053008) gag-pol polyprotein [Glycine max]
10393	GM_159_B2_H11_MR	g3522945	BLASTX	180	3e-12	49	(AC004411) putative cytochrome P450 [Arabidopsis thaliana]
10394	GM_159_B2_H11_T7	g4006885	BLASTN	355	5e-09	63	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No. 2
10395	GM_160_A1_A02_T7	g2462936	BLASTX	273	5e-23	56	(Y12321) open reading frame 2 [Brassica oleracea]
10396	GM_160_A1_A07_T7	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
10397	GM_160_A1_A09_T7	g905361	BLASTX	232	1e-17	34	(U22103) gag-protease polyprotein [Glycine max]
10398	GM_160_A1_A12_T7	g226407	BLASTX	165	5e-10	45	retrotransposon del1-46 [Lilium henryi]
10399	GM_160_A1_B01_T7	g3176774	BLASTN	339	5e-09	61	Homo sapiens allele 3 fragile site locus (FRA10B) minisatellite, 3' sequence
10400	GM_160_A1_B05_MR	g3142328	BLASTN	1756	8e-73	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10401	GM_160_A1_B07_T7	g2443320	BLASTX	221	5e-16	43	(D85597) polyprotein [Oryza australiensis]
10402	GM_160_A1_B09_T7	g3913525	BLASTX	165	3e-10	100	DNA POLYMERASE DELTA CATALYTIC CHAIN >gi 2895198 (AF020193) DNA polymerase delta [Glycine max]
10403	GM_160_A1_C06_T7	g3097320	BLASTN	1014	7e-39	79	Glycine max gene for Bd 30K, complete cds
10404	GM_160_A1_C07_T7	g505129	BLASTN	383	2e-10	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10405	GM_160_A1_D02_T7	g1666236	BLASTX	221	2e-17	33	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10406	GM_160_A1_D05_T7	g2982431	BLASTX	233	2e-17	52	(AL022224) leucine rich repeat-like protein [Arabidopsis thaliana]
10407	GM_160_A1_D07_T7	g2244899	BLASTX	189	6e-13	60	(Z97338) similar to UFD1 protein [Arabidopsis thaliana]
10408	GM_160_A1_E08_T7	g2832258	BLASTN	392	8e-11	74	Medicago sativa ENOD40-2 promoter sequence
10409	GM_160_A1_E10_T7	g1666236	BLASTX	162	9e-11	36	(U76261) unknown [Hordeum vulgare]
10410	GM_160_A1_F01_T7	g4115365	BLASTX	149	2e-10	32	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
10411	GM_160_A1_F04_MR	g3097320	BLASTN	961	2e-36	80	Glycine max gene for Bd 30K, complete cds
10412	GM_160_A1_F04_T7	g226407	BLASTX	389	6e-34	47	retrotransposon del1-46 [Lilium henryi]
10413	GM_160_A1_F05_MR	g1142703	BLASTN	474	6e-15	88	Glycine max satellite STR120-B.1.
10414	GM_160_A1_F06_T7	g3142328	BLASTN	879	6e-42	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10415	GM_160_A1_F10_T7	g3367587	BLASTX	152	7e-10	35	(AL031135) putative protein [Arabidopsis thaliana]
10416	GM_160_A1_G04_MR	g3142328	BLASTN	761	2e-27	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10417	GM_160_A1_G09_MR	g905361	BLASTX	674	2e-65	87	(U22103) gag-protease polyprotein [Glycine max]
10418	GM_160_A1_G09_T7	g3142328	BLASTN	1702	2e-70	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10419	GM_160_A1_G12_T7	g507910	BLASTN	348	4e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10420	GM_160_A1_H01_T7	g2088656	BLASTX	171	6e-11	36	(AF002109) DNA-directed RNA polymerase II isolog [Arabidopsis thaliana]
10421	GM_160_A1_H04_T7	g3777527	BLASTX	231	3e-20	45	(AF053008) gag-pol polyprotein [Glycine max]
10422	GM_160_A1_H09_T7	g116162	BLASTX	218	3e-17	63	G2/MITOTIC-SPECIFIC CYCLIN S13-7 (B-LIKE CYCLIN) gi 2146780 pir S74672 mitotic-specific cyclin S13-7 - soybean (fragment) gi 829266 (X62303) mitotic cyclin [Glycine max]
10423	GM_160_A2_B11_MR	g2181938	BLASTX	149	6e-10	87	(Y13477) mitochondrial elongation factor G [Leishmania mexicana]
10424	GM_160_A2_C03_MR	g18559	BLASTN	1043	3e-40	74	G.max gene for catalase
10425	GM_160_A2_C05_MR	g3777527	BLASTX	405	1e-35	58	(AF053008) gag-pol polyprotein [Glycine max]
10426	GM_160_A2_C09_MR	g1142702	BLASTN	634	4e-22	78	Glycine max satellite STR120-A.4.
10427	GM_160_A2_C12_MR	g4063760	BLASTX	474	4e-43	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10428	GM_160_A2_D03_MR	g18559	BLASTN	1000	3e-38	74	G.max gene for catalase
10429	GM_160_A2_D04_T7	g342952	BLASTN	340	3e-09	66	paramecium species 1,168 mt dna dimer: replication init. region.
10430	GM_160_A2_D05_MR	g3142328	BLASTN	1560	7e-64	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10431	GM_160_A2_D06_MR	g2809253	BLASTX	171	2e-11	32	(AC002560) F21B7.22 [Arabidopsis thaliana]
10432	GM_160_A2_D11_MR	g4063760	BLASTX	152	9e-09	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10433	GM_160_A2_E04_MR	g2995405	BLASTX	296	2e-24	52	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10434	GM_160_A2_E09_T7	g100484	BLASTX	215	9e-16	55	hypothetical protein - garden snapdragon
10435	GM_160_A2_F04_MR	g1666236	BLASTX	221	2e-17	31	(U76261) unknown [Hordeum vulgare]
10436	GM_160_A2_F06_MR	g3023817	BLASTX	259	8e-39	83	GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHOLOROPLAST ISOFORM PRECURSOR (G6PD) gi 1480344 gnl PID e254807 (X99405) glucose-6-phosphate dehydrogenase [Nicotiana tabacum]
10437	GM_160_A2_F08_MR	g3142328	BLASTN	635	9e-22	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10438	GM_160_A2_F09_T7	g4063760	BLASTX	149	3e-13	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10439	GM_160_A2_G03_MR	g541936	BLASTX	199	3e-15	62	4-coumarate--CoA ligase (EC 6.2.1.12) (clone GM4CL14) - soybean (fragment)
10440	GM_160_A2_G06_MR	g905361	BLASTX	119	3e-13	33	(U22103) gag-protease polyprotein [Glycine max]
10441	GM_160_A2_G10_MR	g507910	BLASTN	522	6e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
10442	GM_160_A2_G11_MR	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10443	GM_160_A2_H02_MR	g507910	BLASTN	346	5e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
10444	GM_160_A2_H06_MR	g1769897	BLASTX	156	3e-11	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10445	GM_160_B1_A04_T7	g4063760	BLASTX	334	3e-28	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10446	GM_160_B1_A08_MR	g3777527	BLASTX	318	3e-26	57	(AF053008) gag-pol polyprotein [Glycine max]
10447	GM_160_B1_A10_T7	g3142328	BLASTN	600	4e-20	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10448	GM_160_B1_B06_MR	g2522228	BLASTX	393	9e-36	79	(AB007466) reverse transcriptase-like protein [Vicia faba]
10449	GM_160_B1_B06_T7	g2104945	BLASTN	384	2e-10	70	Glycine max copia-like retrotransposon Tgmr, complete sequence
10450	GM_160_B1_B09_MR	g2462834	BLASTX	138	9e-09	36	(AF000657) hypothetical protein [Arabidopsis thaliana]
10451	GM_160_B1_C09_MR	g421955	BLASTX	173	4e-14	43	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
10452	GM_160_B1_D02_MR	g18559	BLASTN	975	3e-37	77	G.max gene for catalase
10453	GM_160_B1_D06_MR	g2995405	BLASTX	255	6e-20	52	(Y12432) polyprotein [Ananas comosus]
10454	GM_160_B1_D12_MR	g3097320	BLASTN	1277	8e-51	81	Glycine max gene for Bd 30K, complete cds
10455	GM_160_B1_D12_T7	g3142328	BLASTN	1240	3e-49	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10456	GM_160_B1_E10_T7	g4038056	BLASTX	283	6e-23	44	(AC005897) putative transposon [Arabidopsis thaliana]
10457	GM_160_B1_F01_MR	g3142293	BLASTX	348	5e-31	64	(AC002411) Contains similarity to myosin IB heavy chain gb X70400 from Gallus gallus. [Arabidopsis thaliana]
10458	GM_160_B1_F05_T7	g3810584	BLASTN	402	4e-11	66	Arabidopsis thaliana chromosome II BAC T6B13 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10459	GM_160_B1_F08_MR	g2443320	BLASTX	327	2e-27	46	(D85597) polyprotein [Oryza australiensis]
10460	GM_160_B1_F09_T7	g4063760	BLASTX	204	3e-25	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10461	GM_160_B1_G01_MR	g4063770	BLASTX	298	8e-26	56	(AB004906) transposase [Ipomoea purpurea]
10462	GM_160_B1_G03_MR	g3386604	BLASTX	223	1e-16	47	(AC004665) putative protein kinase [Arabidopsis thaliana]
10463	GM_160_B1_G06_MR	g629693	BLASTX	211	5e-16	45	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10464	GM_160_B1_H02_MR	g2501353	BLASTX	188	7e-21	81	TRANSKETOLASE, CHLOROPLAST (TK) gi 1084440 pir S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) gi 664901 (Z46646) transketolase [Craterostigma plantagineum]
10465	GM_160_B1_H06_T7	g3287679	BLASTX	229	5e-17	74	(AC003979) T22J18.6 [Arabidopsis thaliana]
10466	GM_160_B2_A02_T7	g3142328	BLASTN	588	1e-19	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10467	GM_160_B2_A10_T7	g4063760	BLASTX	109	1e-12	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10468	GM_160_B2_B02_MR	g2264320	BLASTN	454	2e-13	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
10469	GM_160_B2_B04_MR	g1666236	BLASTX	182	5e-13	30	(U76261) unknown [Hordeum vulgare]
10470	GM_160_B2_B06_MR	g1666236	BLASTX	148	3e-09	27	(U76261) unknown [Hordeum vulgare]
10471	GM_160_B2_B07_MR	g20861	BLASTN	432	1e-12	69	P.sativum retrotransposon
10472	GM_160_B2_B09_T7	g2522227	BLASTX	209	3e-16	53	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
10473	GM_160_B2_B10_T7	g507910	BLASTN	389	6e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10474	GM_160_B2_C09_T7	g3249064	BLASTX	154	3e-16	60	(AC004473) Strong similarity to trehalose-6-phosphate synthase homolog gb 2245136 from A. thaliana chromosome 4 contig gb Z97344. [Arabidopsis thaliana]
10475	GM_160_B2_D01_T7	g3377855	BLASTX	306	2e-26	71	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
10476	GM_160_B2_D03_MR	g507910	BLASTN	378	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10477	GM_160_B2_E01_T7	g3426334	BLASTN	366	1e-09	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
10478	GM_160_B2_E03_MR	g507910	BLASTN	360	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10479	GM_160_B2_E03_T7	g507910	BLASTN	347	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10480	GM_160_B2_E07_MR	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
10481	GM_160_B2_E09_T7	g4063760	BLASTX	426	5e-38	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10482	GM_160_B2_E10_T7	g4106408	BLASTN	430	1e-12	73	Oryza sativa subsp. indica dispersed centromeric repeat family RCS1
10483	GM_160_B2_E11_MR	g3097320	BLASTN	1076	1e-41	82	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10484	GM_160_B2_F03_MR	g4063760	BLASTX	218	2e-19	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10485	GM_160_B2_F06_MR	g905361	BLASTX	566	2e-56	98	(U22103) gag-protease polyprotein [Glycine max]
10486	GM_160_B2_F12_MR	g130582	BLASTX	159	2e-09	37	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
10487	GM_160_B2_G05_MR	g2495155	BLASTX	233	6e-18	60	GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) gi 1694926 gnl PID d1009544 (D50407) glutamyl-tRNA reductase [Cucumis sativus]
10488	GM_160_B2_G06_T7	g3142328	BLASTN	1376	2e-55	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10489	GM_160_B2_G08_MR	g507910	BLASTN	551	3e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
10490	GM_160_B2_G08_T7	g507910	BLASTN	462	3e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.
10491	GM_160_B2_H07_MR	g3142328	BLASTN	746	8e-27	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10492	GM_161_A1_A03_T7	g4050011	BLASTN	533	4e-17	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
10493	GM_161_A1_A05_T7	g226407	BLASTX	171	1e-10	31	retrotransposon del1-46 [Lilium henryi]
10494	GM_161_A1_A08_T7	g507910	BLASTN	360	1e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10495	GM_161_A1_A09_T7	g421954	BLASTX	299	7e-25	44	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
10496	GM_161_A1_A10_MR	g3777527	BLASTX	583	2e-54	96	(AF053008) gag-pol polyprotein [Glycine max]
10497	GM_161_A1_A11_MR	g3142328	BLASTN	526	8e-17	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10498	GM_161_A1_A11_T7	g3777527	BLASTX	176	3e-11	35	(AF053008) gag-pol polyprotein [Glycine max]
10499	GM_161_A1_B03_T7	g3142328	BLASTN	639	6e-22	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10500	GM_161_A1_B05_T7	g342965	BLASTN	345	5e-09	61	paramecium species 7,227 mt dna dimer: replication init. region.
10501	GM_161_A1_B09_MR	g3449333	BLASTN	355	5e-09	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXF12, complete sequence [Arabidopsis thaliana]
10502	GM_161_A1_B10_MR	g507910	BLASTN	601	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10503	GM_161_A1_D02_T7	g1732513	BLASTX	186	8e-14	68	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]
10504	GM_161_A1_D03_T7	g3097320	BLASTN	525	1e-16	74	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10505	GM_161_A1_D05_MR	g3402749	BLASTX	148	5e-11	43	(AL031187) putative protein [Arabidopsis thaliana]
10506	GM_161_A1_D08_T7	g563247	BLASTX	646	9e-63	90	(U16279) acetolactate synthase precursor [Xanthium sp.]
10507	GM_161_A1_D10_MR	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10508	GM_161_A1_D10_T7	g507910	BLASTN	619	2e-21	85	Glycine max BSR-101 satellite SB92 genomic sequence.
10509	GM_161_A1_D12_MR	g17918	BLASTN	359	4e-10	64	B.oleracea encoding S-receptor kinase protein.
10510	GM_161_A1_E05_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10511	GM_161_A1_E06_MR	g629693	BLASTX	169	2e-11	35	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10512	GM_161_A1_E06_T7	g1076755	BLASTX	528	1e-49	79	protein kinase - rice gi 450300 (L27821) protein kinase [Oryza sativa]
10513	GM_161_A1_E08_MR	g3377848	BLASTX	149	2e-12	49	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
10514	GM_161_A1_F07_T7	g421955	BLASTX	193	4e-30	61	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
10515	GM_161_A1_F08_MR	g114532	BLASTX	432	6e-40	88	ATP SYNTHASE ALPHA CHAIN gi 67824 pir PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast gi 11769 (V00162) alpha subunit of ATPase [Nicotiana tabacum] gi 11811 (Z00044) ATPase alpha subunit [Nicotiana tabacum] gi 225270 prf 1211235E ATPase alpha [Nicotiana tabacum]
10516	GM_161_A1_G10_T7	g507910	BLASTN	367	6e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10517	GM_161_A1_G12_T7	g3142328	BLASTN	724	8e-26	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10518	GM_161_A1_H01_MR	g4063760	BLASTX	257	6e-20	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10519	GM_161_A1_H02_T7	g905361	BLASTX	241	1e-18	41	(U22103) gag-protease polyprotein [Glycine max]
10520	GM_161_A1_H03_T7	g3142328	BLASTN	1499	4e-61	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10521	GM_161_A1_H05_MR	g1769898	BLASTX	199	3e-21	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10522	GM_161_A1_H08_MR	g4063760	BLASTX	373	2e-32	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10523	GM_161_A1_H09_MR	g507910	BLASTN	378	2e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10524	GM_161_A2_B04_MR	g2183226	BLASTN	343	7e-09	62	Dictyostelium discoideum calmodulin-like protein (calB) gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10525	GM_161_A2_B07_MR	g130398	BLASTX	183	4e-12	47	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 297) gi 85089 pir B24872 retrovirus-related pol polyprotein homolog - fruit fly (Drosophila melanogaster) transposon 297
10526	GM_161_A2_B08_MR	g4063760	BLASTX	432	1e-38	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10527	GM_161_A2_B10_T7	g4150930	BLASTN	385	2e-10	61	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
10528	GM_161_A2_B11_MR	g4063760	BLASTX	155	8e-16	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10529	GM_161_A2_B11_T7	g3176795	BLASTN	424	8e-13	63	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
10530	GM_161_A2_B12_T7	g3845148	BLASTN	376	6e-10	61	Plasmodium falciparum chromosome 2, section 23 of 73 of the complete sequence
10531	GM_161_A2_C02_MR	g1532163	BLASTX	206	5e-16	64	(U63815) similar to glutaredoxin encoded by GenBank Accession Number Z49699; localized according to blastn similarity to EST sequences; therefore, the coding span corresponds only to an area of similarity since the initation codon and stop c...
10532	GM_161_A2_C02_T7	g2961349	BLASTX	128	5e-09	34	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
10533	GM_161_A2_C03_T7	g507910	BLASTN	483	3e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
10534	GM_161_A2_C06_MR	g507910	BLASTN	377	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10535	GM_161_A2_C06_T7	g507910	BLASTN	341	8e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10536	GM_161_A2_C09_T7	g1769898	BLASTX	117	5e-10	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10537	GM_161_A2_C11_MR	g2764526	BLASTN	742	2e-26	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
10538	GM_161_A2_D04_MR	g3513745	BLASTX	156	5e-09	32	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
10539	GM_161_A2_D06_MR	g4063760	BLASTX	232	3e-17	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10540	GM_161_A2_D07_MR	g3777527	BLASTX	208	5e-30	88	(AF053008) gag-pol polyprotein [Glycine max]
10541	GM_161_A2_D07_T7	g1167523	BLASTX	358	1e-30	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
10542	GM_161_A2_D10_MR	g3777527	BLASTX	579	4e-54	94	(AF053008) gag-pol polyprotein [Glycine max]
10543	GM_161_A2_D12_T7	g4056486	BLASTX	300	2e-25	47	(AC005896) hypothetical protein [Arabidopsis thaliana]
10544	GM_161_A2_E03_MR	g3426048	BLASTX	353	2e-31	82	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]
10545	GM_161_A2_E06_T7	g3777527	BLASTX	489	1e-68	94	(AF053008) gag-pol polyprotein [Glycine max]
10546	GM_161_A2_E08_MR	g507910	BLASTN	625	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10547	GM_161_A2_E12_MR	g3426334	BLASTN	354	5e-09	60	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
10548	GM_161_A2_F06_MR	g3777527	BLASTX	703	2e-67	95	(AF053008) gag-pol polyprotein [Glycine max]
10549	GM_161_A2_F07_MR	g507910	BLASTN	364	8e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10550	GM_161_A2_F08_MR	g3142328	BLASTN	763	1e-27	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10551	GM_161_A2_F09_T7	g4063760	BLASTX	163	6e-10	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10552	GM_161_A2_F10_MR	g99730	BLASTX	244	3e-26	53	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
10553	GM_161_A2_F11_MR	g2462134	BLASTX	166	9e-11	42	(Y13368) reverse transcriptase [Beta vulgaris]
10554	GM_161_A2_G01_MR	g3142328	BLASTN	905	5e-34	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10555	GM_161_A2_G02_T7	g1041029	BLASTN	370	5e-10	69	Mouse 921-L mRNA for presynaptic protein, complete cds
10556	GM_161_A2_G05_T7	g2995405	BLASTX	537	2e-50	65	(Y12432) polyprotein [Ananas comosus]
10557	GM_161_A2_G08_MR	g505129	BLASTN	389	1e-10	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10558	GM_161_A2_H04_MR	g1840106	BLASTN	519	2e-17	63	Human fragile site locus (FRA16B) minisatellite repeat
10559	GM_161_A2_H06_MR	g3779030	BLASTX	129	5e-15	37	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
10560	GM_161_A2_H10_T7	g541936	BLASTX	233	7e-19	76	4-coumarate--CoA ligase (EC 6.2.1.12) (clone GM4CL14) - soybean (fragment)
10561	GM_161_A2_H11_MR	g3859610	BLASTN	386	2e-10	65	Arabidopsis thaliana BAC T9E19
10562	GM_161_A2_H12_MR	g170080	BLASTN	386	1e-23	65	Soybean seed lectin gene transposable element tgm1.
10563	GM_161_A2_H12_T7	g100484	BLASTX	399	1e-35	52	hypothetical protein - garden snapdragon
10564	GM_161_B1_A01_MR	g905361	BLASTX	225	6e-17	41	(U22103) gag-protease polyprotein [Glycine max]
10565	GM_161_B1_A03_MR	g1769899	BLASTX	202	2e-15	79	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10566	GM_161_B1_A03_T7	g3645899	BLASTX	284	6e-23	58	(U68408) 5' end not determined experimentally [Zea mays]
10567	GM_161_B1_A04_T7	g170605	BLASTN	434	7e-13	58	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
10568	GM_161_B1_A05_T7	g4063760	BLASTX	139	5e-18	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10569	GM_161_B1_A08_MR	g507910	BLASTN	368	5e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10570	GM_161_B1_A08_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10571	GM_161_B1_A09_T7	g4092471	BLASTN	524	1e-16	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
10572	GM_161_B1_B04_MR	g2995405	BLASTX	284	5e-23	52	(Y12432) polyprotein [Ananas comosus]
10573	GM_161_B1_B05_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
10574	GM_161_B1_B05_T7	g507910	BLASTN	391	5e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10575	GM_161_B1_B08_T7	g18559	BLASTN	863	4e-32	76	G.max gene for catalase
10576	GM_161_B1_B09_MR	g18559	BLASTN	1342	7e-54	86	G.max gene for catalase
10577	GM_161_B1_B10_MR	g2443320	BLASTX	308	3e-25	52	(D85597) polyprotein [Oryza australiensis]
10578	GM_161_B1_C11_MR	g3319363	BLASTX	137	2e-15	46	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 33.26) [Arabidopsis thaliana]
10579	GM_161_B1_D01_MR	g507910	BLASTN	389	6e-11	79	Glycine max BSR-101 satellite SB92 genomic sequence.
10580	GM_161_B1_D02_MR	g1666236	BLASTX	149	3e-09	28	(U76261) unknown [Hordeum vulgare]
10581	GM_161_B1_D03_MR	g3645899	BLASTX	199	9e-27	50	(U68408) 5' end not determined experimentally [Zea mays]
10582	GM_161_B1_D03_T7	g2129618	BLASTX	216	1e-15	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10583	GM_161_B1_D08_MR	g99729	BLASTX	212	4e-20	46	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
10584	GM_161_B1_D08_T7	g18559	BLASTN	1213	5e-48	82	G.max gene for catalase
10585	GM_161_B1_E01_MR	g3860167	BLASTX	195	3e-13	42	(AF098964) disease resistance protein RPP1-WsC [Arabidopsis thaliana]
10586	GM_161_B1_E04_T7	g3645899	BLASTX	358	6e-39	62	(U68408) 5' end not determined experimentally [Zea mays]
10587	GM_161_B1_E07_MR	g2129618	BLASTX	163	4e-10	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10588	GM_161_B1_E11_T7	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
10589	GM_161_B1_F02_MR	g3097320	BLASTN	493	3e-15	75	Glycine max gene for Bd 30K, complete cds
10590	GM_161_B1_F04_MR	g3094012	BLASTX	164	2e-11	89	(AF060569) cold-regulated LTCOR12 [Lavatera thuringiaca]
10591	GM_161_B1_F09_MR	g18559	BLASTN	819	4e-30	80	G.max gene for catalase
10592	GM_161_B1_G04_MR	g4063760	BLASTX	470	9e-43	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10593	GM_161_B1_G08_MR	g3777526	BLASTN	442	6e-13	62	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
10594	GM_161_B1_G09_MR	g507910	BLASTN	377	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10595	GM_161_B1_H01_MR	g3142328	BLASTN	1251	9e-50	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10596	GM_161_B1_H03_MR	g3319362	BLASTX	152	4e-16	42	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
10597	GM_161_B1_H11_MR	g342963	BLASTN	422	2e-12	69	paramecium species 5,87 mt dna dimer: replication init. region.
10598	GM_161_B1_H11_T7	g1658062	BLASTX	230	7e-18	68	ACC synthase [Malus domestica]
10599	GM_161_B2_A03_T7	g3777527	BLASTX	175	4e-11	38	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10600	GM_161_B2_A05_T7	g3097320	BLASTN	438	9e-13	70	Glycine max gene for Bd 30K, complete cds
10601	GM_161_B2_A07_MR	g342963	BLASTN	395	3e-11	64	paramecium species 5,87 mt dna dimer: replication init. region.
10602	GM_161_B2_B11_T7	g3021357	BLASTX	254	4e-21	77	(AJ005082) UDP-galactose 4-epimerase [Cyamopsis tetragonoloba]
10603	GM_161_B2_B12_T7	g2443320	BLASTX	235	2e-17	49	(D85597) polyprotein [Oryza australiensis]
10604	GM_161_B2_C01_MR	g3777527	BLASTX	302	1e-35	93	(AF053008) gag-pol polyprotein [Glycine max]
10605	GM_161_B2_C01_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10606	GM_161_B2_C04_MR	g3386534	BLASTX	230	6e-18	61	(AF078934) mariner transposase [Glycine max]
10607	GM_161_B2_C04_T7	g99922	BLASTX	295	2e-47	83	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
10608	GM_161_B2_C09_T7	g2264309	BLASTN	602	4e-20	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]
10609	GM_161_B2_D01_MR	g905361	BLASTX	497	9e-47	90	(U22103) gag-protease polyprotein [Glycine max]
10610	GM_161_B2_D04_MR	g100484	BLASTX	159	7e-10	38	hypothetical protein - garden snapdragon
10611	GM_161_B2_D07_MR	g1142701	BLASTN	1103	2e-43	87	Glycine max satellite STR120-A.3.
10612	GM_161_B2_D10_MR	g4063760	BLASTX	267	5e-21	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10613	GM_161_B2_D10_T7	g1480927	BLASTN	784	9e-29	89	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
10614	GM_161_B2_E01_MR	g507910	BLASTN	374	3e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10615	GM_161_B2_E01_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10616	GM_161_B2_E03_MR	g3702738	BLASTN	311	5e-10	79	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWJ3, complete sequence [Arabidopsis thaliana]
10617	GM_161_B2_E03_T7	g1906825	BLASTN	395	6e-11	88	A.thaliana hsp81.2 gene
10618	GM_161_B2_E04_MR	g3687234	BLASTX	224	2e-16	39	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
10619	GM_161_B2_F06_T7	g2462058	BLASTX	257	2e-21	62	(Y13389) reverse transcriptase [Antirrhinum majus]
10620	GM_161_B2_F07_MR	g2129618	BLASTX	173	4e-11	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10621	GM_161_B2_F07_T7	g18559	BLASTN	674	2e-23	79	G.max gene for catalase
10622	GM_161_B2_F12_MR	g1946279	BLASTX	163	2e-11	36	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
10623	GM_161_B2_G01_T7	g100484	BLASTX	318	7e-27	57	hypothetical protein - garden snapdragon
10624	GM_161_B2_G03_T7	g3142328	BLASTN	941	1e-35	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10625	GM_161_B2_G07_T7	g3142328	BLASTN	1506	2e-61	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10626	GM_161_B2_H03_T7	g100484	BLASTX	334	1e-28	59	hypothetical protein - garden snapdragon
10627	GM_161_B2_H09_MR	g507910	BLASTN	499	6e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
10628	GM_161_B2_H09_T7	g507910	BLASTN	357	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
10629	GM_161_B2_H10_T7	g18559	BLASTN	762	2e-27	78	G.max gene for catalase
10630	GM_161_B2_H11_MR	g1142701	BLASTN	1205	4e-48	85	Glycine max satellite STR120-A.3.
10631	GM_162_A1_A05_MR	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
10632	GM_162_A1_A05_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10633	GM_162_A1_A06_T7	g2522228	BLASTX	218	1e-16	48	(AB007466) reverse transcriptase-like protein [Vicia faba]
10634	GM_162_A1_A07_T7	g3426261	BLASTX	294	7e-24	44	(U81378) disease resistance gene homolog Mi-copy1 [Lycopersicon esculentum]
10635	GM_162_A1_A09_MR	g320564	BLASTX	107	6e-09	42	transposon copia - Arabidopsis thaliana (fragment)
10636	GM_162_A1_B02_MR	g3334349	BLASTX	156	2e-09	47	GLYCYL-TRNA SYNTHETASE (GLYCINE--TRNA LIGASE) (GLYRS) gi 2564215 gnl PID e1181897 (AJ002062) glycyl-tRNA synthetase [Arabidopsis thaliana]
10637	GM_162_A1_B04_MR	g3560028	BLASTN	394	7e-11	67	Schistosoma intercalatum ribosomal intergenic spacer DNA
10638	GM_162_A1_B05_T7	g2443320	BLASTX	281	2e-22	45	(D85597) polyprotein [Oryza australiensis]
10639	GM_162_A1_B10_MR	g3097320	BLASTN	804	2e-29	73	Glycine max gene for Bd 30K, complete cds
10640	GM_162_A1_B11_T7	g2352492	BLASTX	181	3e-12	41	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] gi 2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]
10641	GM_162_A1_C02_MR	g1666236	BLASTX	86	8e-09	26	(U76261) unknown [Hordeum vulgare]
10642	GM_162_A1_C03_MR	g3142328	BLASTN	961	1e-36	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10643	GM_162_A1_C05_MR	g507910	BLASTN	612	5e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
10644	GM_162_A1_C10_MR	g1769898	BLASTX	305	1e-25	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10645	GM_162_A1_D02_MR	g2129618	BLASTX	156	3e-09	37	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10646	GM_162_A1_D09_T7	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
10647	GM_162_A1_E05_MR	g2244915	BLASTX	240	3e-18	40	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
10648	GM_162_A1_E10_MR	g3402711	BLASTX	166	6e-11	48	(AC004261) putative RNA-binding protein [Arabidopsis thaliana]
10649	GM_162_A1_E10_T7	g3193221	BLASTN	1282	5e-51	75	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
10650	GM_162_A1_E11_T7	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10651	GM_162_A1_E12_T7	g3426334	BLASTN	351	7e-09	63	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10652	GM_162_A1_F02_T7	g3777527	BLASTX	215	2e-15	45	(AF053008) gag-pol polyprotein [Glycine max]
10653	GM_162_A1_G05_T7	g531389	BLASTX	156	4e-09	31	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
10654	GM_162_A1_G07_MR	g170029	BLASTN	360	3e-09	76	Glycine max cv. Dare nodulin 26 gene fragment.
10655	GM_162_A1_G08_T7	g3097320	BLASTN	711	4e-25	75	Glycine max gene for Bd 30K, complete cds
10656	GM_162_A1_H01_MR	g507910	BLASTN	530	2e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
10657	GM_162_A1_H01_T7	g3645899	BLASTX	221	1e-20	41	(U68408) 5' end not determined experimentally [Zea mays]
10658	GM_162_A1_H03_T7	g2522228	BLASTX	369	3e-33	64	(AB007466) reverse transcriptase-like protein [Vicia faba]
10659	GM_162_A1_H04_MR	g100484	BLASTX	355	7e-31	61	hypothetical protein - garden snapdragon
10660	GM_162_A1_H06_T7	g2351065	BLASTN	475	2e-14	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15
10661	GM_162_A1_H07_T7	g2618693	BLASTX	103	4e-09	27	(AC002510) putative zinc-finger protein [Arabidopsis thaliana]
10662	GM_162_A1_H08_T7	g507910	BLASTN	593	3e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10663	GM_162_A1_H09_T7	g3097320	BLASTN	457	1e-13	76	Glycine max gene for Bd 30K, complete cds
10664	GM_162_A1_H11_T7	g2160156	BLASTX	256	8e-24	66	(AC000132) Strong similarity to S. pombe leucyl-tRNA synthetase (gb Z73100). [Arabidopsis thaliana]
10665	GM_162_A2_A05_T7	g4115359	BLASTX	150	7e-10	41	(AC005957) putative disease resistance protein [Arabidopsis thaliana]
10666	GM_162_A2_A10_MR	g3947433	BLASTN	451	2e-13	63	Homo sapiens BAC clone RG060P12 from 7q21, complete sequence [Homo sapiens]
10667	GM_162_A2_B03_MR	g2443320	BLASTX	192	2e-14	35	(D85597) polyprotein [Oryza australiensis]
10668	GM_162_A2_B06_MR	g3845197	BLASTN	368	1e-09	63	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
10669	GM_162_A2_B09_MR	g3152629	BLASTN	567	1e-18	67	Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence [Homo sapiens]
10670	GM_162_A2_C02_T7	g100484	BLASTX	290	7e-24	60	hypothetical protein - garden snapdragon
10671	GM_162_A2_C03_MR	g4160362	BLASTN	355	5e-09	63	Saccharomyces cerevisiae complete mitochondrial genome
10672	GM_162_A2_C05_MR	g226407	BLASTX	244	2e-18	46	retrotransposon del1-46 [Lilium henryi]
10673	GM_162_A2_C10_MR	g4140712	BLASTX	331	1e-39	59	(AF110183) putative integrase [Oryza sativa]
10674	GM_162_A2_C12_MR	g2114040	BLASTN	383	7e-11	81	Vigna vexillata DNA for TY1-copia-like retrotransposable element
10675	GM_162_A2_D08_MR	g1769897	BLASTX	137	4e-10	34	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10676	GM_162_A2_D11_MR	g4063760	BLASTX	388	2e-39	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10677	GM_162_A2_D12_MR	g3820757	BLASTN	377	3e-10	60	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
10678	GM_162_A2_E03_MR	g3746069	BLASTX	171	9e-11	40	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10679	GM_162_A2_E05_MR	g507910	BLASTN	392	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10680	GM_162_A2_E05_T7	g507910	BLASTN	403	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10681	GM_162_A2_E07_MR	g99729	BLASTX	342	2e-30	45	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
10682	GM_162_A2_E08_MR	g4063760	BLASTX	175	3e-11	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10683	GM_162_A2_E12_MR	g1167523	BLASTX	103	1e-11	36	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
10684	GM_162_A2_F01_MR	g507910	BLASTN	393	4e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10685	GM_162_A2_F07_MR	g99922	BLASTX	277	3e-31	62	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
10686	GM_162_A2_F09_T7	g3777527	BLASTX	243	3e-18	47	(AF053008) gag-pol polyprotein [Glycine max]
10687	GM_162_A2_G01_T7	g3142328	BLASTN	973	4e-37	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10688	GM_162_A2_G10_T7	g829300	BLASTX	210	2e-16	81	(X01647) open reading frame (ORF 704) [Marchantia polymorpha]
10689	GM_162_B1_A03_MR	g3924609	BLASTX	263	4e-27	59	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
10690	GM_162_B1_A04_T7	g3142328	BLASTN	925	6e-35	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10691	GM_162_B1_A05_MR	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
10692	GM_162_B1_A05_T7	g507910	BLASTN	359	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10693	GM_162_B1_A10_MR	g14227	BLASTN	449	2e-14	61	Yeast cytochrome c oxidase transcription initiation region subunit 1 (COX1) from mitochondrial DNA
10694	GM_162_B1_B03_T7	g1769898	BLASTX	234	1e-19	37	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10695	GM_162_B1_B05_MR	g2335061	BLASTN	471	3e-14	61	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence [Homo sapiens]
10696	GM_162_B1_B10_T7	g1666236	BLASTX	180	9e-13	29	(U76261) unknown [Hordeum vulgare]
10697	GM_162_B1_B11_MR	g3915022	BLASTX	167	5e-25	60	SUCROSE-PHOSPHATE SYNTHASE 2 (UDP-GLUCOSE-FRUCTOSE-PHOSPHATE GLUCOSYLTRANSFERASE 2) >gi 2190350 gnl PID e310970 (Y11795) sucrose-phosphate synthase [Craterostigma plantagineum]
10698	GM_162_B1_C01_T7	g3097320	BLASTN	879	9e-33	75	Glycine max gene for Bd 30K, complete cds
10699	GM_162_B1_C02_MR	g905361	BLASTX	608	2e-58	93	(U22103) gag-protease polyprotein [Glycine max]
10700	GM_162_B1_C04_T7	g3777527	BLASTX	672	5e-64	94	(AF053008) gag-pol polyprotein [Glycine max]
10701	GM_162_B1_C06_T7	g3738114	BLASTN	427	3e-12	65	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10702	GM_162_B1_D01_MR	g2213582	BLASTX	158	3e-09	34	(AC000348) T7N9.2 [Arabidopsis thaliana]
10703	GM_162_B1_D01_T7	g1431738	BLASTN	519	1e-16	88	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
10704	GM_162_B1_D02_MR	g507910	BLASTN	370	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10705	GM_162_B1_D06_MR	g2979597	BLASTN	403	4e-11	60	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
10706	GM_162_B1_E01_MR	g12212	BLASTN	1145	3e-50	93	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
10707	GM_162_B1_E01_T7	g2734665	BLASTX	495	1e-46	70	(U48752) ribosomal protein subunit 2 [Euphrasia sp.]
10708	GM_162_B1_E03_T7	g4063760	BLASTX	268	4e-21	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10709	GM_162_B1_E06_MR	g2708743	BLASTX	203	4e-14	34	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
10710	GM_162_B1_E09_T7	g2443320	BLASTX	350	8e-30	55	(D85597) polyprotein [Oryza australiensis]
10711	GM_162_B1_F01_T7	g3319362	BLASTX	183	3e-12	36	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
10712	GM_162_B1_F05_MR	g4063760	BLASTX	366	2e-31	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10713	GM_162_B1_F06_T7	g2828278	BLASTN	439	9e-13	65	Arabidopsis thaliana DNA chromosome 4, BAC clone T18B16 (ESSAII project)
10714	GM_162_B1_F07_T7	g3777526	BLASTN	1381	2e-55	88	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
10715	GM_162_B1_G01_T7	g507910	BLASTN	384	9e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10716	GM_162_B1_G06_T7	g1518388	BLASTX	210	1e-26	76	(X91172) korean-radish isoperoxidase [Raphanus sativus]
10717	GM_162_B1_G09_MR	g3645899	BLASTX	213	4e-18	44	(U68408) 5' end not determined experimentally [Zea mays]
10718	GM_162_B1_H06_MR	g507910	BLASTN	463	3e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
10719	GM_162_B1_H06_T7	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10720	GM_162_B1_H08_MR	g3097320	BLASTN	1246	2e-49	83	Glycine max gene for Bd 30K, complete cds
10721	GM_162_B1_H10_MR	g507910	BLASTN	362	9e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10722	GM_162_B1_H11_MR	g4063760	BLASTX	390	4e-34	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10723	GM_162_B1_H11_T7	g8540	BLASTN	365	2e-10	63	Drosophila satellite DNA fragment 1.672-614 >gi 158379 gb M29744 DROSAT02 Drosophila satellite DNA fragment 1.672-614.
10724	GM_162_B2_A03_MR	g226407	BLASTX	432	2e-38	46	retrotransposon del1-46 [Lilium henryi]
10725	GM_162_B2_A05_T7	g2129652	BLASTX	210	4e-15	35	myosin heavy chain homolog - Arabidopsis thaliana (fragment) gi 699495 (U19616) myosin heavy chain homolog [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10726	GM_162_B2_A07_MR	g4063760	BLASTX	293	9e-24	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10727	GM_162_B2_A07_T7	g4063760	BLASTX	303	7e-25	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10728	GM_162_B2_A09_MR	g100484	BLASTX	180	8e-14	47	hypothetical protein - garden snapdragon
10729	GM_162_B2_B06_T7	g3777527	BLASTX	563	1e-57	80	(AF053008) gag-pol polyprotein [Glycine max]
10730	GM_162_B2_B08_T7	g3142328	BLASTN	427	2e-20	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10731	GM_162_B2_B11_MR	g99922	BLASTX	533	1e-50	74	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
10732	GM_162_B2_B12_MR	g507910	BLASTN	391	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10733	GM_162_B2_B12_T7	g3097320	BLASTN	446	4e-13	70	Glycine max gene for Bd 30K, complete cds
10734	GM_162_B2_C03_MR	g2275089	BLASTN	650	4e-29	93	Swietenia humilis DNA for simple tandem repeat (340bp)
10735	GM_162_B2_C04_T7	g505337	BLASTN	379	4e-10	61	Plasmodium falciparum (clone Dd2) heat shock protein 86 gene, complete cds.
10736	GM_162_B2_C08_MR	g2738982	BLASTX	187	5e-13	44	(AF022157) CYP71A10 [Glycine max]
10737	GM_162_B2_C08_T7	g225282	BLASTX	474	3e-55	72	RNA polymerase beta [Nicotiana tabacum]
10738	GM_162_B2_C10_MR	g4063760	BLASTX	205	8e-32	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10739	GM_162_B2_E01_MR	g505129	BLASTN	502	9e-16	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10740	GM_162_B2_E04_T7	g3645899	BLASTX	133	5e-16	41	(U68408) 5' end not determined experimentally [Zea mays]
10741	GM_162_B2_E07_MR	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
10742	GM_162_B2_E08_MR	g4038056	BLASTX	278	2e-22	44	(AC005897) putative transposon [Arabidopsis thaliana]
10743	GM_162_B2_E10_T7	g2522230	BLASTX	365	9e-33	44	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
10744	GM_162_B2_E11_MR	g507910	BLASTN	345	6e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10745	GM_162_B2_F01_T7	g4063760	BLASTX	461	1e-41	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10746	GM_162_B2_F05_T7	g2522230	BLASTX	341	3e-30	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
10747	GM_162_B2_F08_T7	g507910	BLASTN	633	5e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10748	GM_162_B2_F09_T7	g4063760	BLASTX	208	5e-31	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10749	GM_162_B2_F11_T7	g3645899	BLASTX	292	8e-24	48	(U68408) 5' end not determined experimentally [Zea mays]
10750	GM_162_B2_G01_MR	g4063760	BLASTX	486	2e-44	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10751	GM_162_B2_G09_MR	g3645899	BLASTX	288	1e-26	41	(U68408) 5' end not determined experimentally [Zea mays]
10752	GM_162_B2_G09_T7	g100484	BLASTX	267	1e-25	56	hypothetical protein - garden snapdragon
10753	GM_163_A1_A02_T7	g4038056	BLASTX	233	4e-23	48	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10754	GM_163_A1_A07_T7	g1335695	BLASTX	248	2e-20	42	(X02600) unidentified open reading frame II (146 aa) [Drosophila melanogaster]
10755	GM_163_A1_A09_T7	g3513747	BLASTX	258	7e-20	47	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
10756	GM_163_A1_B03_T7	g4063760	BLASTX	132	6e-09	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10757	GM_163_A1_B07_T7	g1172441	BLASTX	96	3e-09	81	POSSIBLE TRANSCRIPTION FACTOR POSF21 gi 99685 pir S21883 DNA-binding protein POSF21 - Arabidopsis thaliana gi 16429 (X61031) posF21 gene product [Arabidopsis thaliana]
10758	GM_163_A1_B08_T7	g3650039	BLASTX	258	2e-20	42	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
10759	GM_163_A1_C06_T7	g3142328	BLASTN	1827	4e-76	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10760	GM_163_A1_D03_T7	g2443320	BLASTX	135	1e-16	37	(D85597) polyprotein [Oryza australiensis]
10761	GM_163_A1_D07_T7	g3377856	BLASTX	236	9e-18	38	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 19.54) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 12.35) [Arabidopsis thaliana]
10762	GM_163_A1_D11_T7	g3738133	BLASTN	353	7e-09	69	Human DNA sequence from clone 409O10 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence [Homo sapiens]
10763	GM_163_A1_E01_T7	g2244802	BLASTX	378	1e-32	50	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
10764	GM_163_A1_E04_T7	g629693	BLASTX	254	5e-21	42	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10765	GM_163_A1_E07_T7	g4063760	BLASTX	341	6e-29	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10766	GM_163_A1_E12_T7	g3522932	BLASTN	383	3e-10	62	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]
10767	GM_163_A1_F02_T7	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10768	GM_163_A1_F05_T7	g1045614	BLASTX	185	8e-13	51	(U37088) beta-ketoacyl-CoA synthase [Simmondsia chinensis]
10769	GM_163_A1_G12_T7	g3097320	BLASTN	468	4e-14	73	Glycine max gene for Bd 30K, complete cds
10770	GM_163_A1_H04_T7	g4063760	BLASTX	281	1e-22	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10771	GM_163_A1_H06_T7	g18559	BLASTN	469	3e-14	75	G.max gene for catalase
10772	GM_163_A1_H12_T7	g4038056	BLASTX	356	9e-31	54	(AC005897) putative transposon [Arabidopsis thaliana]
10773	GM_163_A2_C05_MR	g18559	BLASTN	1372	3e-55	79	G.max gene for catalase
10774	GM_163_A2_E05_MR	g1236920	BLASTN	436	8e-13	63	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10775	GM_163_A2_F04_MR	g1335861	BLASTN	374	7e-10	68	Glycine max clathrin heavy chain mRNA, complete cds
10776	GM_163_A2_F10_MR	g522302	BLASTX	260	3e-20	47	(L35053) endonuclease [Magnaporthe grisea]
10777	GM_163_A2_H03_MR	g3738114	BLASTN	352	7e-09	64	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
10778	GM_163_B1_A02_MR	g1480927	BLASTN	1056	2e-41	88	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
10779	GM_163_B1_A07_MR	g3851527	BLASTN	406	2e-11	67	Hordeum vulgare cultivar Bomi starch branching enzyme IIb (sbeIIb) gene, nuclear gene encoding plastid protein, partial cds
10780	GM_163_B1_A11_T7	g508826	BLASTN	381	3e-10	68	Drosophila melanogaster Oregon-R mitochondrial A+T region.
10781	GM_163_B1_B04_MR	g3319362	BLASTX	446	2e-40	61	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
10782	GM_163_B1_B05_MR	g507910	BLASTN	355	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10783	GM_163_B1_B08_MR	g4063760	BLASTX	204	2e-14	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10784	GM_163_B1_C05_T7	g3777527	BLASTX	471	7e-51	88	(AF053008) gag-pol polyprotein [Glycine max]
10785	GM_163_B1_C12_MR	g905361	BLASTX	174	2e-11	34	(U22103) gag-protease polyprotein [Glycine max]
10786	GM_163_B1_D05_T7	g3142328	BLASTN	1099	7e-43	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10787	GM_163_B1_D07_T7	g4063756	BLASTN	418	8e-12	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
10788	GM_163_B1_D09_T7	g3047114	BLASTX	305	2e-26	78	(AF058919) No definition line found [Arabidopsis thaliana]
10789	GM_163_B1_E01_MR	g99922	BLASTX	232	1e-18	66	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
10790	GM_163_B1_E03_T7	g4063760	BLASTX	160	1e-09	30	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10791	GM_163_B1_E05_T7	g507910	BLASTN	561	1e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
10792	GM_163_B1_E06_MR	g4038030	BLASTX	229	2e-17	71	(AC005936) putative protein kinase, 5' partial [Arabidopsis thaliana]
10793	GM_163_B1_E09_MR	g3560028	BLASTN	362	2e-09	64	Schistosoma intercalatum ribosomal intergenic spacer DNA
10794	GM_163_B1_E09_T7	g4092471	BLASTN	437	1e-12	70	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
10795	GM_163_B1_F01_MR	g3449319	BLASTN	494	3e-15	65	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MQP15, complete sequence [Arabidopsis thaliana]
10796	GM_163_B1_F05_T7	g507910	BLASTN	416	3e-12	78	Glycine max BSR-101 satellite SB92 genomic sequence.
10797	GM_163_B1_F06_MR	g507910	BLASTN	478	5e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
10798	GM_163_B1_F09_T7	g1769898	BLASTX	358	1e-34	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10799	GM_163_B1_F11_MR	g1666236	BLASTX	195	2e-14	30	(U76261) unknown [Hordeum vulgare]
10800	GM_163_B1_F12_MR	g507910	BLASTN	511	2e-16	79	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10801	GM_163_B1_G05_T7	g226407	BLASTX	310	2e-25	50	retrotransposon del1-46 [Lilium henryi]
10802	GM_163_B1_G06_T7	g3176799	BLASTN	387	3e-11	65	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite sequence
10803	GM_163_B1_G09_MR	g18559	BLASTN	1141	1e-44	77	G.max gene for catalase
10804	GM_163_B1_G11_T7	g2462054	BLASTX	173	2e-12	40	(Y13373) reverse transcriptase [Allium cepa]
10805	GM_163_B1_H02_MR	g1769898	BLASTX	264	4e-21	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10806	GM_163_B1_H02_T7	g3650039	BLASTX	174	2e-11	40	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
10807	GM_163_B1_H03_MR	g2827713	BLASTX	152	2e-09	82	(AL021684) pyridoxal-phosphate-dependent aminotransferase - like protein [Arabidopsis thaliana]
10808	GM_163_B1_H07_MR	g3142379	BLASTX	277	4e-23	75	(AF053008) envelope-like [Glycine max]
10809	GM_163_B1_H09_T7	g2085783	BLASTN	365	2e-09	67	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
10810	GM_163_B1_H10_MR	g1220442	BLASTN	350	7e-09	61	Plasmodium falciparum clone HB3 d-aminolevulinic acid synthetase gene, complete cds
10811	GM_163_B1_H12_MR	g507910	BLASTN	347	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10812	GM_163_B2_A02_T7	g18559	BLASTN	365	2e-09	71	G.max gene for catalase
10813	GM_163_B2_A03_T7	g2194136	BLASTX	281	9e-28	56	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
10814	GM_163_B2_A04_MR	g3097320	BLASTN	430	2e-12	70	Glycine max gene for Bd 30K, complete cds
10815	GM_163_B2_A05_T7	g18559	BLASTN	530	5e-17	72	G.max gene for catalase
10816	GM_163_B2_A06_MR	g18559	BLASTN	877	1e-32	73	G.max gene for catalase
10817	GM_163_B2_A09_MR	g2443320	BLASTX	155	5e-09	26	(D85597) polyprotein [Oryza australiensis]
10818	GM_163_B2_A10_MR	g3914056	BLASTX	125	2e-13	78	DNA MISMATCH REPAIR PROTEIN MSH2 >gi 2522362 (AF002706) MutS homolog 2 [Arabidopsis thaliana] >gi 2522364 (AF003005) MutS homolog 2 [Arabidopsis thaliana] >gi 2547236 (AF026549) DNA mismatch repair protein MSH2 [Arabidopsis thaliana]
10819	GM_163_B2_B02_MR	g3142328	BLASTN	878	1e-60	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10820	GM_163_B2_B02_T7	g3777527	BLASTX	258	7e-20	37	(AF053008) gag-pol polyprotein [Glycine max]
10821	GM_163_B2_B04_T7	g3319362	BLASTX	260	2e-20	34	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
10822	GM_163_B2_B05_MR	g3777527	BLASTX	416	9e-37	47	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10823	GM_163_B2_B05_T7	g629693	BLASTX	164	3e-25	39	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10824	GM_163_B2_B11_T7	g18559	BLASTN	497	2e-15	76	G.max gene for catalase
10825	GM_163_B2_B12_T7	g2651294	BLASTN	384	3e-10	64	Arabidopsis thaliana chromosome II BAC T2P4 genomic sequence, complete sequence [Arabidopsis thaliana]
10826	GM_163_B2_C02_MR	g1707017	BLASTX	678	5e-66	82	(U78721) RNA helicase isolog [Arabidopsis thaliana]
10827	GM_163_B2_C08_T7	g1171591	BLASTN	409	2e-11	64	P.falciparum complete gene map of plastid-like DNA (IR-B)
10828	GM_163_B2_C10_MR	g3461846	BLASTX	422	2e-37	56	(AC005315) putative zinc-finger protein [Arabidopsis thaliana]
10829	GM_163_B2_C10_T7	g4063770	BLASTX	494	7e-46	56	(AB004906) transposase [Ipomoea purpurea]
10830	GM_163_B2_C12_MR	g3645899	BLASTX	142	2e-12	49	(U68408) 5' end not determined experimentally [Zea mays]
10831	GM_163_B2_D04_T7	g1076389	BLASTX	164	4e-25	84	protein phosphatase 2A pDF1 - Arabidopsis thaliana gi 683502 (X82002) protein phosphatase 2A 65 kDa regulatory subunit [Arabidopsis thaliana]
10832	GM_163_B2_D06_MR	g1769898	BLASTX	339	2e-29	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10833	GM_163_B2_D07_T7	g505129	BLASTN	302	2e-09	68	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
10834	GM_163_B2_D09_T7	g1370199	BLASTN	622	3e-22	71	L.japonicus mRNA for small GTP-binding protein, RAC1
10835	GM_163_B2_E05_MR	g1769897	BLASTX	258	3e-23	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10836	GM_163_B2_E06_MR	g13767	BLASTN	370	1e-10	63	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
10837	GM_163_B2_E10_MR	g3097320	BLASTN	471	3e-14	71	Glycine max gene for Bd 30K, complete cds
10838	GM_163_B2_E12_MR	g2129618	BLASTX	245	8e-19	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10839	GM_163_B2_E12_T7	g3097320	BLASTN	1012	8e-39	76	Glycine max gene for Bd 30K, complete cds
10840	GM_163_B2_F03_MR	g3250688	BLASTX	251	1e-20	43	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
10841	GM_163_B2_F05_MR	g3875246	BLASTX	135	3e-09	50	(Z81490) similar to WD domain, G-beta repeats (2 domains); cDNA EST EMBL:T00482 comes from this gene; cDNA EST EMBL:T00923 comes from this gene; cDNA EST yk449d4.3 comes from this gene; cDNA EST yk449d4.5 comes from this gen...
10842	GM_163_B2_F07_T7	g2586082	BLASTX	422	2e-37	50	(U72725) retrofit [Oryza longistaminata]
10843	GM_163_B2_F09_T7	g18559	BLASTN	495	2e-15	73	G.max gene for catalase
10844	GM_163_B2_F12_MR	g3810596	BLASTX	243	1e-18	37	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10845	GM_163_B2_G01_T7	g905361	BLASTX	433	8e-40	95	(U22103) gag-protease polyprotein [Glycine max]
10846	GM_163_B2_G03_T7	g4063760	BLASTX	593	7e-56	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10847	GM_163_B2_G06_MR	g507910	BLASTN	575	2e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
10848	GM_163_B2_G10_MR	g507910	BLASTN	642	2e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
10849	GM_163_B2_G10_T7	g3777527	BLASTX	411	3e-36	49	(AF053008) gag-pol polyprotein [Glycine max]
10850	GM_163_B2_G12_T7	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
10851	GM_163_B2_H05_T7	g4038056	BLASTX	276	3e-22	37	(AC005897) putative transposon [Arabidopsis thaliana]
10852	GM_163_B2_H06_MR	g507910	BLASTN	372	3e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10853	GM_164_A1_A01_T7	g1769898	BLASTX	406	9e-39	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10854	GM_164_A1_A02_T7	g131772	BLASTX	109	2e-13	79	40S RIBOSOMAL PROTEIN S14 (CLONE MCH1) gi 82723 pir A30097 ribosomal protein S14 (clone MCH1) - maize
10855	GM_164_A1_A03_MR	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
10856	GM_164_A1_A05_T7	g3645899	BLASTX	199	8e-14	49	(U68408) 5' end not determined experimentally [Zea mays]
10857	GM_164_A1_B06_MR	g3097320	BLASTN	1195	4e-47	81	Glycine max gene for Bd 30K, complete cds
10858	GM_164_A1_B07_T7	g170029	BLASTN	383	3e-10	80	Glycine max cv. Dare nodulin 26 gene fragment.
10859	GM_164_A1_B09_MR	g1572834	BLASTN	377	5e-10	62	Caenorhabditis elegans cosmid T01C4
10860	GM_164_A1_C06_MR	g2443320	BLASTX	367	1e-31	54	(D85597) polyprotein [Oryza australiensis]
10861	GM_164_A1_C06_T7	g2708743	BLASTX	171	2e-11	37	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
10862	GM_164_A1_C10_T7	g2921625	BLASTN	348	1e-08	69	Lupinus luteus leghemoglobin (LbI) gene, complete cds
10863	GM_164_A1_C11_T7	g3645899	BLASTX	168	8e-12	50	(U68408) 5' end not determined experimentally [Zea mays]
10864	GM_164_A1_D03_MR	g18559	BLASTN	1017	4e-39	73	G.max gene for catalase
10865	GM_164_A1_D07_T7	g3341443	BLASTX	150	9e-10	82	(AJ223074) acid phosphatase [Glycine max]
10866	GM_164_A1_D10_T7	g4150930	BLASTN	400	5e-11	62	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
10867	GM_164_A1_E01_MR	g1769898	BLASTX	472	4e-44	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10868	GM_164_A1_E04_MR	g507910	BLASTN	693	1e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
10869	GM_164_A1_E05_MR	g3777527	BLASTX	747	4e-72	95	(AF053008) gag-pol polyprotein [Glycine max]
10870	GM_164_A1_E10_MR	g3142328	BLASTN	873	1e-32	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10871	GM_164_A1_F02_MR	g2995405	BLASTX	251	1e-19	57	(Y12432) polyprotein [Ananas comosus]
10872	GM_164_A1_F04_MR	g1769898	BLASTX	183	2e-12	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10873	GM_164_A1_F08_T7	g3142379	BLASTX	289	1e-24	69	(AF053008) envelope-like [Glycine max]
10874	GM_164_A1_G01_T7	g905361	BLASTX	223	9e-17	34	(U22103) gag-protease polyprotein [Glycine max]
10875	GM_164_A1_G03_MR	g905361	BLASTX	389	8e-35	91	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10876	GM_164_A1_G04_MR	g4063756	BLASTN	567	1e-18	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
10877	GM_164_A1_G11_T7	g1769901	BLASTX	206	3e-15	68	(X95737) proline transporter 1 [Arabidopsis thaliana] gi 2088642 (AF002109) proline transporter 1 [Arabidopsis thaliana]
10878	GM_164_A1_H07_T7	g2462744	BLASTX	225	3e-17	36	(AC002292) Hypothetical protein [Arabidopsis thaliana]
10879	GM_164_A1_H08_MR	g3201554	BLASTX	185	1e-12	63	(AJ006501) beta-D-glucosidase [Tropaeolum majus]
10880	GM_164_A1_H09_MR	g3845139	BLASTN	311	5e-09	64	Plasmodium falciparum chromosome 2, section 21 of 73 of the complete sequence
10881	GM_164_A1_H10_MR	g3319362	BLASTX	249	3e-19	50	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
10882	GM_164_A2_A03_T7	g2642431	BLASTX	258	6e-20	36	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
10883	GM_164_A2_A04_T7	g2980640	BLASTN	446	4e-13	71	Arabidopsis thaliana mRNA for putative MRP protein
10884	GM_164_A2_A07_T7	g2586082	BLASTX	184	5e-27	46	(U72725) retrofit [Oryza longistaminata]
10885	GM_164_A2_A08_MR	g114734	BLASTX	166	1e-18	85	AUXIN-INDUCED PROTEIN AUX28 gi 81759 pir A28993 aux28 protein - soybean gi 169921 (J03919) auxin-regulated protein (Aux28) [Glycine max]
10886	GM_164_A2_A09_MR	g2959781	BLASTX	113	3e-15	79	(AJ223508) Zwille protein [Arabidopsis thaliana]
10887	GM_164_A2_A10_MR	g3142328	BLASTN	952	3e-36	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10888	GM_164_A2_A11_MR	g18559	BLASTN	793	6e-29	73	G.max gene for catalase
10889	GM_164_A2_B01_T7	g1666236	BLASTX	118	2e-13	30	(U76261) unknown [Hordeum vulgare]
10890	GM_164_A2_B02_T7	g2864621	BLASTX	101	5e-10	26	hypothetical protein [Arabidopsis thaliana]
10891	GM_164_A2_B06_MR	g3643603	BLASTX	225	1e-16	60	(AC005395) unknown protein [Arabidopsis thaliana]
10892	GM_164_A2_B09_MR	g2522228	BLASTX	157	6e-10	30	(AB007466) reverse transcriptase-like protein [Vicia faba]
10893	GM_164_A2_C02_T7	g4049647	BLASTN	351	8e-09	61	Melanoplus sanguinipes entomopoxvirus, complete genome
10894	GM_164_A2_C03_T7	g3763850	BLASTN	789	1e-28	78	Glycine max GmENOD93 gene for early nodulin, complete cds
10895	GM_164_A2_C04_T7	g421954	BLASTX	183	2e-12	37	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
10896	GM_164_A2_C09_T7	g3820757	BLASTN	390	8e-11	64	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
10897	GM_164_A2_D02_MR	g4063756	BLASTN	516	3e-16	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
10898	GM_164_A2_D03_T7	g4140712	BLASTX	465	2e-43	61	(AF110183) putative integrase [Oryza sativa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10899	GM_164_A2_D04_T7	g3249105	BLASTX	224	2e-23	80	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
10900	GM_164_A2_D08_MR	g2129618	BLASTX	168	1e-10	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10901	GM_164_A2_D11_MR	g2443320	BLASTX	149	6e-12	40	(D85597) polyprotein [Oryza australiensis]
10902	GM_164_A2_D11_T7	g18559	BLASTN	1056	7e-41	74	G.max gene for catalase
10903	GM_164_A2_D12_T7	g1906830	BLASTX	176	7e-17	68	(Y11829) heat shock protein [Arabidopsis thaliana]
10904	GM_164_A2_E05_MR	g2218024	BLASTN	208	6e-10	60	Apis mellifera mitochondrial tRNA-Leu gene
10905	GM_164_A2_E06_T7	g336279	BLASTN	350	9e-09	60	Apis mellifera ligustica complete mitochondrial genome
10906	GM_164_A2_E08_T7	g2781348	BLASTX	220	2e-16	47	(AC003113) F24O1.4 [Arabidopsis thaliana]
10907	GM_164_A2_E09_T7	g3142328	BLASTN	978	2e-37	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10908	GM_164_A2_F01_T7	g18559	BLASTN	1007	1e-38	76	G.max gene for catalase
10909	GM_164_A2_F02_MR	g3097320	BLASTN	1280	6e-51	80	Glycine max gene for Bd 30K, complete cds
10910	GM_164_A2_F04_MR	g1076498	BLASTX	186	6e-18	78	zinc-finger protein (C-terminal) - soybean gi 558543 (Z36749) C-terminal zinc-finger [Glycine max]
10911	GM_164_A2_F11_T7	g100484	BLASTX	383	6e-34	52	hypothetical protein - garden snapdragon
10912	GM_164_A2_G01_T7	g226407	BLASTX	332	8e-28	40	retrotransposon del1-46 [Lilium henryi]
10913	GM_164_A2_G10_T7	g3377848	BLASTX	156	1e-11	38	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
10914	GM_164_A2_H07_T7	g2443320	BLASTX	363	4e-31	50	(D85597) polyprotein [Oryza australiensis]
10915	GM_164_B1_A02_T7	g3650039	BLASTX	222	1e-16	38	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
10916	GM_164_B1_A04_T7	g2129618	BLASTX	211	4e-15	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
10917	GM_164_B1_A05_T7	g2586082	BLASTX	137	5e-09	56	(U72725) retrofit [Oryza longistaminata]
10918	GM_164_B1_A10_MR	g4063770	BLASTX	172	4e-11	43	(AB004906) transposase [Ipomoea purpurea]
10919	GM_164_B1_B01_T7	g18559	BLASTN	434	1e-12	70	G.max gene for catalase
10920	GM_164_B1_B02_T7	g3201608	BLASTN	359	3e-09	62	Arabidopsis thaliana chromosome II BAC F7F1 genomic sequence, complete sequence.
10921	GM_164_B1_B06_MR	g4063760	BLASTX	217	1e-15	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10922	GM_164_B1_B06_T7	g3097320	BLASTN	963	1e-36	82	Glycine max gene for Bd 30K, complete cds
10923	GM_164_B1_B07_T7	g3193221	BLASTN	947	7e-36	70	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
10924	GM_164_B1_B09_MR	g3746070	BLASTX	145	2e-13	73	(AC005311) unknown protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10925	GM_164_B1_B10_T7	g4063760	BLASTX	234	1e-17	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10926	GM_164_B1_C10_MR	g3023281	BLASTX	343	3e-30	59	HIGH AFFINITY AMMONIUM TRANSPORTER gi 2065194 gnl PID e223603 (X95098) ammonium transporter [Lycopersicon esculentum]
10927	GM_164_B1_C10_T7	g2997694	BLASTX	283	4e-24	49	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
10928	GM_164_B1_C11_T7	g2464905	BLASTX	203	1e-15	67	(Z99708) minor allergen [Arabidopsis thaliana]
10929	GM_164_B1_D03_MR	g4140712	BLASTX	158	3e-29	45	(AF110183) putative integrase [Oryza sativa]
10930	GM_164_B1_D03_T7	g4038062	BLASTX	192	8e-16	44	(AC005897) putative transposon MuDR [Arabidopsis thaliana]
10931	GM_164_B1_D05_MR	g3845197	BLASTN	361	3e-09	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
10932	GM_164_B1_D06_T7	g342964	BLASTN	523	1e-17	66	paramecium species 5,311 mt dna dimer: replication init. region.
10933	GM_164_B1_D08_MR	g507910	BLASTN	633	5e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10934	GM_164_B1_D10_MR	g3142328	BLASTN	856	8e-32	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10935	GM_164_B1_D12_MR	g3142328	BLASTN	847	2e-31	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
10936	GM_164_B1_E02_MR	g13773	BLASTN	443	6e-14	65	Torulopsis glabrata mitochondrial genes for tRNAs -Tyr, -Asn, -Ala, -Ile -Trp (from Var1-LrRNA intergenic region) >gi 343959 gb M11906 YSLMTIG09 Yeast (T.glabrata) mitochondrial DNA between var1 and L rRNA genes.
10937	GM_164_B1_E02_T7	g3980359	BLASTN	358	4e-09	64	Human DNA sequence from clone 344I7 on chromosome Xp11.21-11.3. Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8, KRT8) pseudogene, ESTs and a GSS, complete sequence [Homo sapiens]
10938	GM_164_B1_E04_T7	g1769899	BLASTX	190	3e-14	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10939	GM_164_B1_E07_T7	g2764526	BLASTN	501	1e-15	67	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
10940	GM_164_B1_E08_T7	g1666236	BLASTX	103	2e-11	36	(U76261) unknown [Hordeum vulgare]
10941	GM_164_B1_E10_MR	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
10942	GM_164_B1_E10_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10943	GM_164_B1_F01_T7	g2224933	BLASTX	472	4e-44	68	(AF004216) ethylene-insensitive3 [Arabidopsis thaliana] gi 2224935 (AF004217) ethylene-insensitive3 [Arabidopsis thaliana]
10944	GM_164_B1_F02_MR	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
10945	GM_164_B1_F02_T7	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10946	GM_164_B1_F03_T7	g2065531	BLASTX	172	1e-20	83	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
10947	GM_164_B1_F05_MR	g3845197	BLASTN	474	2e-14	66	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
10948	GM_164_B1_F10_T7	g4063760	BLASTX	535	1e-49	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10949	GM_164_B1_G02_MR	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10950	GM_164_B1_G02_T7	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
10951	GM_164_B1_G04_MR	g100484	BLASTX	374	6e-33	62	hypothetical protein - garden snapdragon
10952	GM_164_B1_G04_T7	g2462134	BLASTX	235	3e-18	41	(Y13368) reverse transcriptase [Beta vulgaris]
10953	GM_164_B1_G09_T7	g4063760	BLASTX	166	6e-12	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10954	GM_164_B1_H04_T7	g1769898	BLASTX	415	8e-38	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10955	GM_164_B1_H07_T7	g2462936	BLASTX	402	1e-36	52	(Y12321) open reading frame 2 [Brassica oleracea]
10956	GM_164_B1_H09_MR	g2262178	BLASTX	178	5e-12	55	(AC002329) putative Mlo-like protein [Arabidopsis thaliana]
10957	GM_164_B1_H12_T7	g507910	BLASTN	531	2e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
10958	GM_164_B2_A02_T7	g2462732	BLASTX	292	3e-24	47	(AC002292) Hypothetical Protein [Arabidopsis thaliana]
10959	GM_164_B2_A03_T7	g2244807	BLASTX	253	6e-25	52	(Z97336) hypothetical protein [Arabidopsis thaliana]
10960	GM_164_B2_A07_MR	g3869063	BLASTN	382	3e-10	64	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K17O22, complete sequence [Arabidopsis thaliana]
10961	GM_164_B2_A07_T7	g130582	BLASTX	221	2e-31	45	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
10962	GM_164_B2_A08_T7	g3426334	BLASTN	535	3e-17	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
10963	GM_164_B2_B03_T7	g3845197	BLASTN	470	3e-14	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
10964	GM_164_B2_B06_T7	g2764526	BLASTN	635	1e-21	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
10965	GM_164_B2_B07_MR	g3522943	BLASTX	403	2e-35	71	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]
10966	GM_164_B2_B07_T7	g4063760	BLASTX	128	4e-14	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10967	GM_164_B2_C06_T7	g4063760	BLASTX	707	4e-68	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10968	GM_164_B2_C07_MR	g170605	BLASTN	425	2e-12	63	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
10969	GM_164_B2_C08_T7	g18559	BLASTN	435	1e-12	63	G.max gene for catalase
10970	GM_164_B2_C09_MR	g3550435	BLASTN	524	1e-16	63	Hordeum vulgare Hotr1 gene
10971	GM_164_B2_C10_T7	g3096930	BLASTX	276	1e-22	65	(AL023094) Homeodomain - like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
10972	GM_164_B2_D01_T7	g3249105	BLASTX	218	3e-24	58	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
10973	GM_164_B2_D04_MR	g1769898	BLASTX	330	3e-37	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
10974	GM_164_B2_D09_MR	g18559	BLASTN	361	3e-09	64	G.max gene for catalase
10975	GM_164_B2_D10_MR	g507910	BLASTN	382	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10976	GM_164_B2_D10_T7	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
10977	GM_164_B2_E01_T7	g2213608	BLASTX	187	1e-12	32	(AC000103) F21J9.2 [Arabidopsis thaliana]
10978	GM_164_B2_E03_MR	g4063760	BLASTX	170	1e-10	32	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10979	GM_164_B2_E03_T7	g3928142	BLASTX	231	7e-29	95	(AJ131045) protein phosphatase [Cicer arietinum]
10980	GM_164_B2_E07_T7	g905361	BLASTX	149	8e-09	83	(U22103) gag-protease polyprotein [Glycine max]
10981	GM_164_B2_E09_T7	g2961349	BLASTX	394	4e-38	48	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
10982	GM_164_B2_E12_T7	g4160362	BLASTN	425	4e-14	58	Saccharomyces cerevisiae complete mitochondrial genome
10983	GM_164_B2_F03_MR	g629693	BLASTX	352	2e-31	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
10984	GM_164_B2_F05_MR	g4063760	BLASTX	254	1e-19	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
10985	GM_164_B2_F05_T7	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
10986	GM_164_B2_F06_T7	g507910	BLASTN	469	1e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.
10987	GM_164_B2_F07_T7	g905361	BLASTX	160	5e-10	31	(U22103) gag-protease polyprotein [Glycine max]
10988	GM_164_B2_F10_T7	g3128168	BLASTX	362	4e-37	75	(AC004521) putative carboxyl-terminal peptidase [Arabidopsis thaliana]
10989	GM_164_B2_G01_MR	g2522230	BLASTX	132	1e-13	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
10990	GM_164_B2_G02_MR	g2462936	BLASTX	127	7e-13	42	(Y12321) open reading frame 2 [Brassica oleracea]
10991	GM_164_B2_G04_MR	g1778823	BLASTX	177	7e-13	87	(U82810) early light-induced protein [Glycine max]
10992	GM_164_B2_G05_MR	g4049647	BLASTN	366	2e-09	60	Melanoplus sanguinipes entomopoxvirus, complete genome
10993	GM_164_B2_G05_T7	g2961373	BLASTX	144	6e-14	43	(AL022141) putative disease resistance protein [Arabidopsis thaliana]
10994	GM_164_B2_G06_T7	g2352492	BLASTX	200	6e-24	50	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] gi 2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]
10995	GM_164_B2_G08_MR	g507910	BLASTN	392	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
10996	GM_164_B2_G09_T7	g3643604	BLASTX	180	8e-12	37	(AC005395) receptor-like protein kinase [Arabidopsis thaliana]
10997	GM_164_B2_G10_T7	g507910	BLASTN	603	1e-20	85	Glycine max BSR-101 satellite SB92 genomic sequence.
10998	GM_164_B2_H01_T7	g4038056	BLASTX	336	1e-28	43	(AC005897) putative transposon [Arabidopsis thaliana]
10999	GM_164_B2_H04_T7	g2583130	BLASTX	184	4e-12	30	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11000	GM_164_B2_H07_T7	g2522228	BLASTX	667	8e-65	65	(AB007466) reverse transcriptase-like protein [Vicia faba]
11001	GM_164_B2_H08_T7	g2443320	BLASTX	146	2e-23	43	(D85597) polyprotein [Oryza australiensis]
11002	GM_164_B2_H09_T7	g4063760	BLASTX	423	4e-69	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11003	GM_164_B2_H12_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11004	GM_165_A2_A02_MR	g3776577	BLASTX	144	2e-09	54	(AC005388) T22H22.24 [Arabidopsis thaliana]
11005	GM_165_A2_A07_MR	g2392895	BLASTX	232	3e-17	44	(AF017056) brassinosteroid insensitive 1 [Arabidopsis thaliana]
11006	GM_165_A2_A10_MR	g18559	BLASTN	914	2e-34	77	G.max gene for catalase
11007	GM_165_A2_B03_MR	g3269282	BLASTX	167	3e-10	38	(AL030978) putative protein [Arabidopsis thaliana]
11008	GM_165_A2_B04_MR	g507910	BLASTN	377	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
11009	GM_165_A2_B04_T7	g507910	BLASTN	351	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
11010	GM_165_A2_B09_MR	g507910	BLASTN	379	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11011	GM_165_A2_C02_MR	g507910	BLASTN	520	7e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
11012	GM_165_A2_C02_T7	g507910	BLASTN	549	3e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11013	GM_165_A2_C04_MR	g629693	BLASTX	172	1e-11	33	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
11014	GM_165_A2_C05_T7	g3660471	BLASTX	194	1e-13	82	(AJ001809) succinate dehydrogenase flavoprotein alpha subunit [Arabidopsis thaliana]
11015	GM_165_A2_C07_MR	g585416	BLASTX	122	3e-15	82	LIPOXYGENASE gi 467565 (X71344) lipoxygenase [Lens culinaris]
11016	GM_165_A2_C08_T7	g507910	BLASTN	504	4e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
11017	GM_165_A2_D01_MR	g629693	BLASTX	296	2e-31	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
11018	GM_165_A2_D05_MR	g2598589	BLASTX	115	4e-12	54	(Y15367) MtN19 [Medicago truncatula]
11019	GM_165_A2_D05_T7	g2598589	BLASTX	213	4e-16	45	(Y15367) MtN19 [Medicago truncatula]
11020	GM_165_A2_D07_T7	g2104945	BLASTN	792	7e-29	67	Glycine max copia-like retrotransposon Tgmr, complete sequence
11021	GM_165_A2_D10_MR	g3650039	BLASTX	293	3e-24	45	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
11022	GM_165_A2_E02_MR	g3702736	BLASTN	446	4e-13	71	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRI1, complete sequence [Arabidopsis thaliana]
11023	GM_165_A2_E03_T7	g3695394	BLASTN	349	1e-08	63	Arabidopsis thaliana BAC T5H22
11024	GM_165_A2_E05_T7	g507910	BLASTN	535	1e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
11025	GM_165_A2_E07_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11026	GM_165_A2_E07_T7	g507910	BLASTN	343	7e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11027	GM_165_A2_E12_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11028	GM_165_A2_F01_MR	g170030	BLASTN	1405	1e-56	95	Soybean nodulin-35 (N-35) gene encoding a subunit of uricase II, complete cds.
11029	GM_165_A2_F08_MR	g99922	BLASTX	371	2e-33	79	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
11030	GM_165_A2_F10_MR	g1705678	BLASTX	323	3e-27	76	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP) gi 862480 (U20213) valosin-containing protein [Glycine max]
11031	GM_165_A2_G01_T7	g3142328	BLASTN	918	1e-34	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11032	GM_165_A2_G05_MR	g507910	BLASTN	389	6e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.
11033	GM_165_A2_G05_T7	g507910	BLASTN	358	1e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
11034	GM_165_A2_H01_MR	g2443320	BLASTX	382	3e-33	52	(D85597) polyprotein [Oryza australiensis]
11035	GM_165_A2_H02_MR	g4063760	BLASTX	376	4e-34	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11036	GM_165_A2_H08_MR	g905361	BLASTX	427	4e-39	95	(U22103) gag-protease polyprotein [Glycine max]
11037	GM_165_A2_H11_T7	g3142328	BLASTN	531	5e-17	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11038	GM_165_A2_H12_MR	g3645899	BLASTX	199	2e-29	46	(U68408) 5' end not determined experimentally [Zea mays]
11039	GM_165_B1_A12_MR	g3599418	BLASTN	573	6e-19	79	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
11040	GM_165_B1_B07_T7	g3142328	BLASTN	907	4e-34	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11041	GM_165_B1_D08_MR	g4063760	BLASTX	253	1e-20	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11042	GM_165_B1_E02_T7	g18559	BLASTN	354	5e-09	74	G.max gene for catalase
11043	GM_165_B1_F02_T7	g507910	BLASTN	488	2e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
11044	GM_165_B1_F04_T7	g3650039	BLASTX	177	9e-12	38	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
11045	GM_165_B1_F05_T7	g3810595	BLASTX	159	1e-15	45	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
11046	GM_165_B1_F07_T7	g2995405	BLASTX	245	7e-19	63	(Y12432) polyprotein [Ananas comosus]
11047	GM_165_B1_G02_T7	g507910	BLASTN	591	4e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11048	GM_165_B1_H03_T7	g2583130	BLASTX	211	6e-15	37	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
11049	GM_165_B1_H08_T7	g18559	BLASTN	366	1e-09	71	G.max gene for catalase
11050	GM_165_B1_H10_T7	g100484	BLASTX	159	9e-10	43	hypothetical protein - garden snapdragon
11051	GM_165_B1_H12_T7	g3097320	BLASTN	969	7e-37	79	Glycine max gene for Bd 30K, complete cds
11052	GM_165_B2_A02_T7	g3650039	BLASTX	172	3e-11	42	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11053	GM_165_B2_A03_MR	g2995405	BLASTX	182	2e-15	47	(Y12432) polyprotein [Ananas comosus]
11054	GM_165_B2_A05_T7	g3319351	BLASTX	280	8e-33	45	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
11055	GM_165_B2_A10_T7	g18559	BLASTN	700	1e-24	83	G.max gene for catalase
11056	GM_165_B2_B01_MR	g1621467	BLASTX	369	3e-34	66	(U73106) laccase [Liriodendron tulipifera]
11057	GM_165_B2_B05_MR	g3142328	BLASTN	745	9e-38	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11058	GM_165_B2_B05_T7	g2129618	BLASTX	189	7e-13	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
11059	GM_165_B2_B06_MR	g18559	BLASTN	757	3e-27	75	G.max gene for catalase
11060	GM_165_B2_B07_MR	g1769897	BLASTX	195	7e-14	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11061	GM_165_B2_B10_MR	g1666236	BLASTX	145	7e-09	28	(U76261) unknown [Hordeum vulgare]
11062	GM_165_B2_B10_T7	g507910	BLASTN	549	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
11063	GM_165_B2_C04_MR	g4063760	BLASTX	371	4e-32	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11064	GM_165_B2_D02_MR	g3142328	BLASTN	872	2e-32	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11065	GM_165_B2_D03_MR	g3820976	BLASTN	436	1e-12	65	Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complet...
11066	GM_165_B2_D07_MR	g507910	BLASTN	523	5e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
11067	GM_165_B2_D07_T7	g507910	BLASTN	597	2e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
11068	GM_165_B2_D09_MR	g3193221	BLASTN	755	4e-27	81	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
11069	GM_165_B2_E01_MR	g1480927	BLASTN	537	2e-17	81	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
11070	GM_165_B2_E01_T7	g3097320	BLASTN	816	6e-30	75	Glycine max gene for Bd 30K, complete cds
11071	GM_165_B2_E05_T7	g3702341	BLASTX	343	6e-30	46	(AC005397) hypothetical protein [Arabidopsis thaliana]
11072	GM_165_B2_E06_MR	g507910	BLASTN	373	3e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11073	GM_165_B2_E08_MR	g2827711	BLASTX	304	4e-25	77	(AL021684) oxoglutarate dehydrogenase - like protein [Arabidopsis thaliana]
11074	GM_165_B2_E08_T7	g3355474	BLASTX	396	4e-36	84	(AC004218) unknown protein [Arabidopsis thaliana]
11075	GM_165_B2_E11_T7	g4151321	BLASTX	218	1e-16	72	(AF089085) putative auxin efflux carrier protein; AtPIN1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11076	GM_165_B2_F01_T7	g2760832	BLASTX	185	1e-13	52	(AC003105) similar to barley ids-4 gene product [Arabidopsis thaliana]
11077	GM_165_B2_F02_T7	g3695387	BLASTX	301	9e-25	65	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
11078	GM_165_B2_F07_T7	g3142379	BLASTX	220	8e-17	54	(AF053008) envelope-like [Glycine max]
11079	GM_165_B2_F08_T7	g421948	BLASTX	320	5e-28	55	UDP rhamnose--anthocyanidin-3-glucoside rhamnosyltransferase - garden petunia
11080	GM_165_B2_F09_MR	g2618704	BLASTX	163	1e-11	80	(AC002510) putative thioredoxin reductase [Arabidopsis thaliana]
11081	GM_165_B2_F09_T7	g2995405	BLASTX	249	3e-19	51	(Y12432) polyprotein [Ananas comosus]
11082	GM_165_B2_G01_T7	g18559	BLASTN	862	5e-32	75	G.max gene for catalase
11083	GM_165_B2_G02_MR	g4063760	BLASTX	254	1e-19	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11084	GM_165_B2_G04_MR	g3142328	BLASTN	698	1e-24	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11085	GM_165_B2_G04_T7	g3645899	BLASTX	160	9e-10	47	(U68408) 5' end not determined experimentally [Zea mays]
11086	GM_165_B2_G07_T7	g2522228	BLASTX	226	1e-17	41	(AB007466) reverse transcriptase-like protein [Vicia faba]
11087	GM_165_B2_G11_T7	g218179	BLASTX	171	6e-11	67	(D10207) H-ATPase [Oryza sativa] gi 444339 prf 1906387A H ATPase [Oryza sativa]
11088	GM_165_B2_H02_MR	g3142328	BLASTN	843	3e-31	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11089	GM_165_B2_H05_T7	g3142328	BLASTN	795	5e-29	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11090	GM_166_A2_E03_MR	g3097320	BLASTN	500	1e-15	77	Glycine max gene for Bd 30K, complete cds
11091	GM_166_A2_E05_MR	g1658457	BLASTX	272	6e-23	74	(U75248) reverse transcriptase [Gossypium barbadense]
11092	GM_166_A2_E06_T7	g629693	BLASTX	212	4e-16	49	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
11093	GM_166_A2_F04_T7	g3142328	BLASTN	429	2e-12	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11094	GM_166_A2_F06_MR	g3935157	BLASTX	172	4e-11	66	(AC005106) T25N20.21 [Arabidopsis thaliana]
11095	GM_166_A2_G02_T7	g3176795	BLASTN	470	4e-15	65	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
11096	GM_166_B1_A08_MR	g905361	BLASTX	127	2e-12	33	(U22103) gag-protease polyprotein [Glycine max]
11097	GM_166_B1_A12_T7	g3777527	BLASTX	166	4e-10	36	(AF053008) gag-pol polyprotein [Glycine max]
11098	GM_166_B1_B04_MR	g1946355	BLASTX	288	1e-23	50	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] gi 2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11099	GM_166_B1_C06_T7	g3241935	BLASTN	395	8e-11	65	Arabidopsis thaliana chromosome IV from 19 cM, complete sequence [Arabidopsis thaliana]
11100	GM_166_B1_C09_T7	g421955	BLASTX	185	4e-13	54	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
11101	GM_166_B1_C11_MR	g58340	BLASTN	443	4e-13	64	D.teissieri mitochondrial DNA for tRNA-fmet, tRNA-Ile, tRNA-Gln & tRNA-Val
11102	GM_166_B1_D01_T7	g18559	BLASTN	678	1e-23	76	G.max gene for catalase
11103	GM_166_B1_D02_T7	g3142328	BLASTN	1073	1e-41	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11104	GM_166_B1_D03_MR	g1666236	BLASTX	224	7e-18	32	(U76261) unknown [Hordeum vulgare]
11105	GM_166_B1_D05_T7	g498931	BLASTX	141	5e-09	46	(Z12825) ORF167; homologous to reverse transcriptases from retroviral-like transposons TNT 1-94 from tobacco and COPIA from Drosophila [Beta vulgaris]
11106	GM_166_B1_D06_MR	g3142379	BLASTX	237	1e-18	67	(AF053008) envelope-like [Glycine max]
11107	GM_166_B1_E02_MR	g4063760	BLASTX	288	3e-23	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11108	GM_166_B1_E04_MR	g3142328	BLASTN	784	2e-28	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11109	GM_166_B1_E04_T7	g3142328	BLASTN	528	6e-17	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11110	GM_166_B1_E05_MR	g1673583	BLASTX	317	7e-27	71	(U76687) lipoxygenase [Phaseolus vulgaris]
11111	GM_166_B1_E07_MR	g4115365	BLASTX	197	2e-13	42	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
11112	GM_166_B1_E12_MR	g4063760	BLASTX	195	2e-13	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11113	GM_166_B1_F01_MR	g3142328	BLASTN	1275	7e-51	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11114	GM_166_B1_G01_T7	g99922	BLASTX	375	8e-34	71	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
11115	GM_166_B1_G03_T7	g1091678	BLASTX	179	7e-12	44	activator-like transposable element [Pennisetum glaucum]
11116	GM_166_B1_G05_T7	g3142328	BLASTN	438	8e-13	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11117	GM_166_B1_G06_T7	g3097320	BLASTN	399	5e-11	80	Glycine max gene for Bd 30K, complete cds
11118	GM_166_B1_H01_T7	g3142328	BLASTN	1010	8e-39	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11119	GM_166_B1_H04_T7	g4050011	BLASTN	362	2e-09	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
11120	GM_166_B1_H06_T7	g4063760	BLASTX	297	3e-24	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11121	GM_167_A2_A01_MR	g1352078	BLASTX	168	3e-25	87	BETA-GALACTOSIDASE PRECURSOR (LACTASE) (EXO-(1-->4)-BETA-D-GALACTANASE) gi 507278 (L29451) b-galactosidase-related protein; putative [Malus domestica]
11122	GM_167_A2_A02_MR	g507910	BLASTN	392	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11123	GM_167_A2_A02_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11124	GM_167_A2_A03_T7	g2443320	BLASTX	122	5e-10	58	(D85597) polyprotein [Oryza australiensis]
11125	GM_167_A2_A04_T7	g18559	BLASTN	664	5e-23	71	G.max gene for catalase
11126	GM_167_A2_A08_MR	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11127	GM_167_A2_A08_T7	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
11128	GM_167_A2_A10_MR	g3777527	BLASTX	312	1e-25	51	(AF053008) gag-pol polyprotein [Glycine max]
11129	GM_167_A2_B05_MR	g3873182	BLASTN	368	1e-09	61	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
11130	GM_167_A2_C03_T7	g1666236	BLASTX	183	5e-13	36	(U76261) unknown [Hordeum vulgare]
11131	GM_167_A2_C07_MR	g3763934	BLASTX	191	2e-13	73	(AC004450) hypothetical protein [Arabidopsis thaliana]
11132	GM_167_A2_C11_T7	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11133	GM_167_A2_D03_MR	g3445210	BLASTX	100	2e-10	28	(AC004786) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]
11134	GM_167_A2_D07_T7	g3142328	BLASTN	791	7e-29	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11135	GM_167_A2_D09_T7	g3142328	BLASTN	892	2e-33	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11136	GM_167_A2_D12_T7	g531389	BLASTX	228	3e-18	52	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
11137	GM_167_A2_E01_MR	g507910	BLASTN	436	4e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11138	GM_167_A2_E01_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11139	GM_167_A2_E05_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11140	GM_167_A2_E10_MR	g3930515	BLASTX	109	4e-09	43	(AF059674) putative gag protein [Nicotiana tabacum]
11141	GM_167_A2_F04_T7	g2522230	BLASTX	220	2e-17	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11142	GM_167_A2_F10_MR	g4050011	BLASTN	384	2e-10	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
11143	GM_167_A2_F11_MR	g3033389	BLASTX	182	4e-12	40	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
11144	GM_167_A2_F11_T7	g3033389	BLASTX	169	9e-11	42	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
11145	GM_167_A2_G03_MR	g629722	BLASTX	167	7e-11	33	finger protein pcp1 - potato gi 563623 (X82328) putative DNA/RNA binding protein [Solanum tuberosum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11146	GM_167_A2_G07_T7	g4038056	BLASTX	328	9e-28	56	(AC005897) putative transposon [Arabidopsis thaliana]
11147	GM_167_A2_G08_T7	g3869075	BLASTN	376	2e-12	75	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]
11148	GM_167_A2_G12_MR	g3510538	BLASTX	415	4e-38	93	(U93167) expansin [Prunus armeniaca]
11149	GM_167_A2_H04_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11150	GM_167_A2_H04_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11151	GM_167_A2_H06_T7	g3097320	BLASTN	567	1e-18	79	Glycine max gene for Bd 30K, complete cds
11152	GM_167_A2_H11_T7	g18559	BLASTN	473	2e-14	78	G.max gene for catalase
11153	GM_167_B1_A11_T7	g2443320	BLASTX	158	2e-14	43	(D85597) polyprotein [Oryza australiensis]
11154	GM_167_B1_B01_MR	g3142328	BLASTN	668	6e-43	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11155	GM_167_B1_B01_T7	g2443320	BLASTX	340	1e-28	51	(D85597) polyprotein [Oryza australiensis]
11156	GM_167_B1_B08_MR	g1514643	BLASTX	205	3e-14	53	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
11157	GM_167_B1_C03_T7	g3142328	BLASTN	960	2e-36	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11158	GM_167_B1_C04_MR	g3298551	BLASTX	169	6e-11	52	(AC004681) putative salt-inducible protein [Arabidopsis thaliana]
11159	GM_167_B1_C05_T7	g3142330	BLASTX	644	2e-62	98	(U96295) envelope-like [Glycine max]
11160	GM_167_B1_C06_T7	g4038056	BLASTX	321	5e-27	53	(AC005897) putative transposon [Arabidopsis thaliana]
11161	GM_167_B1_C09_MR	g2995405	BLASTX	339	6e-29	61	(Y12432) polyprotein [Ananas comosus]
11162	GM_167_B1_C09_T7	g1142700	BLASTN	357	8e-14	73	Glycine max satellite STR120-A.2.
11163	GM_167_B1_C12_T7	g3334667	BLASTX	158	6e-10	85	(Y10493) putative cytochrome P450 [Glycine max]
11164	GM_167_B1_D01_T7	g3097320	BLASTN	558	3e-18	78	Glycine max gene for Bd 30K, complete cds
11165	GM_167_B1_D04_MR	g1171591	BLASTN	359	3e-09	63	P.falciparum complete gene map of plastid-like DNA (IR-B)
11166	GM_167_B1_D06_T7	g3243214	BLASTN	465	6e-14	69	Arabidopsis thaliana BAC T19B17 from chromsome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]
11167	GM_167_B1_E01_T7	g3777527	BLASTX	291	2e-23	46	(AF053008) gag-pol polyprotein [Glycine max]
11168	GM_167_B1_E02_T7	g1769898	BLASTX	370	9e-33	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11169	GM_167_B1_E04_MR	g507910	BLASTN	411	6e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
11170	GM_167_B1_F01_MR	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11171	GM_167_B1_F01_T7	g4063760	BLASTX	337	4e-31	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11172	GM_167_B1_F03_MR	g130582	BLASTX	259	2e-25	57	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11173	GM_167_B1_F04_MR	g1167523	BLASTX	387	9e-34	62	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11174	GM_167_B1_F04_T7	g2462134	BLASTX	353	2e-31	50	(Y13368) reverse transcriptase [Beta vulgaris]
11175	GM_167_B1_F05_T7	g3810596	BLASTX	145	3e-14	53	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
11176	GM_167_B1_F06_T7	g2522228	BLASTX	250	3e-20	42	(AB007466) reverse transcriptase-like protein [Vicia faba]
11177	GM_167_B1_G01_MR	g1167523	BLASTX	299	2e-24	53	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11178	GM_167_B1_G05_MR	g507910	BLASTN	526	4e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11179	GM_167_B1_G05_T7	g507910	BLASTN	566	6e-19	79	Glycine max BSR-101 satellite SB92 genomic sequence.
11180	GM_167_B1_G08_T7	g541936	BLASTX	198	4e-15	67	4-coumarate--CoA ligase (EC 6.2.1.12) (clone GM4CL14) - soybean (fragment)
11181	GM_167_B1_G12_T7	g336279	BLASTN	357	4e-09	62	Apis mellifera ligustica complete mitochondrial genome
11182	GM_167_B1_H06_T7	g3142328	BLASTN	1583	6e-65	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11183	GM_167_B1_H08_T7	g2244876	BLASTX	159	3e-19	71	(Z97338) hypothetical protein [Arabidopsis thaliana]
11184	GM_167_B1_H09_MR	g2522230	BLASTX	157	1e-10	36	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11185	GM_168_A1_A09_MR	g507910	BLASTN	458	4e-14	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11186	GM_168_A1_D02_MR	g13767	BLASTN	483	1e-15	68	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
11187	GM_168_A1_H10_MR	g3152629	BLASTN	429	2e-12	66	Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence [Homo sapiens]
11188	GM_168_A2_A01_T7	g1431738	BLASTN	392	8e-11	92	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
11189	GM_168_A2_A03_T7	g1709918	BLASTX	420	1e-38	91	AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) (GPAT) gi 438899 (L23833) glutamine phosphoribosylpyrophosphate amidotransferase [Glycine max]
11190	GM_168_A2_A05_MR	g1769898	BLASTX	444	3e-41	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11191	GM_168_A2_A08_MR	g1171583	BLASTN	349	1e-08	60	P.falciparum complete gene map of plastid-like DNA (IR-A)
11192	GM_168_A2_B01_MR	g1805254	BLASTX	195	4e-30	73	(U62622) monogalactosyldiacylglycerol synthase [Cucumis sativus]
11193	GM_168_A2_B04_MR	g3777527	BLASTX	200	9e-14	31	(AF053008) gag-pol polyprotein [Glycine max]
11194	GM_168_A2_B06_MR	g3319351	BLASTX	245	1e-18	44	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11195	GM_168_A2_B07_MR	g3097320	BLASTN	586	2e-19	75	Glycine max gene for Bd 30K, complete cds
11196	GM_168_A2_B09_MR	g905361	BLASTX	667	9e-65	96	(U22103) gag-protease polyprotein [Glycine max]
11197	GM_168_A2_B09_T7	g4038056	BLASTX	131	4e-15	44	(AC005897) putative transposon [Arabidopsis thaliana]
11198	GM_168_A2_C08_T7	g4063760	BLASTX	201	2e-21	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11199	GM_168_A2_C10_T7	g905361	BLASTX	420	2e-38	92	(U22103) gag-protease polyprotein [Glycine max]
11200	GM_168_A2_D01_MR	g2522230	BLASTX	263	6e-22	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11201	GM_168_A2_D02_T7	g1514643	BLASTX	173	6e-11	56	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
11202	GM_168_A2_D03_T7	g2760832	BLASTX	262	7e-22	62	(AC003105) similar to barley ids-4 gene product [Arabidopsis thaliana]
11203	GM_168_A2_D04_MR	g2145358	BLASTX	121	5e-12	56	(Y10922) HD-Zip protein [Arabidopsis thaliana]
11204	GM_168_A2_D07_MR	g178823	BLASTN	333	7e-09	61	Human apolipoprotein B gene hypervariable region, 3' flank.
11205	GM_168_A2_D10_MR	g2995405	BLASTX	434	3e-39	61	(Y12432) polyprotein [Ananas comosus]
11206	GM_168_A2_D12_MR	g3777527	BLASTX	639	2e-60	96	(AF053008) gag-pol polyprotein [Glycine max]
11207	GM_168_A2_E06_T7	g3023281	BLASTX	194	8e-14	50	HIGH AFFINITY AMMONIUM TRANSPORTER gi 2065194 gnl PID e223603 (X95098) ammonium transporter [Lycopersicon esculentum]
11208	GM_168_A2_E09_MR	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
11209	GM_168_A2_E09_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11210	GM_168_A2_E12_MR	g99922	BLASTX	360	4e-58	82	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
11211	GM_168_A2_F05_T7	g2702264	BLASTX	143	3e-09	41	(AC003033) similar to disease resistance protein (Cf-2.2) [Arabidopsis thaliana]
11212	GM_168_A2_F07_T7	g1167523	BLASTX	348	1e-29	69	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11213	GM_168_A2_F10_T7	g3777527	BLASTX	477	3e-43	94	(AF053008) gag-pol polyprotein [Glycine max]
11214	GM_168_A2_G01_MR	g2959767	BLASTX	150	4e-18	54	(AJ002584) AtMRP4 [Arabidopsis thaliana]
11215	GM_168_A2_G07_T7	g170080	BLASTN	737	2e-26	91	Soybean seed lectin gene transposable element tgm1.
11216	GM_168_A2_G08_MR	g2853072	BLASTX	311	4e-27	54	(AL021768) putative protein [Arabidopsis thaliana]
11217	GM_168_A2_G12_MR	g3860167	BLASTX	156	3e-09	40	(AF098964) disease resistance protein RPP1-WsC [Arabidopsis thaliana]
11218	GM_168_A2_H03_MR	g905361	BLASTX	185	1e-12	62	(U22103) gag-protease polyprotein [Glycine max]
11219	GM_168_A2_H04_T7	g2264309	BLASTN	582	3e-19	75	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]
11220	GM_168_A2_H05_T7	g3063690	BLASTN	444	5e-13	77	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11221	GM_168_A2_H06_MR	g4159702	BLASTN	581	3e-19	69	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2N11, complete sequence [Arabidopsis thaliana]
11222	GM_168_A2_H12_MR	g2495155	BLASTX	92	2e-13	61	GLUTAMYL-TRNA REDUCTASE 1 PRECURSOR (GLUTR) gi 1694926 gnl PID d1009544 (D50407) glutamyl-tRNA reductase [Cucumis sativus]
11223	GM_168_B1_A01_T7	g862479	BLASTN	434	1e-12	81	Glycine max valosin-containing protein mRNA, complete cds.
11224	GM_168_B1_A04_T7	g100484	BLASTX	121	5e-13	48	hypothetical protein - garden snapdragon
11225	GM_168_B1_A07_MR	g2894502	BLASTN	352	6e-09	65	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-102, complete sequence [Plasmodium falciparum]
11226	GM_168_B1_A09_MR	g18559	BLASTN	487	5e-15	73	G.max gene for catalase
11227	GM_168_B1_B01_T7	g4063770	BLASTX	185	2e-12	37	(AB004906) transposase [Ipomoea purpurea]
11228	GM_168_B1_B04_MR	g1171591	BLASTN	358	4e-09	63	P.falciparum complete gene map of plastid-like DNA (IR-B)
11229	GM_168_B1_B06_T7	g3777527	BLASTX	548	8e-51	96	(AF053008) gag-pol polyprotein [Glycine max]
11230	GM_168_B1_B07_T7	g2982444	BLASTX	184	2e-13	43	(AL022224) CLV1 receptor kinase like protein [Arabidopsis thaliana]
11231	GM_168_B1_B08_T7	g3452136	BLASTN	339	4e-09	79	Glycine max mRNA for glucose-6-phosphate-dehydrogenase, partial
11232	GM_168_B1_B09_MR	g3738114	BLASTN	364	2e-09	62	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
11233	GM_168_B1_B09_T7	g282881	BLASTX	224	1e-16	49	receptor-like protein kinase precursor - Arabidopsis thaliana gi 166846 (M84658) receptor-like protein kinase [Arabidopsis thaliana]
11234	GM_168_B1_B10_MR	g1514643	BLASTX	128	5e-14	56	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
11235	GM_168_B1_C03_T7	g1769898	BLASTX	225	5e-17	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11236	GM_168_B1_C09_MR	g2995405	BLASTX	394	7e-35	62	(Y12432) polyprotein [Ananas comosus]
11237	GM_168_B1_D03_T7	g3688600	BLASTX	266	1e-27	70	(AB009030) beta-Amyrin Synthase [Panax ginseng]
11238	GM_168_B1_D04_MR	g3142328	BLASTN	766	1e-27	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11239	GM_168_B1_D11_MR	g2145358	BLASTX	196	1e-13	77	(Y10922) HD-Zip protein [Arabidopsis thaliana]
11240	GM_168_B1_E01_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11241	GM_168_B1_E02_T7	g3176686	BLASTX	320	5e-27	69	(AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomyces occidentalis. [Arabidopsis thaliana]
11242	GM_168_B1_E03_T7	g3283026	BLASTX	150	3e-11	62	putative transposase [Arabidopsis thaliana]
11243	GM_168_B1_E05_T7	g1236920	BLASTN	356	4e-09	65	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11244	GM_168_B1_E06_MR	g3097320	BLASTN	361	3e-09	78	Glycine max gene for Bd 30K, complete cds
11245	GM_168_B1_E11_MR	g3142328	BLASTN	554	4e-18	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11246	GM_168_B1_F02_MR	g1085621	BLASTX	179	2e-12	89	alcohol dehydrogenase (EC 1.1.1.1) 1CN - Phaseolus acutifolius gi 452767 (Z23171) alcohol dehydrogenase-1CN [Phaseolus acutifolius]
11247	GM_168_B1_F07_MR	g4063760	BLASTX	253	1e-19	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11248	GM_168_B1_F10_MR	g3810596	BLASTX	213	2e-15	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
11249	GM_168_B1_G08_T7	g576754	BLASTN	347	5e-09	64	Myrmecia pilosula HI87-128 mitochondrion cytochrome b gene, partial cds.
11250	GM_168_B1_H02_MR	g507910	BLASTN	518	8e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
11251	GM_168_B1_H06_MR	g2586083	BLASTX	254	1e-19	46	(U72725) receptor kinase-like protein [Oryza longistaminata]
11252	GM_168_B1_H06_T7	g3250688	BLASTX	210	2e-16	47	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
11253	GM_168_B1_H07_MR	g2522228	BLASTX	165	7e-11	49	(AB007466) reverse transcriptase-like protein [Vicia faba]
11254	GM_168_B1_H09_MR	g18559	BLASTN	598	4e-20	74	G.max gene for catalase
11255	GM_168_B1_H09_T7	g3789709	BLASTN	402	4e-11	66	Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence [Homo sapiens]
11256	GM_168_B1_H10_T7	g3142328	BLASTN	527	7e-17	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11257	GM_168_B2_B01_MR	g3549652	BLASTX	109	8e-09	83	(AJ224982) MAP3K epsilon protein kinase [Arabidopsis thaliana]
11258	GM_168_B2_B02_MR	g505129	BLASTN	371	8e-10	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
11259	GM_168_B2_B04_T7	g4063760	BLASTX	335	3e-28	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11260	GM_168_B2_B07_MR	g3777527	BLASTX	694	2e-66	94	(AF053008) gag-pol polyprotein [Glycine max]
11261	GM_168_B2_C07_MR	g2443320	BLASTX	342	6e-29	49	(D85597) polyprotein [Oryza australiensis]
11262	GM_168_B2_D03_MR	g2497486	BLASTX	114	8e-16	65	URIDYLATE KINASE (UK) (URIDINE MONOPHOSPHATE KINASE) (UMP KINASE) gi 2121275 (AF000147) UMP/CMP kinase [Arabidopsis thaliana]
11263	GM_168_B2_D04_T7	g3777527	BLASTX	619	2e-58	94	(AF053008) gag-pol polyprotein [Glycine max]
11264	GM_168_B2_D07_MR	g3142328	BLASTN	658	8e-23	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11265	GM_168_B2_D08_MR	g4006828	BLASTX	119	1e-12	31	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
11266	GM_168_B2_E04_MR	g3097320	BLASTN	363	2e-09	73	Glycine max gene for Bd 30K, complete cds
11267	GM_168_B2_G04_MR	g2995405	BLASTX	317	3e-31	62	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11268	GM_168_B2_G09_MR	g3283026	BLASTX	174	2e-11	30	putative transposase [Arabidopsis thaliana]
11269	GM_168_B2_G09_T7	g2522228	BLASTX	198	2e-14	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
11270	GM_168_B2_G10_MR	g2624372	BLASTN	365	2e-09	60	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-64, complete sequence [Plasmodium falciparum]
11271	GM_168_B2_H05_MR	g2429543	BLASTX	237	8e-18	44	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]
11272	GM_168_B2_H06_MR	g99922	BLASTX	365	8e-33	73	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
11273	GM_168_B2_H10_T7	g2828183	BLASTN	404	3e-11	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPL12, complete sequence [Arabidopsis thaliana]
11274	GM_168_B2_H11_MR	g100484	BLASTX	173	3e-11	45	hypothetical protein - garden snapdragon
11275	GM_169_A1_A04_MR	g2522230	BLASTX	265	3e-22	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11276	GM_169_A1_A05_MR	g1167523	BLASTX	429	3e-38	68	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11277	GM_169_A1_A06_MR	g3097320	BLASTN	511	4e-16	73	Glycine max gene for Bd 30K, complete cds
11278	GM_169_A1_A07_MR	g507910	BLASTN	678	5e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
11279	GM_169_A1_B05_MR	g905361	BLASTX	178	7e-12	40	(U22103) gag-protease polyprotein [Glycine max]
11280	GM_169_A1_B06_MR	g4063756	BLASTN	447	4e-13	66	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11281	GM_169_A1_C07_MR	g1666236	BLASTX	174	4e-12	30	(U76261) unknown [Hordeum vulgare]
11282	GM_169_A1_C12_MR	g2398681	BLASTX	366	6e-33	93	(Y14798) 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase [Morinda citrifolia]
11283	GM_169_A1_D05_MR	g2129832	BLASTX	323	2e-28	78	heat shock transcription factor 5 - soybean gi 671868 (Z46956) heat shock transcription factor 5 [Glycine max]
11284	GM_169_A1_D06_MR	g1771160	BLASTX	389	2e-34	65	(X98929) SBT1 [Lycopersicon esculentum] gi 3687305 gnl PID e1299610 (AJ006378) subtilisin-like protease [Lycopersicon esculentum]
11285	GM_169_A1_D07_MR	g3777527	BLASTX	508	2e-46	92	(AF053008) gag-pol polyprotein [Glycine max]
11286	GM_169_A1_D08_MR	g1142701	BLASTN	1188	2e-47	85	Glycine max satellite STR120-A.3.
11287	GM_169_A1_D10_MR	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
11288	GM_169_A1_E06_MR	g18559	BLASTN	492	3e-15	71	G.max gene for catalase
11289	GM_169_A1_E07_MR	g4063760	BLASTX	407	6e-36	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11290	GM_169_A1_E08_MR	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11291	GM_169_A1_E11_MR	g4063760	BLASTX	178	8e-16	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11292	GM_169_A1_F04_MR	g4063756	BLASTN	429	2e-12	73	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11293	GM_169_A1_G01_MR	g2760839	BLASTX	212	1e-15	42	(AC003105) putative receptor kinase [Arabidopsis thaliana]
11294	GM_169_A1_G09_MR	g3319366	BLASTX	185	1e-13	42	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
11295	GM_169_A1_H02_MR	g421955	BLASTX	321	4e-28	58	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
11296	GM_169_A1_H03_MR	g3097320	BLASTN	667	4e-23	81	Glycine max gene for Bd 30K, complete cds
11297	GM_169_A2_A04_T7	g1167523	BLASTX	181	8e-12	38	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11298	GM_169_A2_A06_T7	g2522230	BLASTX	160	4e-11	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11299	GM_169_A2_A07_MR	g4063760	BLASTX	154	6e-09	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11300	GM_169_A2_A08_T7	g3097320	BLASTN	990	8e-38	78	Glycine max gene for Bd 30K, complete cds
11301	GM_169_A2_B02_MR	g3319345	BLASTX	140	5e-11	42	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
11302	GM_169_A2_B03_MR	g3097320	BLASTN	1424	2e-57	81	Glycine max gene for Bd 30K, complete cds
11303	GM_169_A2_B04_MR	g905361	BLASTX	297	2e-29	70	(U22103) gag-protease polyprotein [Glycine max]
11304	GM_169_A2_B07_T7	g3097320	BLASTN	405	3e-11	68	Glycine max gene for Bd 30K, complete cds
11305	GM_169_A2_C04_MR	g3869176	BLASTX	215	6e-17	81	(AB019518) cyclophilin [Trichophyton mentagrophytes]
11306	GM_169_A2_C07_MR	g1769898	BLASTX	420	2e-38	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11307	GM_169_A2_C07_T7	g3097320	BLASTN	988	1e-37	77	Glycine max gene for Bd 30K, complete cds
11308	GM_169_A2_D02_MR	g1167523	BLASTX	153	7e-15	32	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11309	GM_169_A2_D09_MR	g3097320	BLASTN	368	1e-09	75	Glycine max gene for Bd 30K, complete cds
11310	GM_169_A2_D09_T7	g99922	BLASTX	374	1e-33	57	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
11311	GM_169_A2_E01_MR	g130582	BLASTX	231	9e-23	36	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
11312	GM_169_A2_E04_MR	g18767	BLASTN	382	9e-17	70	Soybean Tgm6 transposable element 5' end
11313	GM_169_A2_E06_MR	g905361	BLASTX	199	4e-14	36	(U22103) gag-protease polyprotein [Glycine max]
11314	GM_169_A2_F01_MR	g530207	BLASTX	198	3e-26	68	(L35272) heat shock protein [Glycine max]
11315	GM_169_A2_F04_T7	g3980405	BLASTX	220	2e-17	75	(AC004561) putative tropinone reductase [Arabidopsis thaliana]
11316	GM_169_A2_F05_MR	g1813979	BLASTX	184	1e-13	49	(Y10860) hypothetical protein [Musa acuminata]
11317	GM_169_A2_F06_MR	g3746069	BLASTX	256	8e-20	41	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11318	GM_169_A2_F07_T7	g343789	BLASTN	359	3e-09	62	Yeast (S.cerevisiae) mitochondrial cytochrome oxi1 gene and flanks.
11319	GM_169_A2_F11_MR	g3367528	BLASTX	147	7e-09	30	(AC004392) Strong similarity to gi 2160138 F19K23.6 gene product from A. thaliana BAC gb AC000375. [Arabidopsis thaliana]
11320	GM_169_A2_G01_MR	g2462936	BLASTX	533	1e-50	55	(Y12321) open reading frame 2 [Brassica oleracea]
11321	GM_169_A2_G02_MR	g4063770	BLASTX	160	8e-20	37	(AB004906) transposase [Ipomoea purpurea]
11322	GM_169_A2_G03_MR	g505129	BLASTN	349	8e-09	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
11323	GM_169_A2_G05_MR	g992916	BLASTN	1210	1e-47	71	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
11324	GM_169_A2_G10_MR	g4063760	BLASTX	388	6e-34	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11325	GM_169_A2_G12_MR	g18559	BLASTN	879	8e-33	71	G.max gene for catalase
11326	GM_169_A2_H02_T7	g1167523	BLASTX	486	3e-44	54	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11327	GM_169_A2_H04_MR	g2160155	BLASTN	373	3e-21	69	Sequence of BAC F21M12 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
11328	GM_169_A2_H05_MR	g1730796	BLASTX	210	5e-15	40	HYPOTHETICAL 124.5 KD PROTEIN IN SKO1-RPL44A INTERGENIC REGION gi 2132760 pir S60964 probable membrane protein YNL163c - yeast (Saccharomyces cerevisiae) gi 1050790 (X92517) N1718 gene product [Saccharomyces cerevisiae] gi 1302132 gnl PID e239817 (Z71439) ORF YNL163c [Saccharomyces cerevisiae]
11329	GM_169_A2_H06_T7	g130405	BLASTX	241	3e-18	35	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 17.6) gi 74642 pir GNFF17 retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) transposon 17.6 gi 1335613 gnl PID e1849 (X01472) ORF 2, pot. reverse transcriptase [Drosophila melanogaster] gi 224319 prf 1101404B ORF 2 [Drosophila melanogaster]
11330	GM_169_A2_H09_MR	g507910	BLASTN	367	6e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11331	GM_169_B1_A02_MR	g100484	BLASTX	372	1e-32	53	hypothetical protein - garden snapdragon
11332	GM_169_B1_A02_T7	g576754	BLASTN	351	3e-09	63	Myrmecia pilosula HI87-128 mitochondrion cytochrome b gene, partial cds.
11333	GM_169_B1_A07_MR	g18559	BLASTN	351	7e-09	73	G.max gene for catalase
11334	GM_169_B1_A10_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11335	GM_169_B1_A10_T7	g507910	BLASTN	402	1e-11	84	Glycine max BSR-101 satellite SB92 genomic sequence.
11336	GM_169_B1_B07_T7	g1769899	BLASTX	286	2e-24	74	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11337	GM_169_B1_C08_MR	g3785980	BLASTX	283	3e-23	42	(AC005560) hypothetical protein [Arabidopsis thaliana]
11338	GM_169_B1_C09_MR	g2982169	BLASTN	358	4e-09	61	Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence [Homo sapiens]
11339	GM_169_B1_C09_T7	g340796	BLASTN	405	3e-12	64	Figure 6. DNA sequence of three 3' apoB VNTR alleles.
11340	GM_169_B1_C12_MR	g2335097	BLASTX	269	2e-21	83	(AC002339) putative receptor-like protein kinase [Arabidopsis thaliana]
11341	GM_169_B1_D03_MR	g2522230	BLASTX	345	1e-30	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11342	GM_169_B1_D04_MR	g3334667	BLASTX	324	4e-28	43	(Y10493) putative cytochrome P450 [Glycine max]
11343	GM_169_B1_D04_T7	g3334667	BLASTX	177	4e-14	75	(Y10493) putative cytochrome P450 [Glycine max]
11344	GM_169_B1_D09_T7	g507910	BLASTN	346	5e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11345	GM_169_B1_D11_T7	g18559	BLASTN	452	2e-13	80	G.max gene for catalase
11346	GM_169_B1_E03_MR	g4063760	BLASTX	324	4e-27	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11347	GM_169_B1_E04_MR	g452593	BLASTX	162	1e-14	57	(D21814) ORF [Lilium longiflorum]
11348	GM_169_B1_E07_MR	g2492675	BLASTX	156	8e-10	76	ACTIN-LIKE PROTEIN 3 >gi 1718497 (U79737) actin-related protein 3 [Neurospora crassa]
11349	GM_169_B1_F01_MR	g3184285	BLASTX	208	3e-16	52	(AC004136) hypothetical protein [Arabidopsis thaliana]
11350	GM_169_B1_F03_MR	g1769898	BLASTX	428	1e-41	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11351	GM_169_B1_F04_MR	g3250687	BLASTX	264	1e-24	40	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
11352	GM_169_B1_F04_T7	g1769896	BLASTN	387	2e-10	66	A.thaliana lectin receptor kinase gene
11353	GM_169_B1_F08_MR	g507910	BLASTN	406	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11354	GM_169_B1_G09_MR	g992916	BLASTN	414	1e-11	63	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
11355	GM_169_B1_G10_MR	g1906369	BLASTX	400	7e-36	61	(Y11998) hypothetical protein [Pseudomonas fluorescens]
11356	GM_169_B1_G10_T7	g1906369	BLASTX	300	2e-38	50	(Y11998) hypothetical protein [Pseudomonas fluorescens]
11357	GM_169_B1_H02_MR	g3024387	BLASTX	297	1e-25	66	POLYGALACTURONASE PRECURSOR (PG) (PECTINASE) gi 668998 (U20431) polygalacturonase [Medicago sativa]
11358	GM_169_B1_H04_T7	g2244803	BLASTX	280	9e-24	44	(Z97336) reverse transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11359	GM_169_B1_H05_MR	g2501460	BLASTX	154	5e-19	66	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) gi 1545952 gnl PID e244584 (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]
11360	GM_169_B1_H08_MR	g2194117	BLASTX	439	3e-40	60	(AC002062) Strong similarity to Arabidopsis receptor protein kinase PR5K (gb ATU48698). [Arabidopsis thaliana]
11361	GM_169_B1_H12_T7	g18768	BLASTN	386	4e-11	76	Soybean Tgm6 transposable element 3' end
11362	GM_169_B2_A03_T7	g2462936	BLASTX	164	2e-11	44	(Y12321) open reading frame 2 [Brassica oleracea]
11363	GM_169_B2_A08_MR	g3142328	BLASTN	741	1e-26	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11364	GM_169_B2_B02_MR	g507910	BLASTN	363	8e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
11365	GM_169_B2_B03_MR	g4063756	BLASTN	542	2e-17	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11366	GM_169_B2_B06_T7	g18559	BLASTN	1112	2e-43	84	G.max gene for catalase
11367	GM_169_B2_B09_MR	g99922	BLASTX	205	4e-31	60	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
11368	GM_169_B2_B10_MR	g4156182	BLASTN	432	2e-12	64	Homo sapiens clone DJ0815D20, complete sequence [Homo sapiens]
11369	GM_169_B2_B11_MR	g2264320	BLASTN	547	1e-17	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
11370	GM_169_B2_B11_T7	g3894387	BLASTX	151	9e-09	46	(AF053995) Hcr2-0B [Lycopersicon esculentum]
11371	GM_169_B2_C05_MR	g3650036	BLASTX	185	1e-12	30	(AC005396) putative transposase [Arabidopsis thaliana]
11372	GM_169_B2_C12_T7	g3599418	BLASTN	525	9e-17	64	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
11373	GM_169_B2_D06_MR	g3377848	BLASTX	216	6e-23	56	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
11374	GM_169_B2_D12_MR	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
11375	GM_169_B2_E07_MR	g1799782	BLASTX	238	4e-19	92	BILE ACID-INDUCIBLE OPERON PROTEIN F. [Escherichia coli]
11376	GM_169_B2_E07_T7	g1799782	BLASTX	196	3e-14	100	BILE ACID-INDUCIBLE OPERON PROTEIN F. [Escherichia coli]
11377	GM_169_B2_E09_T7	g99922	BLASTX	341	5e-42	80	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
11378	GM_169_B2_E11_MR	g2522228	BLASTX	327	9e-29	74	(AB007466) reverse transcriptase-like protein [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11379	GM_169_B2_F01_MR	g3142328	BLASTN	681	1e-38	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11380	GM_169_B2_F01_T7	g3738337	BLASTX	214	2e-15	38	(AC005170) putative reverse transcriptase [Arabidopsis thaliana]
11381	GM_169_B2_F09_MR	g3645899	BLASTX	286	2e-24	47	(U68408) 5' end not determined experimentally [Zea mays]
11382	GM_169_B2_F10_MR	g1209754	BLASTN	375	6e-10	64	Trypanosoma cruzi kinetoplast maxicircle DNA, clone TRCKPMAX
11383	GM_169_B2_F12_MR	g3645899	BLASTX	285	5e-23	48	(U68408) 5' end not determined experimentally [Zea mays]
11384	GM_169_B2_G07_T7	g4063760	BLASTX	347	2e-29	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11385	GM_169_B2_G10_T7	g18559	BLASTN	887	3e-33	77	G.max gene for catalase
11386	GM_169_B2_G11_MR	g4063756	BLASTN	377	5e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11387	GM_169_B2_G11_T7	g507910	BLASTN	698	6e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
11388	GM_169_B2_G12_MR	g3097320	BLASTN	406	2e-11	70	Glycine max gene for Bd 30K, complete cds
11389	GM_169_B2_G12_T7	g3645899	BLASTX	197	1e-13	56	(U68408) 5' end not determined experimentally [Zea mays]
11390	GM_169_B2_H01_T7	g3319366	BLASTX	192	2e-14	43	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
11391	GM_170_A2_A01_T7	g3650039	BLASTX	144	2e-12	54	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
11392	GM_170_A2_A03_MR	g2326264	BLASTN	429	2e-12	61	Arabidopsis thaliana DNA for CCT alpha/TCP-1, complete cds.
11393	GM_170_A2_A06_MR	g2654226	BLASTX	97	2e-09	58	(AJ003069) aminoacyl-t-RNA synthetase [Arabidopsis thaliana]
11394	GM_170_A2_A06_T7	g1946355	BLASTX	153	4e-09	33	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] gi 2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]
11395	GM_170_A2_A08_MR	g507910	BLASTN	401	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11396	GM_170_A2_A09_MR	g13774	BLASTN	347	6e-09	61	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
11397	GM_170_A2_A10_MR	g1871190	BLASTX	305	2e-29	52	(U90439) Ser/Thr kinase isolog [Arabidopsis thaliana]
11398	GM_170_A2_A10_T7	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
11399	GM_170_A2_B08_MR	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
11400	GM_170_A2_B08_T7	g4063760	BLASTX	389	5e-34	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11401	GM_170_A2_B09_MR	g3176726	BLASTX	164	3e-10	51	(AC002392) putative serine proteinase [Arabidopsis thaliana]
11402	GM_170_A2_B11_MR	g3779030	BLASTX	168	6e-12	32	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
11403	GM_170_A2_B12_MR	g4063760	BLASTX	194	4e-17	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11404	GM_170_A2_B12_T7	g507910	BLASTN	456	5e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
11405	GM_170_A2_C01_T7	g18559	BLASTN	961	2e-36	94	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11406	GM_170_A2_C02_T7	g3142328	BLASTN	1448	9e-59	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11407	GM_170_A2_D11_MR	g18559	BLASTN	388	1e-10	76	G.max gene for catalase
11408	GM_170_A2_E01_T7	g3777526	BLASTN	675	2e-23	81	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
11409	GM_170_A2_E04_MR	g1666236	BLASTX	249	2e-20	33	(U76261) unknown [Hordeum vulgare]
11410	GM_170_A2_E05_T7	g100484	BLASTX	301	5e-25	58	hypothetical protein - garden snapdragon
11411	GM_170_A2_E08_MR	g421955	BLASTX	216	1e-16	37	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
11412	GM_170_A2_E11_MR	g905361	BLASTX	384	3e-34	95	(U22103) gag-protease polyprotein [Glycine max]
11413	GM_170_A2_F04_MR	g112609	BLASTX	193	1e-14	45	jacalin a' - jackfruit
11414	GM_170_A2_F05_MR	g3264544	BLASTN	403	4e-11	61	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
11415	GM_170_A2_G02_T7	g2129618	BLASTX	181	5e-12	46	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
11416	GM_170_A2_G03_T7	g507910	BLASTN	534	2e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
11417	GM_170_A2_G04_MR	g3142328	BLASTN	479	1e-14	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11418	GM_170_A2_G06_MR	g4038056	BLASTX	345	1e-29	48	(AC005897) putative transposon [Arabidopsis thaliana]
11419	GM_170_A2_G10_MR	g507910	BLASTN	432	6e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11420	GM_170_A2_H02_MR	g479357	BLASTX	174	2e-11	33	hypothetical protein 612 - maize transposon MuA2 gi 22375 (X62251) ORF [Zea mays]
11421	GM_170_A2_H04_MR	g3142328	BLASTN	483	7e-15	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11422	GM_170_A2_H07_MR	g3646936	BLASTN	410	2e-11	62	Caenorhabditis elegans cosmid Y47D3B, complete sequence [Caenorhabditis elegans]
11423	GM_170_B2_A09_T7	g2316016	BLASTX	282	2e-22	49	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
11424	GM_170_B2_B01_MR	g2443320	BLASTX	170	1e-10	34	(D85597) polyprotein [Oryza australiensis]
11425	GM_170_B2_B07_T7	g507910	BLASTN	592	4e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11426	GM_170_B2_B11_MR	g2832304	BLASTX	126	6e-14	57	(AF044489) receptor-like protein kinase [Oryza sativa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11427	GM_170_B2_C03_T7	g122106	BLASTX	235	4e-19	69	HISTONE H4 gi 70771 pir HSZM4 histone H4 - maize gi 81642 pir S06904 histone H4 - Arabidopsis thaliana gi 2119028 pir S60475 histone H4 - garden pea gi 21795 (X00043) histone H4 [Triticum aestivum] gi 166740 (M17132) histone H4 [Arabidopsis thaliana] gi 166742 (M17133) histone H4 [Arabidopsis thaliana] gi 168499 (M36659) histone H4 (H4C13) [Zea mays] gi 168501 (M13370) histone H4 [Zea mays] gi 168503 (M13377) histone H4 [Zea mays] gi 498898 (U10042) histone H4 homolog [Pisum sativum] gi 1806285 gnl PID e263432 (Z79638) histone H4 homologue [Sesbania rostrata] gi 225838 prf 1314298A histone H4 [Arabidopsis thaliana]
11428	GM_170_B2_C05_MR	g1514643	BLASTX	152	5e-24	75	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
11429	GM_170_B2_C09_T7	g3645899	BLASTX	366	1e-31	49	(U68408) 5' end not determined experimentally [Zea mays]
11430	GM_170_B2_D03_MR	g507910	BLASTN	339	1e-08	69	Glycine max BSR-101 satellite SB92 genomic sequence.
11431	GM_170_B2_D05_T7	g2522230	BLASTX	327	9e-29	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11432	GM_170_B2_D06_T7	g3056601	BLASTX	369	3e-33	80	(AC004255) T1F9.22 [Arabidopsis thaliana]
11433	GM_170_B2_D07_T7	g3319372	BLASTX	240	4e-18	40	(AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]
11434	GM_170_B2_D10_MR	g18559	BLASTN	702	8e-25	76	G.max gene for catalase
11435	GM_170_B2_D10_T7	g100484	BLASTX	262	8e-21	44	hypothetical protein - garden snapdragon
11436	GM_170_B2_E05_MR	g2454214	BLASTN	382	2e-10	63	Glycine max nodule-specific phosphoribosylpyrophosphate amidotransferase (PRAT) gene, 5' upstream sequence and partial cds
11437	GM_170_B2_E07_T7	g905361	BLASTX	396	1e-35	89	(U22103) gag-protease polyprotein [Glycine max]
11438	GM_170_B2_E10_MR	g4063760	BLASTX	349	9e-30	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11439	GM_170_B2_F01_T7	g629693	BLASTX	148	4e-09	41	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
11440	GM_170_B2_F04_T7	g2995405	BLASTX	564	2e-53	57	(Y12432) polyprotein [Ananas comosus]
11441	GM_170_B2_F05_T7	g1666236	BLASTX	200	5e-15	29	(U76261) unknown [Hordeum vulgare]
11442	GM_170_B2_G02_T7	g3021265	BLASTX	206	6e-18	59	(AL022347) protein kinase - like protein [Arabidopsis thaliana] gi 3292839 gnl PID e1310082 (AL031018) protein kinase - like protein [Arabidopsis thaliana]
11443	GM_170_B2_G03_T7	g2522227	BLASTX	163	1e-16	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
11444	GM_170_B2_G04_T7	g3097320	BLASTN	432	2e-12	70	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11445	GM_170_B2_G06_T7	g3097320	BLASTN	1038	6e-40	81	Glycine max gene for Bd 30K, complete cds
11446	GM_170_B2_G09_T7	g3097320	BLASTN	402	4e-11	66	Glycine max gene for Bd 30K, complete cds
11447	GM_170_B2_G12_MR	g4063760	BLASTX	274	9e-22	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11448	GM_170_B2_H01_MR	g3777527	BLASTX	183	9e-13	39	(AF053008) gag-pol polyprotein [Glycine max]
11449	GM_170_B2_H03_T7	g4038056	BLASTX	365	1e-31	47	(AC005897) putative transposon [Arabidopsis thaliana]
11450	GM_170_B2_H04_MR	g4063760	BLASTX	103	5e-10	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11451	GM_170_B2_H04_T7	g1402877	BLASTX	159	2e-10	60	(X98130) unknown [Arabidopsis thaliana] gi 1495257 gnl PID e242925 (X97485) orf03 [Arabidopsis thaliana]
11452	GM_170_B2_H06_MR	g507910	BLASTN	350	3e-09	87	Glycine max BSR-101 satellite SB92 genomic sequence.
11453	GM_170_B2_H09_T7	g3688172	BLASTX	162	1e-11	50	(AL031804) putative protein [Arabidopsis thaliana]
11454	GM_171_A1_A03_MR	g18559	BLASTN	626	2e-21	74	G.max gene for catalase
11455	GM_171_A1_A09_T7	g3097320	BLASTN	511	4e-16	76	Glycine max gene for Bd 30K, complete cds
11456	GM_171_A1_A10_MR	g3063460	BLASTX	145	4e-12	69	(AC003981) F22O13.22 [Arabidopsis thaliana]
11457	GM_171_A1_A10_T7	g3859610	BLASTN	427	3e-12	64	Arabidopsis thaliana BAC T9E19
11458	GM_171_A1_B06_MR	g3645899	BLASTX	207	1e-14	42	(U68408) 5' end not determined experimentally [Zea mays]
11459	GM_171_A1_B08_T7	g2651303	BLASTX	215	4e-17	64	(AC002336) putative potassium transporter [Arabidopsis thaliana]
11460	GM_171_A1_C02_MR	g3142328	BLASTN	1274	8e-51	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11461	GM_171_A1_C11_T7	g3645899	BLASTX	154	5e-09	45	(U68408) 5' end not determined experimentally [Zea mays]
11462	GM_171_A1_C12_MR	g507910	BLASTN	461	3e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
11463	GM_171_A1_D03_MR	g507910	BLASTN	572	3e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11464	GM_171_A1_D04_T7	g2388577	BLASTX	274	6e-22	59	(AC000098) Similar to Arabidopsis putative ion-channel PID:g2262157 (gb AC002329). [Arabidopsis thaliana]
11465	GM_171_A1_D05_T7	g3142328	BLASTN	1382	9e-56	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11466	GM_171_A1_D08_MR	g2522230	BLASTX	167	8e-12	36	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11467	GM_171_A1_D11_MR	g507910	BLASTN	567	5e-19	85	Glycine max BSR-101 satellite SB92 genomic sequence.
11468	GM_171_A1_E03_T7	g4063760	BLASTX	323	6e-27	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11469	GM_171_A1_E10_MR	g509768	BLASTN	455	1e-13	67	Glycine max seed-specific low molecular weight sulfur-rich protein.
11470	GM_171_A1_F06_T7	g18559	BLASTN	430	2e-12	67	G.max gene for catalase
11471	GM_171_A1_F09_T7	g342960	BLASTN	356	5e-10	64	paramecium mutant 4.51clm-cl mt dna dimer: repl. init. region, clone 2.
11472	GM_171_A1_F12_T7	g4063760	BLASTX	261	2e-20	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11473	GM_171_A1_G09_T7	g18559	BLASTN	728	6e-26	75	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11474	GM_171_A1_H01_MR	g342954	BLASTN	394	9e-12	60	paramecium species 4.51b mt dna dimer: replication init. region, clone-1.
11475	GM_171_A1_H05_T7	g4063770	BLASTX	164	3e-10	41	(AB004906) transposase [Ipomoea purpurea]
11476	GM_171_A1_H12_T7	g507910	BLASTN	341	8e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11477	GM_171_A2_A03_MR	g100488	BLASTX	175	2e-11	34	TNP2 protein - garden snapdragon
11478	GM_171_A2_A04_MR	g905361	BLASTX	109	2e-12	42	(U22103) gag-protease polyprotein [Glycine max]
11479	GM_171_A2_B10_MR	g3810596	BLASTX	334	2e-28	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
11480	GM_171_A2_C10_MR	g1946279	BLASTX	278	1e-23	46	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
11481	GM_171_A2_D04_MR	g21098	BLASTN	426	6e-13	66	Tomato U1 small nuclear RNA gene U1.5
11482	GM_171_A2_D05_MR	g3063708	BLASTX	240	5e-18	46	(AL022537) putative protein [Arabidopsis thaliana]
11483	GM_171_A2_D10_MR	g1946279	BLASTX	303	3e-26	47	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
11484	GM_171_A2_E03_MR	g131026	BLASTX	170	4e-12	47	PATHOGENESIS-RELATED PROTEIN STH-2 gi 479691 pir S35161 STH-2 protein - potato gi 169551 (M25155) pSTH-2 protein [Solanum tuberosum] gi 169576 (M29041) STH-2 protein [Solanum tuberosum]
11485	GM_171_A2_E11_MR	g18559	BLASTN	562	1e-31	79	G.max gene for catalase
11486	GM_171_A2_F06_MR	g2522230	BLASTX	313	3e-27	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11487	GM_171_A2_G07_MR	g3142328	BLASTN	775	4e-28	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11488	GM_171_A2_G08_MR	g2961349	BLASTX	160	1e-09	40	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
11489	GM_171_A2_G09_MR	g13584	BLASTN	438	3e-13	62	Yeast mitochondrial oxi3 gene exon 1 for cytochrome c oxidase subunit I
11490	GM_171_A2_G12_MR	g2995405	BLASTX	218	2e-17	46	(Y12432) polyprotein [Ananas comosus]
11491	GM_171_A2_H03_MR	g100484	BLASTX	133	6e-16	41	hypothetical protein - garden snapdragon
11492	GM_171_A2_H04_MR	g1171591	BLASTN	350	9e-09	62	P.falciparum complete gene map of plastid-like DNA (IR-B)
11493	GM_171_A2_H06_MR	g3193311	BLASTN	363	2e-09	76	Arabidopsis thaliana BAC F6N15
11494	GM_171_A2_H09_MR	g99922	BLASTX	519	4e-49	69	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
11495	GM_171_A2_H11_MR	g3668083	BLASTX	158	4e-10	60	(AC004667) hypothetical protein [Arabidopsis thaliana]
11496	GM_171_B2_A08_MR	g507910	BLASTN	655	6e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
11497	GM_171_B2_A09_MR	g2462936	BLASTX	211	1e-16	32	(Y12321) open reading frame 2 [Brassica oleracea]
11498	GM_171_B2_A12_MR	g507910	BLASTN	347	4e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11499	GM_171_B2_C06_MR	g3097320	BLASTN	373	7e-10	71	Glycine max gene for Bd 30K, complete cds
11500	GM_171_B2_D09_MR	g507910	BLASTN	559	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11501	GM_171_B2_E10_MR	g3377848	BLASTX	105	7e-16	66	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
11502	GM_171_B2_F01_MR	g1374720	BLASTN	381	2e-10	62	Neocallimastix patriciarum cellobiohydrolase precursor (celA) mRNA, complete cds
11503	GM_171_B2_F11_MR	g100484	BLASTX	348	4e-30	58	hypothetical protein - garden snapdragon
11504	GM_171_B2_G01_MR	g13769	BLASTN	241	2e-11	66	Torulopsis glabrata mitochondrial DNA for tRNA-Met and tRNA-Pro downstream of cytochrome b gene >gi 343952 gb M11873 YSLMTIG02 Yeast (T.glabrata) mitochondrial DNA between cytochrome b and cytochrome oxidase subunit 1 genes.
11505	GM_172_A1_A08_MR	g3142328	BLASTN	817	5e-30	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11506	GM_172_A1_B03_T7	g1769898	BLASTX	419	2e-38	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11507	GM_172_A1_B06_MR	g1769898	BLASTX	208	3e-19	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11508	GM_172_A1_B12_MR	g507910	BLASTN	361	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11509	GM_172_A1_C05_MR	g629693	BLASTX	398	3e-36	57	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
11510	GM_172_A1_C05_T7	g3097320	BLASTN	454	2e-13	67	Glycine max gene for Bd 30K, complete cds
11511	GM_172_A1_C09_MR	g3413322	BLASTX	94	1e-10	56	(Y11118) polygalacturonase [Medicago sativa]
11512	GM_172_A1_D01_MR	g18559	BLASTN	421	5e-12	73	G.max gene for catalase
11513	GM_172_A1_E04_MR	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11514	GM_172_A1_E10_T7	g2995405	BLASTX	240	2e-18	42	(Y12432) polyprotein [Ananas comosus]
11515	GM_172_A1_F07_MR	g1769897	BLASTX	187	5e-13	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11516	GM_172_A1_F09_T7	g3264565	BLASTN	372	9e-10	63	Homo sapiens chromosome 17, clone hRPC.1037_O_7, complete sequence [Homo sapiens]
11517	GM_172_A1_G01_MR	g3176811	BLASTN	360	3e-10	61	Homo sapiens allele 18 fragile site locus (FRA10B) minisatellite, 3' sequence
11518	GM_172_A1_G03_MR	g2323254	BLASTN	383	3e-10	62	Human Chromosome X, complete sequence [Homo sapiens]
11519	GM_172_A1_G03_T7	g3860167	BLASTX	159	2e-09	41	(AF098964) disease resistance protein RPP1-WsC [Arabidopsis thaliana]
11520	GM_172_A1_G05_MR	g3142328	BLASTN	778	3e-51	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11521	GM_172_A1_G07_MR	g3063445	BLASTX	255	8e-20	61	(AC003981) F22O13.7 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11522	GM_172_A1_H01_MR	g2522230	BLASTX	313	3e-27	45	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11523	GM_172_A1_H04_MR	g3075383	BLASTN	534	4e-17	69	Arabidopsis thaliana chromosome II BAC T1D16 genomic sequence, complete sequence [Arabidopsis thaliana]
11524	GM_172_A1_H08_MR	g13584	BLASTN	381	2e-10	63	Yeast mitochondrial oxi3 gene exon 1 for cytochrome c oxidase subunit I
11525	GM_172_A1_H08_T7	g3688428	BLASTX	409	2e-37	72	(AJ011534) sucrose synthase [Lycopersicon esculentum]
11526	GM_172_A1_H11_T7	g1658457	BLASTX	212	1e-16	69	(U75248) reverse transcriptase [Gossypium barbadense]
11527	GM_172_A1_H12_MR	g2781345	BLASTX	170	7e-11	37	(AC003113) F24O1.2 [Arabidopsis thaliana]
11528	GM_172_A2_A03_T7	g4063760	BLASTX	305	4e-25	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11529	GM_172_A2_A04_T7	g905361	BLASTX	119	2e-10	33	(U22103) gag-protease polyprotein [Glycine max]
11530	GM_172_A2_A05_T7	g2996647	BLASTN	405	3e-11	64	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
11531	GM_172_A2_A08_T7	g392991	BLASTN	402	4e-11	71	Phaseolus vulgaris nitrate reductase (PVNR2) gene, complete cds.
11532	GM_172_A2_B02_MR	g4159699	BLASTN	381	4e-10	65	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K16E1, complete sequence [Arabidopsis thaliana]
11533	GM_172_A2_B02_T7	g3928116	BLASTN	438	9e-13	62	, complete sequence [Homo sapiens]
11534	GM_172_A2_B03_T7	g3337395	BLASTN	436	1e-12	62	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
11535	GM_172_A2_B04_MR	g4115943	BLASTX	208	1e-20	80	(AF118223) contains similarity to eukaryotic protein kinase domains (Pfam: PF00069, score=312.6, E=4.7e-90, N=1) and EF hand domains (Pfam: PF00036, score=131, E=2.1e-35, N=4) [Arabidopsis thaliana]
11536	GM_172_A2_B11_MR	g4063760	BLASTX	357	1e-30	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11537	GM_172_A2_C01_MR	g2244901	BLASTN	510	5e-16	69	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 4
11538	GM_172_A2_C03_MR	g4063760	BLASTX	198	1e-13	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11539	GM_172_A2_C04_T7	g18559	BLASTN	722	1e-25	73	G.max gene for catalase
11540	GM_172_A2_C12_T7	g507910	BLASTN	609	7e-21	81	Glycine max BSR-101 satellite SB92 genomic sequence.
11541	GM_172_A2_D06_T7	g2995405	BLASTX	304	3e-25	61	(Y12432) polyprotein [Ananas comosus]
11542	GM_172_A2_D08_MR	g3599418	BLASTN	382	3e-10	72	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
11543	GM_172_A2_D11_MR	g2443320	BLASTX	308	3e-25	52	(D85597) polyprotein [Oryza australiensis]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11544	GM_172_A2_E02_T7	g13767	BLASTN	365	2e-10	68	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
11545	GM_172_A2_E07_MR	g100484	BLASTX	304	2e-25	54	hypothetical protein - garden snapdragon
11546	GM_172_A2_F06_T7	g3142328	BLASTN	1609	4e-66	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11547	GM_172_A2_F11_MR	g18559	BLASTN	875	1e-32	76	G.max gene for catalase
11548	GM_172_A2_G04_T7	g1666236	BLASTX	207	7e-16	31	(U76261) unknown [Hordeum vulgare]
11549	GM_172_A2_G05_T7	g2618602	BLASTN	411	2e-11	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSJ1, complete sequence [Arabidopsis thaliana]
11550	GM_172_A2_G07_MR	g3702339	BLASTX	212	3e-16	54	(AC005397) unknown protein [Arabidopsis thaliana]
11551	GM_172_A2_G11_MR	g2292907	BLASTX	165	4e-10	32	(Y10099) P-glycoprotein homologue [Hordeum vulgare]
11552	GM_172_A2_H06_MR	g3777527	BLASTX	445	8e-40	94	(AF053008) gag-pol polyprotein [Glycine max]
11553	GM_172_A2_H09_T7	g4140712	BLASTX	218	3e-17	56	(AF110183) putative integrase [Oryza sativa]
11554	GM_172_B1_A07_T7	g1769898	BLASTX	118	1e-18	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11555	GM_172_B1_A08_MR	g4038056	BLASTX	99	1e-10	53	(AC005897) putative transposon [Arabidopsis thaliana]
11556	GM_172_B1_A08_T7	g507910	BLASTN	367	6e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11557	GM_172_B1_A09_MR	g342965	BLASTN	339	1e-08	61	paramecium species 7,227 mt dna dimer: replication init. region.
11558	GM_172_B1_B01_T7	g3153873	BLASTX	552	1e-52	79	(AF065393) putative G-binding protein [Homo sapiens]
11559	GM_172_B1_B02_T7	g3176686	BLASTX	334	2e-28	61	(AC003671) Similar to high affinity potassium transporter, HAK1 protein gb U22945 from Schwanniomyces occidentalis. [Arabidopsis thaliana]
11560	GM_172_B1_B07_T7	g421954	BLASTX	128	2e-15	38	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
11561	GM_172_B1_B12_MR	g2522228	BLASTX	207	2e-15	46	(AB007466) reverse transcriptase-like protein [Vicia faba]
11562	GM_172_B1_C01_MR	g3924609	BLASTX	90	2e-09	62	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
11563	GM_172_B1_C04_MR	g1666236	BLASTX	106	8e-09	32	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11564	GM_172_B1_C04_T7	g125271	BLASTX	180	9e-13	84	CASEIN KINASE II, ALPHA CHAIN (CK II) (CK2-ALPHA) gi 100860 pir S19726 casein kinase II (EC 2.7.1.-) alpha chain - maize gi 3318993 pdb 1A6O Protein Kinase Ck2 (Catalytic Subunit) From Zea Mays Transferase, SerineTHREONINE-Protein Kinase, Casein Kinase, SerTHR KINASE Mol_id: 1; Molecule: Protein Kinase Ck2ALPHA-Subunit; Chain: Null; Ec: 2.7.1.37; Engineered: Yes gi 22117 (X61387) casein kinase II alpha subunit [Zea mays]
11565	GM_172_B1_C08_MR	g2564050	BLASTN	527	9e-17	76	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA22, complete sequence [Arabidopsis thaliana]
11566	GM_172_B1_D03_MR	g3142328	BLASTN	705	6e-25	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11567	GM_172_B1_D09_T7	g3643611	BLASTX	129	2e-16	95	(AC005395) putative casein kinase [Arabidopsis thaliana]
11568	GM_172_B1_D10_MR	g3142328	BLASTN	571	7e-19	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11569	GM_172_B1_D12_T7	g3142330	BLASTX	353	8e-31	88	(U96295) envelope-like [Glycine max]
11570	GM_172_B1_E09_MR	g507910	BLASTN	611	5e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
11571	GM_172_B1_E09_T7	g507910	BLASTN	544	6e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
11572	GM_172_B1_F03_MR	g1167523	BLASTX	279	3e-22	43	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11573	GM_172_B1_F07_T7	g629693	BLASTX	299	7e-26	52	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
11574	GM_172_B1_F12_MR	g3445210	BLASTX	189	2e-13	45	(AC004786) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]
11575	GM_172_B1_G03_T7	g4159700	BLASTN	377	5e-10	69	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K1L20, complete sequence [Arabidopsis thaliana]
11576	GM_172_B1_G04_MR	g905361	BLASTX	479	7e-45	85	(U22103) gag-protease polyprotein [Glycine max]
11577	GM_172_B1_G05_T7	g2982303	BLASTX	270	9e-23	79	(AF051236) hypothetical protein [Picea mariana]
11578	GM_172_B1_G07_MR	g2598589	BLASTX	191	1e-13	51	(Y15367) MtN19 [Medicago truncatula]
11579	GM_172_B1_H02_MR	g507910	BLASTN	565	6e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11580	GM_172_B1_H03_T7	g4063760	BLASTX	380	4e-33	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11581	GM_172_B2_A04_MR	g1076755	BLASTX	332	2e-43	75	protein kinase - rice gi 450300 (L27821) protein kinase [Oryza sativa]
11582	GM_172_B2_A08_MR	g2864613	BLASTX	171	5e-11	62	(AL021811) S-receptor kinase -like protein [Arabidopsis thaliana]
11583	GM_172_B2_A12_MR	g3953471	BLASTX	289	7e-41	64	(AC002328) F22O2.16 [Arabidopsis thaliana]
11584	GM_172_B2_A12_T7	g1769898	BLASTX	212	1e-15	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11585	GM_172_B2_B01_MR	g1346113	BLASTX	298	1e-25	67	GTP CYCLOHYDROLASE II gi 1084339 pir JC4209 GTP cyclohydrolase II (EC 3.5.4.25) - Arabidopsis thaliana gi 940383 gnl PID d1008704 (D45165) GTP cyclohydrolase II [Arabidopsis thaliana]
11586	GM_172_B2_B04_MR	g2827621	BLASTX	178	8e-12	44	(AL021636) putative protein [Arabidopsis thaliana]
11587	GM_172_B2_B04_T7	g3851529	BLASTN	558	1e-18	97	Glycine max nodulin mRNA, complete cds
11588	GM_172_B2_B09_T7	g2062167	BLASTX	98	5e-11	60	(AC001645) Proline-rich protein APG isolog [Arabidopsis thaliana]
11589	GM_172_B2_B10_T7	g4115536	BLASTX	212	1e-16	48	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]
11590	GM_172_B2_C02_MR	g1769898	BLASTX	131	3e-10	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11591	GM_172_B2_C03_T7	g4063756	BLASTN	373	8e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11592	GM_172_B2_C05_MR	g2443320	BLASTX	192	2e-14	40	(D85597) polyprotein [Oryza australiensis]
11593	GM_172_B2_C08_MR	g4063760	BLASTX	248	6e-19	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11594	GM_172_B2_C12_MR	g1167523	BLASTX	181	9e-12	44	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11595	GM_172_B2_D07_MR	g4063756	BLASTN	518	2e-16	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11596	GM_172_B2_D07_T7	g3777527	BLASTX	588	5e-55	97	(AF053008) gag-pol polyprotein [Glycine max]
11597	GM_172_B2_E03_MR	g2129618	BLASTX	203	2e-14	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
11598	GM_172_B2_E08_T7	g170606	BLASTN	685	2e-24	69	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
11599	GM_172_B2_E10_T7	g1769899	BLASTX	242	8e-20	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11600	GM_172_B2_E12_T7	g4063760	BLASTX	237	7e-18	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11601	GM_172_B2_F03_T7	g4063760	BLASTX	186	2e-12	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11602	GM_172_B2_F05_T7	g3513745	BLASTX	171	5e-14	40	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
11603	GM_172_B2_F07_T7	g18664	BLASTN	298	1e-12	76	Soybean leghaemoglobin gene lba promoter region
11604	GM_172_B2_F12_T7	g3184283	BLASTX	129	1e-09	70	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]
11605	GM_172_B2_G01_T7	g4115365	BLASTX	302	1e-24	49	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
11606	GM_172_B2_G09_MR	g3142328	BLASTN	564	1e-18	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11607	GM_172_B2_G11_T7	g507910	BLASTN	534	2e-17	81	Glycine max BSR-101 satellite SB92 genomic sequence.
11608	GM_172_B2_H01_T7	g3097320	BLASTN	638	7e-22	71	Glycine max gene for Bd 30K, complete cds
11609	GM_172_B2_H02_T7	g3777527	BLASTX	577	7e-54	93	(AF053008) gag-pol polyprotein [Glycine max]
11610	GM_173_A1_A05_T7	g1840106	BLASTN	498	1e-16	68	Human fragile site locus (FRA16B) minisatellite repeat

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11611	GM_173_A1_A09_MR	g2665890	BLASTX	213	8e-16	71	(AF035944) calcium-dependent protein kinase [Fragaria x ananassa]
11612	GM_173_A1_A10_T7	g3047068	BLASTX	182	4e-12	36	(AF058825) similar to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
11613	GM_173_A1_A11_T7	g3777527	BLASTX	350	9e-30	95	(AF053008) gag-pol polyprotein [Glycine max]
11614	GM_173_A1_B01_MR	g3319362	BLASTX	225	1e-16	41	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
11615	GM_173_A1_B02_MR	g4063756	BLASTN	551	7e-18	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11616	GM_173_A1_B03_MR	g2739003	BLASTN	709	2e-25	82	Glycine max cytochrome P450 monooxygenase CYP82C1p (CYP82C1) mRNA, complete cds
11617	GM_173_A1_B05_MR	g3649752	BLASTN	352	7e-09	64	Plasmodium falciparum MAL3P3, complete sequence [Plasmodium falciparum]
11618	GM_173_A1_B08_MR	g507910	BLASTN	455	6e-14	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11619	GM_173_A1_B08_T7	g507910	BLASTN	534	2e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
11620	GM_173_A1_B09_MR	g3426334	BLASTN	501	1e-15	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
11621	GM_173_A1_B11_T7	g3097320	BLASTN	387	2e-10	68	Glycine max gene for Bd 30K, complete cds
11622	GM_173_A1_B12_MR	g507910	BLASTN	342	7e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11623	GM_173_A1_B12_T7	g507910	BLASTN	365	7e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11624	GM_173_A1_C07_MR	g4165194	BLASTX	171	8e-11	35	(AJ009736) Pol protein [Drosophila melanogaster]
11625	GM_173_A1_D02_T7	g3319359	BLASTN	377	2e-14	62	Arabidopsis thaliana BAC T7M24
11626	GM_173_A1_D07_T7	g4160362	BLASTN	412	1e-11	60	Saccharomyces cerevisiae complete mitochondrial genome
11627	GM_173_A1_E01_T7	g505129	BLASTN	429	2e-12	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
11628	GM_173_A1_E05_T7	g2443320	BLASTX	131	1e-14	48	(D85597) polyprotein [Oryza australiensis]
11629	GM_173_A1_E07_MR	g4063762	BLASTX	128	3e-10	27	(AC005561) putative retrotransposon [Arabidopsis thaliana]
11630	GM_173_A1_F01_MR	g1480927	BLASTN	1115	4e-44	85	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
11631	GM_173_A1_F04_T7	g2191150	BLASTX	209	6e-16	80	(AF007269) similar to mitochondrial carrier family [Arabidopsis thaliana]
11632	GM_173_A1_F05_MR	g1769898	BLASTX	178	9e-18	39	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11633	GM_173_A1_F07_MR	g4063760	BLASTX	371	4e-32	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11634	GM_173_A1_G03_MR	g3355463	BLASTN	671	3e-23	67	Arabidopsis thaliana chromosome II BAC F12L6 genomic sequence, complete sequence [Arabidopsis thaliana]
11635	GM_173_A1_G04_MR	g3452273	BLASTX	157	2e-23	91	(AF043110) phosphatidylinositol 4-kinase alpha [Daucus carota]
11636	GM_173_A1_G04_T7	g4063770	BLASTX	122	4e-09	40	(AB004906) transposase [Ipomoea purpurea]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11637	GM_173_A1_G06_MR	g2495365	BLASTX	250	1e-19	79	HEAT SHOCK PROTEIN 81-2 (HSP81-2) gi 445127 prf 1908431B heat shock protein HSP81-2 [Arabidopsis thaliana]
11638	GM_173_A1_G10_T7	g505129	BLASTN	361	2e-09	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
11639	GM_173_A1_G11_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11640	GM_173_A1_H01_T7	g2764526	BLASTN	443	6e-25	66	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
11641	GM_173_A1_H05_MR	g2194136	BLASTX	207	1e-14	48	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
11642	GM_173_A1_H06_MR	g3319351	BLASTX	263	1e-20	43	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
11643	GM_173_A1_H08_MR	g3142328	BLASTN	1131	3e-44	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11644	GM_173_A1_H09_T7	g336279	BLASTN	489	5e-15	63	Apis mellifera ligustica complete mitochondrial genome
11645	GM_173_A1_H10_MR	g1658457	BLASTX	216	5e-17	68	(U75248) reverse transcriptase [Gossypium barbadense]
11646	GM_173_B1_A05_MR	g1850550	BLASTX	97	3e-09	43	(U88030) reverse transcriptase [Secale cereale]
11647	GM_173_B1_B05_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11648	GM_173_B1_B05_T7	g507910	BLASTN	358	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11649	GM_173_B1_D05_MR	g507910	BLASTN	348	4e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11650	GM_173_B1_D05_T7	g4063760	BLASTX	352	4e-30	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11651	GM_173_B1_D07_MR	g507910	BLASTN	354	2e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11652	GM_173_B1_D10_MR	g158813	BLASTN	383	7e-11	67	Drosophila hydei Y chromosome lampbrush loop transcribed repeats.
11653	GM_173_B1_E10_T7	g114411	BLASTX	158	6e-10	73	ATP SYNTHASE ALPHA CHAIN, MITOCHONDRIAL gi 320126 pir S26979 H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - kidney bean mitochondrion gi 169318 (M64246) adenosine triphosphatase [Phaseolus vulgaris]
11654	GM_173_B1_G05_MR	g3645899	BLASTX	233	2e-17	50	(U68408) 5' end not determined experimentally [Zea mays]
11655	GM_173_B1_G08_MR	g3281853	BLASTX	173	5e-19	64	(AL031004) putative protein [Arabidopsis thaliana]
11656	GM_173_B1_G08_T7	g3281850	BLASTX	214	6e-16	68	(AL031004) monogalactosyldiacylglycerol synthase - like protein [Arabidopsis thaliana]
11657	GM_173_B1_G10_T7	g3645899	BLASTX	205	2e-14	45	(U68408) 5' end not determined experimentally [Zea mays]
11658	GM_173_B1_H02_T7	g1769898	BLASTX	290	5e-24	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11659	GM_173_B1_H10_T7	g2244915	BLASTX	179	9e-12	39	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11660	GM_173_B2_A07_MR	g3142328	BLASTN	737	2e-26	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11661	GM_173_B2_A10_MR	g2827637	BLASTX	235	6e-18	41	(AL021636) putative protein [Arabidopsis thaliana]
11662	GM_173_B2_B10_T7	g2522230	BLASTX	141	6e-09	32	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11663	GM_173_B2_C03_T7	g2833380	BLASTX	143	1e-08	82	RIBOSE-PHOSPHATE PYROPHOSPHOKINASE 2 (PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE 2) (PRS II) gi 2146772 pir S71262 ribose-phosphate pyrophosphokinase (EC 2.7.6.1) II - Arabidopsis thaliana (fragment) gi 1064885 (X92974) phosphoribosyl pyrophosphate synthetase II [Arabidopsis thaliana]
11664	GM_173_B2_C04_T7	g507910	BLASTN	900	5e-34	99	Glycine max BSR-101 satellite SB92 genomic sequence.
11665	GM_173_B2_C09_MR	g4063760	BLASTX	188	1e-12	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11666	GM_173_B2_C09_T7	g507910	BLASTN	347	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11667	GM_173_B2_C12_MR	g4063760	BLASTX	409	3e-36	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11668	GM_173_B2_D03_MR	g4063760	BLASTX	273	1e-21	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11669	GM_173_B2_D03_T7	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11670	GM_173_B2_D05_MR	g4063756	BLASTN	484	8e-15	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11671	GM_173_B2_F02_T7	g531389	BLASTX	221	2e-23	45	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
11672	GM_173_B2_F04_T7	g422028	BLASTX	222	1e-17	71	transcription factor OBF3.1, ocs element-binding - maize gi 297020 (X69153) ocs-element binding factor 3.1 [Zea mays]
11673	GM_173_B2_F09_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
11674	GM_173_B2_G02_T7	g1840106	BLASTN	412	2e-12	62	Human fragile site locus (FRA16B) minisatellite repeat
11675	GM_173_B2_G03_T7	g4063760	BLASTX	418	4e-37	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11676	GM_173_B2_G05_T7	g507910	BLASTN	573	3e-19	83	Glycine max BSR-101 satellite SB92 genomic sequence.
11677	GM_173_B2_G10_MR	g3513747	BLASTX	271	3e-21	54	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
11678	GM_173_B2_H05_T7	g3080421	BLASTX	327	1e-27	65	(AL022604) putative protein [Arabidopsis thaliana]
11679	GM_174_A1_A01_MR	g18559	BLASTN	816	6e-30	78	G.max gene for catalase
11680	GM_174_A1_A02_T7	g2865424	BLASTX	167	3e-10	33	(AF039371) polyprotein [Arabidopsis thaliana]
11681	GM_174_A1_A03_T7	g3142328	BLASTN	855	9e-32	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11682	GM_174_A1_A07_T7	g4063760	BLASTX	291	1e-23	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11683	GM_174_A1_A10_T7	g1666236	BLASTX	198	8e-15	33	(U76261) unknown [Hordeum vulgare]
11684	GM_174_A1_B04_MR	g2522228	BLASTX	345	1e-30	71	(AB007466) reverse transcriptase-like protein [Vicia faba]
11685	GM_174_A1_B05_MR	g2522228	BLASTX	324	2e-28	70	(AB007466) reverse transcriptase-like protein [Vicia faba]
11686	GM_174_A1_B06_T7	g531389	BLASTX	214	3e-15	48	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
11687	GM_174_A1_B07_MR	g133872	BLASTX	209	9e-16	74	30S RIBOSOMAL PROTEIN S1, CHLOROPLAST PRECURSOR (CS1) gi 282838 pir S26494 ribosomal protein S1, chloroplast - spinach gi 322404 pir A44121 small subunit ribosomal protein CS1, CS-S2 - spinach gi 18060 (X66135) ribosomal protein S1 [Spinacia oleracea] gi 170143 (M82923) chloroplast ribosomal protein S1 [Spinacia oleracea]
11688	GM_174_A1_B08_MR	g1840106	BLASTN	522	1e-17	66	Human fragile site locus (FRA16B) minisatellite repeat
11689	GM_174_A1_B10_MR	g3269291	BLASTX	99	4e-10	73	(AL030978) putative receptor protein kinase [Arabidopsis thaliana]
11690	GM_174_A1_B11_MR	g3777527	BLASTX	159	3e-21	42	(AF053008) gag-pol polyprotein [Glycine max]
11691	GM_174_A1_C11_MR	g3097320	BLASTN	1257	7e-50	82	Glycine max gene for Bd 30K, complete cds
11692	GM_174_A1_D02_T7	g4063760	BLASTX	232	3e-17	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11693	GM_174_A1_D03_MR	g4063756	BLASTN	491	4e-15	67	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11694	GM_174_A1_D05_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
11695	GM_174_A1_D08_T7	g2760839	BLASTX	159	7e-10	48	(AC003105) putative receptor kinase [Arabidopsis thaliana]
11696	GM_174_A1_E04_MR	g3319362	BLASTX	188	1e-12	47	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
11697	GM_174_A1_E05_T7	g1769897	BLASTX	189	3e-13	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11698	GM_174_A1_E08_MR	g507910	BLASTN	584	9e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11699	GM_174_A1_E11_T7	g3319362	BLASTX	212	9e-20	48	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
11700	GM_174_A1_F01_T7	g1167523	BLASTX	335	3e-28	44	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11701	GM_174_A1_F02_MR	g905361	BLASTX	398	7e-36	92	(U22103) gag-protease polyprotein [Glycine max]
11702	GM_174_A1_F02_T7	g18559	BLASTN	691	3e-24	73	G.max gene for catalase
11703	GM_174_A1_F04_T7	g13767	BLASTN	346	2e-09	63	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
11704	GM_174_A1_F07_T7	g169669	BLASTX	307	1e-26	69	(M96069) tyrosine decarboxylase [Petroselinum crispum]
11705	GM_174_A1_F11_T7	g4063760	BLASTX	202	2e-15	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11706	GM_174_A1_G08_T7	g2586082	BLASTX	323	6e-27	48	(U72725) retrofit [Oryza longistaminata]
11707	GM_174_A1_H04_MR	g3142328	BLASTN	601	3e-20	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11708	GM_174_A1_H05_T7	g3777527	BLASTX	333	7e-28	47	(AF053008) gag-pol polyprotein [Glycine max]
11709	GM_174_A1_H07_T7	g3777527	BLASTX	326	5e-40	84	(AF053008) gag-pol polyprotein [Glycine max]
11710	GM_174_A2_A01_MR	g2244835	BLASTX	145	2e-11	57	(Z97337) protein kinase homolog [Arabidopsis thaliana]
11711	GM_174_A2_A04_T7	g1946279	BLASTX	249	2e-20	48	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
11712	GM_174_A2_A09_MR	g18559	BLASTN	682	7e-24	72	G.max gene for catalase
11713	GM_174_A2_B09_MR	g4115536	BLASTX	251	8e-21	59	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]
11714	GM_174_A2_B11_MR	g2921625	BLASTN	590	1e-19	68	Lupinus luteus leghemoglobin (LbI) gene, complete cds
11715	GM_174_A2_C03_MR	g4063760	BLASTX	523	2e-48	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11716	GM_174_A2_C05_MR	g507910	BLASTN	472	1e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
11717	GM_174_A2_C07_MR	g507910	BLASTN	492	1e-15	79	Glycine max BSR-101 satellite SB92 genomic sequence.
11718	GM_174_A2_C08_MR	g1654140	BLASTX	424	5e-38	71	(U37840) lipoxygenase [Lycopersicon esculentum]
11719	GM_174_A2_D06_MR	g4063756	BLASTN	354	6e-09	70	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11720	GM_174_A2_D12_T7	g99755	BLASTX	265	2e-21	51	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
11721	GM_174_A2_F01_MR	g2961358	BLASTX	151	1e-09	38	(AL022140) serine/threonine protein kinase like protein [Arabidopsis thaliana]
11722	GM_174_A2_F02_T7	g1256830	BLASTX	408	2e-37	82	(U52970) cysteine endopeptidase 1 [Phaseolus vulgaris] gi 2959418 gnl PID e1264083 (AJ224766) cysteine protease [Phaseolus vulgaris]
11723	GM_174_A2_F04_MR	g905361	BLASTX	176	1e-11	28	(U22103) gag-protease polyprotein [Glycine max]
11724	GM_174_A2_F10_MR	g3763969	BLASTN	561	3e-18	67	Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE ...
11725	GM_174_A2_G05_MR	g2522228	BLASTX	215	2e-28	65	(AB007466) reverse transcriptase-like protein [Vicia faba]
11726	GM_174_A2_G05_T7	g1165321	BLASTN	527	7e-17	71	Glycine max extensin (SbHRGP3) gene, complete cds
11727	GM_174_A2_G10_MR	g3550983	BLASTX	127	3e-13	70	(AB010690) mutM homologue-2 [Arabidopsis thaliana]
11728	GM_174_B1_A02_MR	g3777527	BLASTX	359	1e-30	80	(AF053008) gag-pol polyprotein [Glycine max]
11729	GM_174_B1_A02_T7	g1666236	BLASTX	153	8e-10	30	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11730	GM_174_B1_A04_T7	g3492889	BLASTN	378	5e-10	62	Homo sapiens chromosome 17, clone hRPK.746_E_8, complete sequence [Homo sapiens]
11731	GM_174_B1_A08_MR	g507910	BLASTN	375	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11732	GM_174_B1_A08_T7	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11733	GM_174_B1_A09_MR	g3142328	BLASTN	1302	4e-52	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11734	GM_174_B1_A11_MR	g3522943	BLASTX	380	5e-33	80	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]
11735	GM_174_B1_B01_MR	g507910	BLASTN	556	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11736	GM_174_B1_B01_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11737	GM_174_B1_B02_T7	g4063756	BLASTN	364	2e-09	71	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11738	GM_174_B1_B06_MR	g422418	BLASTX	193	3e-13	39	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
11739	GM_174_B1_B06_T7	g3142328	BLASTN	1187	7e-47	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11740	GM_174_B1_B09_MR	g3046704	BLASTX	254	1e-19	44	(AL022223) putative protein [Arabidopsis thaliana]
11741	GM_174_B1_B10_MR	g1666229	BLASTN	454	1e-13	73	Pisum sativum actin (PEAc9) mRNA, complete cds gi 1724138 gb U81047 PSU81047 Pisum sativum actin (PEAc9) mRNA, complete cds
11742	GM_174_B1_B11_T7	g100484	BLASTX	400	9e-36	52	hypothetical protein - garden snapdragon
11743	GM_174_B1_C10_T7	g3097320	BLASTN	422	4e-12	71	Glycine max gene for Bd 30K, complete cds
11744	GM_174_B1_D01_MR	g3097320	BLASTN	493	3e-15	65	Glycine max gene for Bd 30K, complete cds
11745	GM_174_B1_D02_T7	g3687234	BLASTX	206	1e-14	41	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
11746	GM_174_B1_D03_MR	g3142328	BLASTN	712	2e-47	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11747	GM_174_B1_D08_T7	g3645899	BLASTX	182	4e-15	51	(U68408) 5' end not determined experimentally [Zea mays]
11748	GM_174_B1_D09_T7	g2443320	BLASTX	232	1e-20	50	(D85597) polyprotein [Oryza australiensis]
11749	GM_174_B1_D11_MR	g556421	BLASTN	754	3e-41	77	Stylosanthes humilis cinnamyl alcohol dehydrogenase (CAD1) mRNA, complete cds.
11750	GM_174_B1_D11_T7	g3600030	BLASTX	130	3e-10	35	(AF080119) contains similarity to ankyrin repeats (Pfam: ank.hmm, score: 13.93, 14.93 and 27.78) [Arabidopsis thaliana]
11751	GM_174_B1_E01_T7	g1752734	BLASTX	190	5e-23	72	(D78510) beta-glucan-elicitor receptor [Glycine max]
11752	GM_174_B1_E04_MR	g1769897	BLASTX	377	5e-34	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11753	GM_174_B1_E07_MR	g3097320	BLASTN	663	5e-23	73	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11754	GM_174_B1_E08_MR	g507910	BLASTN	379	2e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11755	GM_174_B1_E08_T7	g507910	BLASTN	363	8e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11756	GM_174_B1_E09_MR	g2462058	BLASTX	269	1e-22	53	(Y13389) reverse transcriptase [Antirrhinum majus]
11757	GM_174_B1_F01_MR	g1084334	BLASTX	233	4e-18	75	calcium-dependent protein kinase (EC 2.7.1.-) 1 - Arabidopsis thaliana gi 604880 gnl PID d1005364 (D21805) calcium-dependent protein kinase [Arabidopsis thaliana]
11758	GM_174_B1_G03_MR	g2443320	BLASTX	203	8e-31	51	(D85597) polyprotein [Oryza australiensis]
11759	GM_174_B1_G04_T7	g3513747	BLASTX	229	7e-26	58	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
11760	GM_174_B1_H01_MR	g507910	BLASTN	357	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
11761	GM_174_B1_H05_MR	g1167523	BLASTX	287	4e-23	42	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11762	GM_174_B1_H07_MR	g507910	BLASTN	407	9e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
11763	GM_174_B1_H08_T7	g3097320	BLASTN	583	2e-19	76	Glycine max gene for Bd 30K, complete cds
11764	GM_174_B2_A05_MR	g2194136	BLASTX	264	1e-20	53	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
11765	GM_174_B2_C05_MR	g1142703	BLASTN	293	5e-14	75	Glycine max satellite STR120-B.1.
11766	GM_174_B2_D02_MR	g2191135	BLASTX	115	1e-12	61	(AF007269) A_IG002N01.14 gene product [Arabidopsis thaliana]
11767	GM_174_B2_D03_MR	g3513747	BLASTX	163	9e-10	42	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
11768	GM_174_B2_E01_MR	g2129618	BLASTX	184	3e-12	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
11769	GM_174_B2_E12_MR	g3548808	BLASTX	315	7e-27	80	(AC005313) unknown protein [Arabidopsis thaliana]
11770	GM_174_B2_F03_MR	g3650039	BLASTX	271	7e-22	45	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
11771	GM_174_B2_F12_MR	g4038056	BLASTX	111	9e-15	40	(AC005897) putative transposon [Arabidopsis thaliana]
11772	GM_174_B2_G03_MR	g2522228	BLASTX	156	1e-15	59	(AB007466) reverse transcriptase-like protein [Vicia faba]
11773	GM_174_B2_H04_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
11774	GM_174_B2_H06_MR	g1666236	BLASTX	182	6e-13	33	(U76261) unknown [Hordeum vulgare]
11775	GM_174_B2_H07_MR	g507910	BLASTN	359	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11776	GM_174_B2_H11_MR	g100484	BLASTX	393	5e-35	55	hypothetical protein - garden snapdragon
11777	GM_175_A1_A03_T7	g99719	BLASTX	201	3e-23	65	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Landsberg) (fragment) gi 16384 (X53976) orf 2 [Arabidopsis thaliana]
11778	GM_175_A1_A05_T7	g507910	BLASTN	644	2e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11779	GM_175_A1_A06_MR	g2522230	BLASTX	260	1e-21	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11780	GM_175_A1_A08_MR	g3548806	BLASTX	227	5e-17	55	(AC005313) unknown protein [Arabidopsis thaliana]
11781	GM_175_A1_A08_T7	g22491	BLASTX	165	8e-11	33	(X01380) ORF2 [Zea mays]
11782	GM_175_A1_A09_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
11783	GM_175_A1_A09_T7	g3777527	BLASTX	617	4e-58	96	(AF053008) gag-pol polyprotein [Glycine max]
11784	GM_175_A1_A10_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11785	GM_175_A1_A10_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11786	GM_175_A1_A11_MR	g2129618	BLASTX	203	2e-14	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
11787	GM_175_A1_B03_MR	g4063760	BLASTX	321	9e-27	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11788	GM_175_A1_B04_T7	g3953458	BLASTX	195	7e-14	82	(AC002328) F20N2.3 [Arabidopsis thaliana]
11789	GM_175_A1_B06_MR	g320565	BLASTX	166	1e-11	50	transposon TA1-1 KAS-1 - Arabidopsis thaliana (fragment)
11790	GM_175_A1_B08_T7	g1666236	BLASTX	146	5e-09	27	(U76261) unknown [Hordeum vulgare]
11791	GM_175_A1_C01_T7	g4038056	BLASTX	190	6e-13	36	(AC005897) putative transposon [Arabidopsis thaliana]
11792	GM_175_A1_C04_T7	g4063760	BLASTX	139	1e-11	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11793	GM_175_A1_C05_MR	g507910	BLASTN	385	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11794	GM_175_A1_C05_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
11795	GM_175_A1_C10_T7	g3845197	BLASTN	379	4e-10	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
11796	GM_175_A1_C11_MR	g1742959	BLASTX	192	5e-22	81	(Z71450) CLC-d chloride channel protein [Arabidopsis thaliana]
11797	GM_175_A1_C11_T7	g2244834	BLASTX	305	1e-25	91	(Z97337) hypothetical protein [Arabidopsis thaliana]
11798	GM_175_A1_D04_MR	g479178	BLASTX	227	1e-16	46	pol polyprotein - Volvox carteri f. nagariensis retrotransposon Osser gi 288597 (X69552) gag,protease,endonuclease, reverse transcriptase,RNaseH [Volvox carteri]
11799	GM_175_A1_D07_MR	g2522227	BLASTX	200	2e-15	48	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
11800	GM_175_A1_D07_T7	g2995405	BLASTX	370	3e-32	55	(Y12432) polyprotein [Ananas comosus]
11801	GM_175_A1_D08_T7	g2995405	BLASTX	181	2e-26	50	(Y12432) polyprotein [Ananas comosus]
11802	GM_175_A1_D09_MR	g3097320	BLASTN	621	4e-21	78	Glycine max gene for Bd 30K, complete cds
11803	GM_175_A1_E08_MR	g2191130	BLASTX	461	6e-43	76	(AF007269) A_IG002N01.7 gene product [Arabidopsis thaliana]
11804	GM_175_A1_E10_T7	g507910	BLASTN	401	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11805	GM_175_A1_F01_MR	g421954	BLASTX	152	8e-21	43	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
11806	GM_175_A1_F06_MR	g4038056	BLASTX	257	4e-20	45	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11807	GM_175_A1_F08_T7	g2801423	BLASTN	419	7e-12	64	Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence [Homo sapiens]
11808	GM_175_A1_F09_MR	g3142328	BLASTN	663	5e-23	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11809	GM_175_A1_F09_T7	g3319362	BLASTX	331	5e-30	57	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
11810	GM_175_A1_F10_MR	g3170525	BLASTX	234	5e-18	45	(AF054615) cellulase [Fragaria x ananassa]
11811	GM_175_A1_G05_T7	g1174498	BLASTX	156	1e-10	68	SYNAPTOBREVIN-RELATED PROTEIN gi 600710 (M90418) formerly called HAT24; synaptobrevin-related protein [Arabidopsis thaliana]
11812	GM_175_A1_G06_T7	g2522228	BLASTX	396	4e-36	59	(AB007466) reverse transcriptase-like protein [Vicia faba]
11813	GM_175_A1_G07_T7	g130582	BLASTX	237	9e-18	44	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
11814	GM_175_A1_G11_T7	g4063756	BLASTN	392	1e-10	68	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11815	GM_175_A1_G12_T7	g3738114	BLASTN	395	8e-11	65	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
11816	GM_175_A1_H02_T7	g3687234	BLASTX	196	2e-13	53	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
11817	GM_175_A1_H05_MR	g1666236	BLASTX	180	9e-13	29	(U76261) unknown [Hordeum vulgare]
11818	GM_175_A1_H07_MR	g1142700	BLASTN	400	1e-11	72	Glycine max satellite STR120-A.2.
11819	GM_175_A1_H08_T7	g4063760	BLASTX	478	2e-43	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11820	GM_175_A1_H11_MR	g905361	BLASTX	420	3e-38	95	(U22103) gag-protease polyprotein [Glycine max]
11821	GM_175_A1_H12_T7	g1931641	BLASTX	164	3e-10	50	(U95973) unknown protein [Arabidopsis thaliana]
11822	GM_175_A2_A03_T7	g3097320	BLASTN	744	1e-26	73	Glycine max gene for Bd 30K, complete cds
11823	GM_175_A2_A04_MR	g22491	BLASTX	119	3e-13	36	(X01380) ORF2 [Zea mays]
11824	GM_175_A2_B01_MR	g507910	BLASTN	619	2e-21	85	Glycine max BSR-101 satellite SB92 genomic sequence.
11825	GM_175_A2_B02_T7	g3869069	BLASTN	543	2e-17	73	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]
11826	GM_175_A2_B05_MR	g1326016	BLASTX	98	5e-11	47	TY3-2 orfB

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11827	GM_175_A2_B07_MR	g3059060	BLASTN	374	7e-10	62	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
11828	GM_175_A2_B07_T7	g1805654	BLASTX	154	5e-09	37	(X99972) calmodulin-stimulated calcium-ATPase [Brassica oleracea]
11829	GM_175_A2_B09_T7	g3738114	BLASTN	354	6e-09	61	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
11830	GM_175_A2_B11_MR	g4063756	BLASTN	477	2e-14	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
11831	GM_175_A2_C03_MR	g2462058	BLASTX	170	4e-27	56	(Y13389) reverse transcriptase [Antirrhinum majus]
11832	GM_175_A2_C07_T7	g3212847	BLASTX	310	6e-27	61	(AC004005) putative polygalacturonase [Arabidopsis thaliana]
11833	GM_175_A2_C08_MR	g905361	BLASTX	566	4e-54	92	(U22103) gag-protease polyprotein [Glycine max]
11834	GM_175_A2_D04_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11835	GM_175_A2_D06_T7	g3650039	BLASTX	150	7e-09	42	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
11836	GM_175_A2_E07_MR	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
11837	GM_175_A2_E11_MR	g3915165	BLASTX	205	4e-15	78	TRYPTOPHAN SYNTHASE BETA CHAIN 2 PRECURSOR >gi 2792520 (AF042320) tryptophan synthase beta subunit [Camptotheca acuminata] >gi 2801771 (AF042321) tryptophan synthase beta [Camptotheca acuminata]
11838	GM_175_A2_F06_MR	g507910	BLASTN	566	6e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11839	GM_175_A2_F10_T7	g2995405	BLASTX	256	5e-20	62	(Y12432) polyprotein [Ananas comosus]
11840	GM_175_A2_G02_T7	g4063760	BLASTX	177	2e-11	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11841	GM_175_A2_G03_MR	g507910	BLASTN	571	3e-19	79	Glycine max BSR-101 satellite SB92 genomic sequence.
11842	GM_175_A2_G03_T7	g4063760	BLASTX	279	3e-22	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11843	GM_175_A2_G04_T7	g3142328	BLASTN	859	6e-32	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11844	GM_175_A2_G06_MR	g1142703	BLASTN	293	8e-17	75	Glycine max satellite STR120-B.1.
11845	GM_175_A2_G06_T7	g2995405	BLASTX	161	7e-16	65	(Y12432) polyprotein [Ananas comosus]
11846	GM_175_A2_H04_MR	g975703	BLASTN	958	2e-36	74	P.sativum GR gene
11847	GM_175_A2_H05_MR	g99730	BLASTX	109	8e-11	48	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
11848	GM_175_A2_H10_MR	g3319362	BLASTX	292	8e-31	61	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11849	GM_175_A2_H11_MR	g507910	BLASTN	400	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
11850	GM_175_B1_A02_MR	g4063760	BLASTX	162	8e-10	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11851	GM_175_B1_A05_T7	g2997591	BLASTX	409	2e-37	83	(AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum]
11852	GM_175_B1_A09_T7	g3645899	BLASTX	222	3e-16	42	(U68408) 5' end not determined experimentally [Zea mays]
11853	GM_175_B1_A11_MR	g4063760	BLASTX	275	7e-22	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11854	GM_175_B1_A11_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
11855	GM_175_B1_B01_T7	g2224927	BLASTX	422	8e-39	80	(AF004213) ethylene-insensitive3-like1 [Arabidopsis thaliana]
11856	GM_175_B1_B08_MR	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
11857	GM_175_B1_B12_MR	g3777527	BLASTX	178	2e-11	50	(AF053008) gag-pol polyprotein [Glycine max]
11858	GM_175_B1_C01_T7	g2522230	BLASTX	365	9e-33	44	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
11859	GM_175_B1_C03_T7	g3142328	BLASTN	1175	3e-46	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11860	GM_175_B1_C04_T7	g2335061	BLASTN	476	2e-14	65	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence [Homo sapiens]
11861	GM_175_B1_C06_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
11862	GM_175_B1_C10_T7	g507910	BLASTN	619	2e-21	85	Glycine max BSR-101 satellite SB92 genomic sequence.
11863	GM_175_B1_C12_T7	g1666236	BLASTX	169	1e-11	32	(U76261) unknown [Hordeum vulgare]
11864	GM_175_B1_D01_T7	g3599418	BLASTN	1240	3e-49	86	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
11865	GM_175_B1_D04_MR	g3142289	BLASTX	427	2e-39	68	(AC002411) Strong similarity to beta-keto-Coa synthase gb U37088 from Simmondsia chinensis. [Arabidopsis thaliana]
11866	GM_175_B1_D05_T7	g3176774	BLASTN	371	1e-10	60	Homo sapiens allele 3 fragile site locus (FRA10B) minisatellite, 3' sequence
11867	GM_175_B1_D06_MR	g3810596	BLASTX	266	5e-21	50	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
11868	GM_175_B1_E01_T7	g2735745	BLASTN	364	9e-10	60	Oncorhynchus kisutch growth hormone 1 gene, intron C, complete sequence
11869	GM_175_B1_E08_MR	g3269281	BLASTX	139	8e-11	50	(AL030978) putative protein [Arabidopsis thaliana]
11870	GM_175_B1_E11_MR	g3135962	BLASTN	490	4e-15	65	Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence [Homo sapiens]
11871	GM_175_B1_E11_T7	g1785739	BLASTX	237	3e-19	45	(Y08502) orf240b [Arabidopsis thaliana]
11872	GM_175_B1_F01_MR	g3777527	BLASTX	239	7e-18	97	(AF053008) gag-pol polyprotein [Glycine max]
11873	GM_175_B1_F03_MR	g2995405	BLASTX	329	7e-28	55	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11874	GM_175_B1_F10_MR	g1171583	BLASTN	456	1e-13	62	P.falciparum complete gene map of plastid-like DNA (IR-A)
11875	GM_175_B1_F12_MR	g3287156	BLASTN	468	4e-14	65	Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence [Homo sapiens]
11876	GM_175_B1_G07_MR	g4063760	BLASTX	511	5e-47	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11877	GM_175_B1_G07_T7	g343537	BLASTN	416	9e-12	64	T.brucei mitochondrial maxicircle DNA encoding cytochrome c oxidase subunit I (COI), and NADH dehydrogenase subunits 4 and 5, complete cds.
11878	GM_175_B1_G11_MR	g3322325	BLASTX	210	4e-15	60	(AE001191) ATP-dependent Clp protease subunit B (clpB) [Treponema pallidum]
11879	GM_175_B1_H06_MR	g3097320	BLASTN	1223	2e-48	84	Glycine max gene for Bd 30K, complete cds
11880	GM_175_B1_H10_MR	g3059060	BLASTN	399	6e-11	62	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
11881	GM_175_B2_A02_T7	g99729	BLASTX	138	2e-15	64	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
11882	GM_175_B2_A11_T7	g2642431	BLASTX	293	1e-23	67	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
11883	GM_175_B2_A12_T7	g507910	BLASTN	578	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
11884	GM_175_B2_B02_T7	g2160694	BLASTX	209	2e-15	56	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
11885	GM_175_B2_C02_MR	g2558962	BLASTX	306	2e-26	98	(AF025667) histone H2B1 [Gossypium hirsutum]
11886	GM_175_B2_C08_T7	g3777527	BLASTX	359	1e-30	89	(AF053008) gag-pol polyprotein [Glycine max]
11887	GM_175_B2_D05_T7	g4063760	BLASTX	251	3e-19	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11888	GM_175_B2_D10_MR	g3142328	BLASTN	400	4e-11	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11889	GM_175_B2_E04_MR	g3193221	BLASTN	401	4e-11	82	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
11890	GM_175_B2_E07_T7	g507910	BLASTN	399	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11891	GM_175_B2_F06_MR	g3548808	BLASTX	285	1e-23	80	(AC005313) unknown protein [Arabidopsis thaliana]
11892	GM_175_B2_F07_T7	g3777527	BLASTX	409	6e-36	91	(AF053008) gag-pol polyprotein [Glycine max]
11893	GM_175_B2_F11_MR	g905361	BLASTX	417	6e-38	84	(U22103) gag-protease polyprotein [Glycine max]
11894	GM_175_B2_G09_MR	g3650039	BLASTX	206	7e-15	46	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11895	GM_175_B2_H06_T7	g100484	BLASTX	134	4e-14	57	hypothetical protein - garden snapdragon
11896	GM_175_B2_H11_MR	g3142328	BLASTN	452	2e-13	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11897	GM_176_A1_A04_T7	g18559	BLASTN	816	6e-30	79	G.max gene for catalase
11898	GM_176_A1_A09_MR	g18559	BLASTN	661	6e-25	72	G.max gene for catalase
11899	GM_176_A1_A11_T7	g4063760	BLASTX	310	1e-25	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11900	GM_176_A1_A12_T7	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
11901	GM_176_A1_B04_MR	g4063760	BLASTX	311	1e-25	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11902	GM_176_A1_B04_T7	g4063760	BLASTX	253	1e-19	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11903	GM_176_A1_B06_T7	g507910	BLASTN	370	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
11904	GM_176_A1_B07_T7	g2586082	BLASTX	205	3e-14	44	(U72725) retrofit [Oryza longistaminata]
11905	GM_176_A1_B08_T7	g507910	BLASTN	407	9e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
11906	GM_176_A1_B09_T7	g1142702	BLASTN	256	3e-12	72	Glycine max satellite STR120-A.4.
11907	GM_176_A1_B11_T7	g3047073	BLASTX	180	4e-12	44	(AF058825) contains similarity to retrotransposon-like proteins [Arabidopsis thaliana]
11908	GM_176_A1_C02_T7	g1040717	BLASTN	360	4e-10	66	D.polychroa microsatellite sequence (clone Dp ch1 F3)
11909	GM_176_A1_C03_T7	g3097320	BLASTN	861	6e-32	78	Glycine max gene for Bd 30K, complete cds
11910	GM_176_A1_C06_T7	g3142328	BLASTN	793	6e-45	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11911	GM_176_A1_C10_T7	g905361	BLASTX	431	1e-39	93	(U22103) gag-protease polyprotein [Glycine max]
11912	GM_176_A1_C11_T7	g3645899	BLASTX	283	9e-23	53	(U68408) 5' end not determined experimentally [Zea mays]
11913	GM_176_A1_D01_T7	g2190548	BLASTX	153	3e-16	49	(AC001229) EST gb ATTS1121 comes from this gene. [Arabidopsis thaliana]
11914	GM_176_A1_D04_MR	g507910	BLASTN	354	2e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11915	GM_176_A1_D06_MR	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
11916	GM_176_A1_D12_T7	g2231046	BLASTX	181	2e-12	91	(Y12618) PPF-1 protein [Pisum sativum]
11917	GM_176_A1_E02_T7	g3142328	BLASTN	758	2e-27	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11918	GM_176_A1_E06_T7	g1769898	BLASTX	265	3e-21	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11919	GM_176_A1_E07_T7	g3650035	BLASTX	225	1e-16	43	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
11920	GM_176_A1_E11_T7	g2522228	BLASTX	158	3e-10	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
11921	GM_176_A1_F04_T7	g2522227	BLASTX	147	3e-09	47	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
11922	GM_176_A1_F05_T7	g1769899	BLASTX	146	1e-09	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11923	GM_176_A1_F06_T7	g2252828	BLASTX	142	4e-09	37	(AF013293) No definition line found [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11924	GM_176_A1_F10_MR	g2244878	BLASTX	284	3e-23	71	(Z97338) hypothetical protein [Arabidopsis thaliana]
11925	GM_176_A1_F11_T7	g3135269	BLASTX	214	2e-15	44	(AC003058) unknown protein [Arabidopsis thaliana]
11926	GM_176_A1_G01_T7	g507910	BLASTN	535	1e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
11927	GM_176_A1_G10_T7	g1167523	BLASTX	234	2e-17	51	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
11928	GM_176_A1_H02_MR	g2462749	BLASTX	220	2e-16	60	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]
11929	GM_176_A1_H02_T7	g13581	BLASTN	390	2e-11	66	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTCG10 Saccharomyces cerevisiae mitochondrion DNA segment.
11930	GM_176_A1_H06_MR	g2462749	BLASTX	183	2e-12	55	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]
11931	GM_176_A1_H07_T7	g2246449	BLASTN	486	6e-15	67	Lycopersicon esculentum copia-like retrotransposon ToRTL1, 3-hydroxy-3-methylglutaryl CoA reductase 2 (HMG2) gene, complete cds.
11932	GM_176_A2_A05_MR	g507910	BLASTN	498	7e-16	79	Glycine max BSR-101 satellite SB92 genomic sequence.
11933	GM_176_A2_A05_T7	g507910	BLASTN	591	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
11934	GM_176_A2_A08_T7	g2914758	BLASTN	398	6e-11	58	Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds
11935	GM_176_A2_B05_MR	g18559	BLASTN	828	2e-30	68	G.max gene for catalase
11936	GM_176_A2_B05_T7	g2995405	BLASTX	497	5e-46	56	(Y12432) polyprotein [Ananas comosus]
11937	GM_176_A2_C04_T7	g3142328	BLASTN	742	4e-53	83	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11938	GM_176_A2_C08_T7	g2995405	BLASTX	282	6e-27	46	(Y12432) polyprotein [Ananas comosus]
11939	GM_176_A2_C09_MR	g3142328	BLASTN	1061	4e-41	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11940	GM_176_A2_D07_MR	g1666171	BLASTX	167	2e-11	85	(Y09105) unknown [Nicotiana plumbaginifolia]
11941	GM_176_A2_D08_MR	g1707642	BLASTX	216	1e-15	33	(Y07748) TMK [Oryza sativa]
11942	GM_176_A2_D09_MR	g2852447	BLASTX	174	2e-16	57	(D88206) protein kinase [Arabidopsis thaliana]
11943	GM_176_A2_E01_T7	g4063760	BLASTX	198	1e-13	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11944	GM_176_A2_E03_T7	g4063760	BLASTX	273	1e-21	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11945	GM_176_A2_E05_T7	g421954	BLASTX	160	1e-18	43	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
11946	GM_176_A2_F02_T7	g1769897	BLASTX	169	5e-11	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11947	GM_176_A2_G02_T7	g4063760	BLASTX	175	3e-11	31	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11948	GM_176_A2_G04_T7	g2979597	BLASTN	349	1e-08	67	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
11949	GM_176_A2_G07_MR	g2642431	BLASTX	224	3e-16	45	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
11950	GM_176_A2_G09_T7	g2522228	BLASTX	348	9e-44	65	(AB007466) reverse transcriptase-like protein [Vicia faba]
11951	GM_176_A2_H03_MR	g3142328	BLASTN	796	4e-29	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11952	GM_176_A2_H10_T7	g3142328	BLASTN	657	9e-23	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11953	GM_176_B1_A03_MR	g3004480	BLASTX	96	5e-11	51	(AJ228333) reverse transcriptase [Pinus elliottii]
11954	GM_176_B1_A05_T7	g1418331	BLASTX	207	4e-15	39	(X95909) receptor like protein kinase [Arabidopsis thaliana]
11955	GM_176_B1_A09_MR	g4050011	BLASTN	411	1e-11	60	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
11956	GM_176_B1_B01_MR	g3860272	BLASTX	157	1e-13	96	(AC005824) putative suppressor protein [Arabidopsis thaliana]
11957	GM_176_B1_B04_T7	g4106406	BLASTN	405	4e-12	64	Sorghum bicolor centromere specific element pHind22, complete sequence
11958	GM_176_B1_B09_MR	g100484	BLASTX	298	1e-24	58	hypothetical protein - garden snapdragon
11959	GM_176_B1_C05_T7	g4063760	BLASTX	270	2e-21	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11960	GM_176_B1_C08_MR	g905361	BLASTX	591	1e-56	95	(U22103) gag-protease polyprotein [Glycine max]
11961	GM_176_B1_D02_T7	g4063760	BLASTX	215	5e-27	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11962	GM_176_B1_D10_T7	g3135962	BLASTN	355	5e-09	67	Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence [Homo sapiens]
11963	GM_176_B1_E02_MR	g3282250	BLASTX	193	7e-14	67	(AF009337) CDPK-related protein kinase [Tradescantia virginiana]
11964	GM_176_B1_E03_T7	g2708331	BLASTX	228	5e-17	53	(AF038557) ligand gated channel-like protein [Arabidopsis thaliana]
11965	GM_176_B1_E10_MR	g2618683	BLASTN	380	4e-10	67	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]
11966	GM_176_B1_F04_MR	g3645899	BLASTX	212	3e-15	41	(U68408) 5' end not determined experimentally [Zea mays]
11967	GM_176_B1_F08_MR	g507910	BLASTN	571	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
11968	GM_176_B1_F10_T7	g3097320	BLASTN	429	2e-12	67	Glycine max gene for Bd 30K, complete cds
11969	GM_176_B1_G01_T7	g13373	BLASTN	347	1e-09	63	Terminal inverted repeat from Paramecium mitochondrion >gi 342968 gb J01432 PARMTDIN1 paramecium species 1 mitochondria dimer initiation region dna.
11970	GM_176_B1_G02_T7	g4063760	BLASTX	265	7e-21	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11971	GM_176_B1_G05_MR	g2832608	BLASTX	167	2e-11	33	(AL021637) leucine rich repeat-like protein (fragment) [Arabidopsis thaliana]
11972	GM_176_B1_H03_MR	g2967687	BLASTX	250	7e-20	52	(AF035630) epidermal germacrene C synthase [Lycopersicon esculentum]
11973	GM_176_B1_H03_T7	g1769898	BLASTX	335	6e-29	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
11974	GM_176_B1_H09_MR	g3319362	BLASTX	170	2e-14	40	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
11975	GM_176_B2_A05_T7	g3461840	BLASTX	249	6e-19	48	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
11976	GM_176_B2_B06_T7	g507910	BLASTN	405	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
11977	GM_176_B2_C09_T7	g507910	BLASTN	391	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
11978	GM_176_B2_C11_T7	g507910	BLASTN	351	3e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
11979	GM_176_B2_C12_T7	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
11980	GM_176_B2_D12_T7	g2809246	BLASTX	206	4e-15	51	(AC002560) F24O1.15 [Arabidopsis thaliana]
11981	GM_176_B2_F06_T7	g507910	BLASTN	369	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
11982	GM_176_B2_F08_T7	g18683	BLASTN	456	1e-13	75	G.max N-20t gene
11983	GM_176_B2_F11_T7	g3184283	BLASTX	160	4e-13	80	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]
11984	GM_176_B2_G06_T7	g3142328	BLASTN	644	4e-22	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11985	GM_176_B2_G11_T7	g3142328	BLASTN	790	8e-29	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
11986	GM_177_A2_A02_MR	g2792208	BLASTX	190	3e-14	38	(AF032682) NBS-LRR type resistance protein [Hordeum vulgare]
11987	GM_177_A2_A11_MR	g116570	BLASTX	146	1e-09	30	CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) gi 105602 pir A32760 cellular nucleic acid-binding protein - human gi 1083628 pir JC2512 cellular nucleic acid binding protein - rat gi 643576 (M28372) SRE-binding protein [Homo sapiens] gi 790571 (U19765) nucleic acid binding protein [Homo sapiens] gi 809511 gnl PID d1008807 (D45254) Cellular Nucleic Acid Binding Protein [Rattus rattus]
11988	GM_177_A2_B05_MR	g2522228	BLASTX	252	1e-20	48	(AB007466) reverse transcriptase-like protein [Vicia faba]
11989	GM_177_A2_B09_MR	g1742955	BLASTX	253	8e-20	68	(Z71446) CLC-b chloride channel protein [Arabidopsis thaliana]
11990	GM_177_A2_B10_MR	g2464905	BLASTX	210	2e-16	55	(Z99708) minor allergen [Arabidopsis thaliana]
11991	GM_177_A2_C04_MR	g4063760	BLASTX	486	2e-44	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
11992	GM_177_A2_C05_MR	g2911054	BLASTX	215	1e-20	42	(AL021961) putative protein [Arabidopsis thaliana]
11993	GM_177_A2_C09_MR	g4033335	BLASTX	138	9e-15	70	(AJ012745) RH27 helicase [Arabidopsis thaliana]
11994	GM_177_A2_D04_MR	g507910	BLASTN	512	2e-16	81	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
11995	GM_177_A2_D07_MR	g3287270	BLASTX	199	1e-13	51	(Y09533) involved in starch metabalism [Solanum tuberosum]
11996	GM_177_A2_D09_MR	g719276	BLASTN	735	3e-26	67	Arabidopsis thaliana SABRE gene, exon 1
11997	GM_177_A2_E02_MR	g3894211	BLASTN	428	3e-12	62	Homo sapiens PAC clone DJ0888A21 from 7q31, complete sequence [Homo sapiens]
11998	GM_177_A2_E03_MR	g905360	BLASTN	763	9e-28	87	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
11999	GM_177_A2_F03_MR	g4038056	BLASTX	177	1e-11	43	(AC005897) putative transposon [Arabidopsis thaliana]
12000	GM_177_A2_F05_MR	g3645899	BLASTX	277	4e-25	57	(U68408) 5' end not determined experimentally [Zea mays]
12001	GM_177_A2_H09_MR	g1666236	BLASTX	186	2e-13	33	(U76261) unknown [Hordeum vulgare]
12002	GM_177_A2_H11_MR	g2522227	BLASTX	204	1e-15	52	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
12003	GM_177_B2_A01_T7	g1769898	BLASTX	149	8e-09	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12004	GM_177_B2_A02_T7	g3355478	BLASTX	146	4e-09	43	(AC004218) hypothetical protein [Arabidopsis thaliana]
12005	GM_177_B2_A03_T7	g3377848	BLASTX	165	7e-11	44	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
12006	GM_177_B2_A04_MR	g1934877	BLASTN	408	2e-11	63	Human DNA sequence from PAC 447N6 on chromosome X contains ESTs and STS
12007	GM_177_B2_A05_T7	g507910	BLASTN	392	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12008	GM_177_B2_A06_T7	g905361	BLASTX	345	6e-30	95	(U22103) gag-protease polyprotein [Glycine max]
12009	GM_177_B2_A08_T7	g3047086	BLASTX	222	7e-18	42	(AF058914) similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31) [Arabidopsis thaliana]
12010	GM_177_B2_A09_T7	g2760839	BLASTX	421	8e-41	63	(AC003105) putative receptor kinase [Arabidopsis thaliana]
12011	GM_177_B2_A12_T7	g3645899	BLASTX	282	1e-22	48	(U68408) 5' end not determined experimentally [Zea mays]
12012	GM_177_B2_B03_T7	g2995405	BLASTX	472	3e-43	56	(Y12432) polyprotein [Ananas comosus]
12013	GM_177_B2_B06_MR	g18559	BLASTN	354	5e-09	64	G.max gene for catalase
12014	GM_177_B2_B12_MR	g4150930	BLASTN	381	4e-10	63	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
12015	GM_177_B2_C04_MR	g905361	BLASTX	422	2e-38	95	(U22103) gag-protease polyprotein [Glycine max]
12016	GM_177_B2_C04_T7	g3777527	BLASTX	592	2e-55	89	(AF053008) gag-pol polyprotein [Glycine max]
12017	GM_177_B2_C10_MR	g2501495	BLASTX	185	4e-13	36	FLAVONOL 3-O-GLUCOSYLTRANSFERASE 6 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 6) gi 542016 pir S41952 UTP-glucose glucosyltransferase - cassava (fragment) gi 453251 (X77463) UTP-glucose glucosyltransferase [Manihot esculenta]
12018	GM_177_B2_C12_MR	g2522228	BLASTX	242	2e-19	61	(AB007466) reverse transcriptase-like protein [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12019	GM_177_B2_D01_T7	g4063760	BLASTX	568	4e-53	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12020	GM_177_B2_D02_MR	g507910	BLASTN	477	6e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
12021	GM_177_B2_D10_MR	g2708744	BLASTX	171	2e-11	76	(AC003952) putative Bop-like zinc-finger protein [Arabidopsis thaliana]
12022	GM_177_B2_E03_T7	g2995405	BLASTX	390	2e-34	57	(Y12432) polyprotein [Ananas comosus]
12023	GM_177_B2_E05_MR	g3142328	BLASTN	664	4e-23	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12024	GM_177_B2_E06_T7	g531389	BLASTX	166	4e-10	32	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
12025	GM_177_B2_E08_T7	g3650039	BLASTX	187	8e-13	51	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
12026	GM_177_B2_E10_MR	g507910	BLASTN	520	7e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
12027	GM_177_B2_E10_T7	g507910	BLASTN	422	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
12028	GM_177_B2_E11_T7	g3873182	BLASTN	396	7e-11	64	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
12029	GM_177_B2_E12_T7	g1840106	BLASTN	470	3e-15	61	Human fragile site locus (FRA16B) minisatellite repeat
12030	GM_177_B2_F06_T7	g1236920	BLASTN	402	3e-11	59	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
12031	GM_177_B2_F12_MR	g3915037	BLASTX	329	6e-28	84	SUCROSE SYNTHASE 2 (SUCROSE-UDP GLUCOSYLTRANSFERASE 2) >gi 2570067 gnl PID e1154401 (AJ001071) second sucrose synthase [Pisum sativum]
12032	GM_177_B2_G05_T7	g507910	BLASTN	445	2e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
12033	GM_177_B2_G08_T7	g4050011	BLASTN	639	7e-22	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
12034	GM_177_B2_H06_T7	g3097320	BLASTN	1350	4e-54	79	Glycine max gene for Bd 30K, complete cds
12035	GM_177_B2_H09_T7	g507910	BLASTN	431	7e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
12036	GM_178_A1_A03_MR	g1066856	BLASTN	698	2e-24	73	Glycine max acetyl coenzyme A carboxylase (ACCase-B) gene, 5' end of cds.
12037	GM_178_A1_A05_MR	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12038	GM_178_A1_B01_T7	g1865677	BLASTX	156	3e-09	94	(Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]
12039	GM_178_A1_B02_T7	g3645899	BLASTX	166	9e-19	46	(U68408) 5' end not determined experimentally [Zea mays]
12040	GM_178_A1_B03_MR	g2522228	BLASTX	341	3e-30	61	(AB007466) reverse transcriptase-like protein [Vicia faba]
12041	GM_178_A1_B07_MR	g3695395	BLASTX	205	8e-15	40	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12042	GM_178_A1_B08_MR	g4063760	BLASTX	155	2e-18	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12043	GM_178_A1_B10_MR	g3860246	BLASTX	144	8e-09	33	(AC005824) putative reverse-transcriptase protein [Arabidopsis thaliana]
12044	GM_178_A1_B10_T7	g413796	BLASTN	355	5e-09	65	Cloning vector pMAMneoBlue, complete sequence
12045	GM_178_A1_C06_MR	g81800	BLASTX	179	4e-13	66	nodulin-26 precursor - soybean
12046	GM_178_A1_C09_MR	g4063760	BLASTX	332	6e-28	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12047	GM_178_A1_C11_MR	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12048	GM_178_A1_C11_T7	g4063760	BLASTX	367	1e-31	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12049	GM_178_A1_D01_T7	g2316016	BLASTX	174	6e-11	60	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
12050	GM_178_A1_D03_T7	g18559	BLASTN	1521	5e-62	90	G.max gene for catalase
12051	GM_178_A1_D11_MR	g3097320	BLASTN	814	8e-30	78	Glycine max gene for Bd 30K, complete cds
12052	GM_178_A1_D11_T7	g3930515	BLASTX	122	7e-10	42	(AF059674) putative gag protein [Nicotiana tabacum]
12053	GM_178_A1_E05_MR	g18559	BLASTN	842	4e-31	79	G.max gene for catalase
12054	GM_178_A1_E05_T7	g2522228	BLASTX	124	6e-15	41	(AB007466) reverse transcriptase-like protein [Vicia faba]
12055	GM_178_A1_E06_MR	g3377855	BLASTX	188	9e-14	40	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
12056	GM_178_A1_E09_MR	g4063760	BLASTX	294	6e-24	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12057	GM_178_A1_E09_T7	g507910	BLASTN	444	2e-13	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12058	GM_178_A1_E12_MR	g4063760	BLASTX	398	5e-35	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12059	GM_178_A1_G05_MR	g3241923	BLASTN	370	1e-09	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MMN10, complete sequence [Arabidopsis thaliana]
12060	GM_178_A1_G12_MR	g3810596	BLASTX	182	4e-12	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
12061	GM_178_A1_H02_MR	g2129618	BLASTX	211	3e-15	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
12062	GM_178_A1_H04_MR	g1236920	BLASTN	371	7e-10	60	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
12063	GM_178_A1_H08_MR	g4115365	BLASTX	155	2e-18	43	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
12064	GM_178_A1_H09_MR	g3513747	BLASTX	315	6e-26	53	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
12065	GM_178_A1_H09_T7	g4160362	BLASTN	391	1e-10	65	Saccharomyces cerevisiae complete mitochondrial genome
12066	GM_178_A1_H10_T7	g3323609	BLASTX	181	8e-13	59	(AF064093) KE04p [Homo sapiens]
12067	GM_178_A1_H11_MR	g3941725	BLASTN	355	5e-09	66	Homo sapiens clone BAC 72m22 chromosome 8 map 8p21, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12068	GM_178_A1_H12_MR	g2181190	BLASTX	260	1e-21	70	(Y12531) serine/threonine kinase [Brassica oleracea]
12069	GM_178_A1_H12_T7	g1783312	BLASTX	150	6e-10	54	(X98520) receptor-like kinase [Brassica oleracea]
12070	GM_178_B1_A07_MR	g3097320	BLASTN	712	3e-25	78	Glycine max gene for Bd 30K, complete cds
12071	GM_178_B1_B01_MR	g2522228	BLASTX	173	1e-11	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
12072	GM_178_B1_B06_MR	g1769897	BLASTX	172	2e-11	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12073	GM_178_B1_C01_MR	g507910	BLASTN	346	5e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
12074	GM_178_B1_C01_T7	g507910	BLASTN	363	8e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12075	GM_178_B1_C06_T7	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12076	GM_178_B1_D05_T7	g1946279	BLASTX	224	2e-22	50	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
12077	GM_178_B1_D12_T7	g2497702	BLASTX	140	5e-09	47	OUTER MEMBRANE LIPOPROTEIN BLC PRECURSOR gi 2121019 pir I40710 outer membrane lipoprotein - Citrobacter freundii gi 717136 (U21727) lipocalin precursor [Citrobacter freundii]
12078	GM_178_B1_E02_T7	g4063760	BLASTX	251	2e-19	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12079	GM_178_B1_E03_T7	g99922	BLASTX	346	9e-31	75	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
12080	GM_178_B1_E05_MR	g4092470	BLASTN	559	3e-18	70	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
12081	GM_178_B1_F04_T7	g4092471	BLASTN	429	2e-12	67	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
12082	GM_178_B1_G04_MR	g1480927	BLASTN	376	4e-10	98	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
12083	GM_178_B1_G06_MR	g507910	BLASTN	414	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
12084	GM_178_B1_G06_T7	g3142328	BLASTN	739	2e-26	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12085	GM_178_B1_H02_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12086	GM_178_B1_H05_T7	g1350680	BLASTX	324	2e-28	77	60S RIBOSOMAL PROTEIN L1
12087	GM_178_B1_H11_T7	g2522230	BLASTX	167	8e-12	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
12088	GM_178_B2_F05_MR	g2429543	BLASTX	190	8e-13	42	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]
12089	GM_179_A1_A04_T7	g4006831	BLASTX	203	3e-14	42	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
12090	GM_179_A1_A05_T7	g3402709	BLASTX	252	6e-20	43	(AC004261) hypothetical protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12091	GM_179_A1_A09_MR	g3777527	BLASTX	561	3e-52	89	(AF053008) gag-pol polyprotein [Glycine max]
12092	GM_179_A1_B07_T7	g2914758	BLASTN	361	3e-09	63	Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds
12093	GM_179_A1_C09_T7	g3645899	BLASTX	155	3e-09	38	(U68408) 5' end not determined experimentally [Zea mays]
12094	GM_179_A1_D04_T7	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12095	GM_179_A1_D10_MR	g99726	BLASTX	199	9e-25	49	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Landsberg) (fragment) gi 1345515 gnl PID e32696 (X53976) orf 3 [Arabidopsis thaliana]
12096	GM_179_A1_E05_MR	g4063760	BLASTX	278	4e-22	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12097	GM_179_A1_E05_T7	g3687234	BLASTX	191	6e-13	50	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
12098	GM_179_A1_E07_T7	g4038056	BLASTX	271	1e-21	47	(AC005897) putative transposon [Arabidopsis thaliana]
12099	GM_179_A1_E09_T7	g3142328	BLASTN	653	3e-33	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12100	GM_179_A1_E10_MR	g1666236	BLASTX	108	7e-10	33	(U76261) unknown [Hordeum vulgare]
12101	GM_179_A1_F04_MR	g3650039	BLASTX	224	8e-17	40	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
12102	GM_179_A1_F05_MR	g2073447	BLASTN	487	6e-15	66	L.japonicus gln1, pge1 & krm genes
12103	GM_179_A1_F06_T7	g2443320	BLASTX	334	4e-28	54	(D85597) polyprotein [Oryza australiensis]
12104	GM_179_A1_F10_MR	g1769899	BLASTX	183	1e-13	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12105	GM_179_A1_G01_T7	g4063756	BLASTN	403	4e-11	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12106	GM_179_A1_G06_MR	g2522226	BLASTN	568	9e-19	70	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
12107	GM_179_A1_G07_MR	g4038056	BLASTX	241	2e-18	46	(AC005897) putative transposon [Arabidopsis thaliana]
12108	GM_179_A1_H01_MR	g505129	BLASTN	351	7e-09	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
12109	GM_179_A1_H02_T7	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12110	GM_179_A2_A03_MR	g3063444	BLASTX	247	3e-20	70	(AC003981) F22O13.5 [Arabidopsis thaliana]
12111	GM_179_A2_A09_MR	g99922	BLASTX	426	3e-39	62	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
12112	GM_179_A2_B03_MR	g629693	BLASTX	304	2e-26	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
12113	GM_179_A2_B09_MR	g3650039	BLASTX	227	4e-17	42	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12114	GM_179_A2_C01_MR	g1045530	BLASTN	375	4e-10	63	Magnaporthe grisea host-species specificity (Pwl1) gene, complete cds.
12115	GM_179_A2_C04_MR	g4150930	BLASTN	349	1e-08	60	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
12116	GM_179_A2_C11_MR	g12212	BLASTN	982	1e-42	92	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
12117	GM_179_A2_D05_MR	g18695	BLASTN	394	6e-11	69	Soybean nodulin 22 gene
12118	GM_179_A2_D08_MR	g2462058	BLASTX	150	1e-13	45	(Y13389) reverse transcriptase [Antirrhinum majus]
12119	GM_179_A2_E03_MR	g1167523	BLASTX	246	1e-18	39	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
12120	GM_179_A2_E07_MR	g2055374	BLASTX	145	1e-20	63	(U29095) serine-threonine protein kinase [Triticum aestivum]
12121	GM_179_A2_E09_MR	g99755	BLASTX	359	1e-31	55	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
12122	GM_179_A2_F03_MR	g3097320	BLASTN	632	1e-21	80	Glycine max gene for Bd 30K, complete cds
12123	GM_179_A2_F11_MR	g2522228	BLASTX	392	1e-35	59	(AB007466) reverse transcriptase-like protein [Vicia faba]
12124	GM_179_A2_G05_MR	g3097320	BLASTN	445	4e-13	71	Glycine max gene for Bd 30K, complete cds
12125	GM_179_A2_H01_MR	g1769898	BLASTX	318	5e-27	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12126	GM_179_A2_H02_MR	g1040717	BLASTN	338	4e-09	64	D.polychroa microsatellite sequence (clone Dp ch1 F3)
12127	GM_179_A2_H10_MR	g3810596	BLASTX	98	5e-09	32	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
12128	GM_179_B1_A02_MR	g3461834	BLASTN	364	2e-09	68	Arabidopsis thaliana chromosome II BAC T9I4 genomic sequence, complete sequence [Arabidopsis thaliana]
12129	GM_179_B1_A04_T7	g507910	BLASTN	372	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12130	GM_179_B1_A05_T7	g2924729	BLASTN	875	2e-32	74	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]
12131	GM_179_B1_A06_MR	g507910	BLASTN	580	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12132	GM_179_B1_A06_T7	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12133	GM_179_B1_A09_T7	g2522228	BLASTX	401	1e-36	76	(AB007466) reverse transcriptase-like protein [Vicia faba]
12134	GM_179_B1_B02_T7	g505129	BLASTN	379	4e-10	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
12135	GM_179_B1_B03_T7	g1666236	BLASTX	101	2e-10	31	(U76261) unknown [Hordeum vulgare]
12136	GM_179_B1_B04_MR	g3845197	BLASTN	349	1e-08	67	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
12137	GM_179_B1_B04_T7	g3947733	BLASTX	237	2e-18	42	(AJ009719) NL25 [Solanum tuberosum]
12138	GM_179_B1_B05_MR	g3777527	BLASTX	480	2e-43	96	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12139	GM_179_B1_B11_T7	g3142328	BLASTN	1808	3e-75	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12140	GM_179_B1_C02_T7	g3142328	BLASTN	580	3e-41	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12141	GM_179_B1_C03_MR	g4063760	BLASTX	198	1e-13	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12142	GM_179_B1_C03_T7	g507910	BLASTN	585	8e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12143	GM_179_B1_C08_MR	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12144	GM_179_B1_C11_T7	g2160165	BLASTX	274	6e-22	44	(AC000132) F21M12.11 gene product [Arabidopsis thaliana]
12145	GM_179_B1_C12_MR	g4063760	BLASTX	186	2e-12	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12146	GM_179_B1_C12_T7	g507910	BLASTN	621	2e-21	86	Glycine max BSR-101 satellite SB92 genomic sequence.
12147	GM_179_B1_D01_MR	g2832404	BLASTX	200	1e-17	60	(Y14207) R2R3-MYB transcription factor [Arabidopsis thaliana]
12148	GM_179_B1_D03_T7	g4156188	BLASTN	597	6e-20	67	Homo sapiens clone DJ0784G16, complete sequence [Homo sapiens]
12149	GM_179_B1_D04_T7	g2801536	BLASTX	99	1e-09	80	(AF039531) lysophospholipase homolog [Oryza sativa]
12150	GM_179_B1_D07_T7	g3885328	BLASTX	105	1e-12	71	(AC005623) putative serine/threonine protein kinase [Arabidopsis thaliana]
12151	GM_179_B1_E02_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12152	GM_179_B1_E02_T7	g3777527	BLASTX	378	1e-32	53	(AF053008) gag-pol polyprotein [Glycine max]
12153	GM_179_B1_E04_T7	g1236920	BLASTN	366	1e-09	62	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
12154	GM_179_B1_E07_T7	g3142328	BLASTN	890	2e-33	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12155	GM_179_B1_E10_MR	g2342686	BLASTX	143	7e-09	45	(AC000106) Similar to Saccharomyces hypothetical protein YDR051c (gb Z49209). ESTs gb T44436,gb 42252 come from this gene. [Arabidopsis thaliana]
12156	GM_179_B1_E10_T7	g3650039	BLASTX	190	4e-13	36	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
12157	GM_179_B1_F02_T7	g2245003	BLASTX	278	3e-23	44	(Z97341) similarity to a membrane-associated salt-inducible protein - Nicotiana tabacum [Arabidopsis thaliana]
12158	GM_179_B1_F04_T7	g421955	BLASTX	232	2e-18	58	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
12159	GM_179_B1_F09_MR	g3645899	BLASTX	279	2e-22	55	(U68408) 5' end not determined experimentally [Zea mays]
12160	GM_179_B1_F11_MR	g507910	BLASTN	353	2e-09	76	Glycine max BSR-101 satellite SB92 genomic sequence.
12161	GM_179_B1_G02_MR	g2995405	BLASTX	298	1e-24	62	(Y12432) polyprotein [Ananas comosus]
12162	GM_179_B1_G03_T7	g2191181	BLASTN	708	6e-25	69	Arabidopsis thaliana BAC TM021B04

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12163	GM_179_B1_G05_T7	g4056428	BLASTX	159	7e-10	82	(AC005322) Similar to gb U43629 integral membrane protein from Beta vulgaris and a member of sugar transporter family PF 00083. [Arabidopsis thaliana]
12164	GM_179_B1_G07_T7	g905361	BLASTX	188	6e-13	29	(U22103) gag-protease polyprotein [Glycine max]
12165	GM_179_B1_G08_MR	g984307	BLASTN	426	3e-12	82	Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precurso...
12166	GM_179_B1_G10_MR	g905361	BLASTX	154	3e-09	40	(U22103) gag-protease polyprotein [Glycine max]
12167	GM_179_B1_H02_T7	g4063756	BLASTN	487	6e-15	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12168	GM_179_B1_H09_MR	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12169	GM_179_B2_A03_MR	g3133272	BLASTN	386	2e-10	62	Genomic sequence for Arabidopsis thaliana BAC T17H7, complete sequence.
12170	GM_179_B2_A03_T7	g226407	BLASTX	111	8e-12	48	retrotransposon del1-46 [Lilium henryi]
12171	GM_179_B2_A06_MR	g3319362	BLASTX	194	2e-13	32	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12172	GM_179_B2_A06_T7	g1755162	BLASTX	332	6e-42	72	(U75192) germin-like protein [Arabidopsis thaliana]
12173	GM_179_B2_A07_T7	g3142328	BLASTN	1494	7e-61	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12174	GM_179_B2_A11_MR	g2980770	BLASTX	362	1e-32	64	(AL022198) putative protein kinase [Arabidopsis thaliana]
12175	GM_179_B2_A11_T7	g4063760	BLASTX	186	1e-13	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12176	GM_179_B2_B04_T7	g3810596	BLASTX	266	4e-21	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
12177	GM_179_B2_B06_T7	g18559	BLASTN	435	2e-20	73	G.max gene for catalase
12178	GM_179_B2_B07_T7	g3510505	BLASTX	115	5e-14	48	(AF030881) pol polyprotein [Fugu rubripes]
12179	GM_179_B2_B09_T7	g507910	BLASTN	446	1e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
12180	GM_179_B2_B10_T7	g905361	BLASTX	330	3e-28	75	(U22103) gag-protease polyprotein [Glycine max]
12181	GM_179_B2_B12_T7	g18559	BLASTN	984	1e-37	77	G.max gene for catalase
12182	GM_179_B2_C01_T7	g3513747	BLASTX	234	5e-24	48	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
12183	GM_179_B2_C03_MR	g2129618	BLASTX	190	6e-13	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
12184	GM_179_B2_C04_MR	g3021283	BLASTX	312	4e-26	70	(AL022347) serine/threonine kinase - like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12185	GM_179_B2_C04_T7	g3142328	BLASTN	701	9e-25	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12186	GM_179_B2_C06_MR	g507910	BLASTN	426	1e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
12187	GM_179_B2_C10_T7	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12188	GM_179_B2_D01_T7	g1666236	BLASTX	157	3e-10	30	(U76261) unknown [Hordeum vulgare]
12189	GM_179_B2_D02_T7	g3097320	BLASTN	439	8e-13	70	Glycine max gene for Bd 30K, complete cds
12190	GM_179_B2_D05_MR	g2792161	BLASTX	170	4e-12	51	(AJ223558) reverse transcriptase [Alstroemeria ligtu]
12191	GM_179_B2_D06_MR	g3758836	BLASTN	358	4e-09	72	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
12192	GM_179_B2_D06_T7	g3142379	BLASTX	210	5e-30	91	(AF053008) envelope-like [Glycine max]
12193	GM_179_B2_D08_MR	g320565	BLASTX	215	7e-17	48	transposon TA1-1 KAS-1 - Arabidopsis thaliana (fragment)
12194	GM_179_B2_D08_T7	g1431738	BLASTN	395	6e-11	83	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
12195	GM_179_B2_D11_T7	g2522227	BLASTX	201	2e-15	47	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
12196	GM_179_B2_D12_MR	g3777527	BLASTX	720	3e-69	95	(AF053008) gag-pol polyprotein [Glycine max]
12197	GM_179_B2_D12_T7	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12198	GM_179_B2_E05_MR	g18559	BLASTN	1030	1e-39	76	G.max gene for catalase
12199	GM_179_B2_E12_MR	g2801681	BLASTN	921	3e-35	86	Glycine max telomere-associated sequence STAS10
12200	GM_179_B2_F02_T7	g2864613	BLASTX	260	1e-20	61	(AL021811) S-receptor kinase -like protein [Arabidopsis thaliana]
12201	GM_179_B2_F03_MR	g1769898	BLASTX	366	2e-32	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12202	GM_179_B2_F04_MR	g3047066	BLASTX	97	8e-09	31	(AF058825) contains similarity to retrovirus-related POL polyproteins [Arabidopsis thaliana]
12203	GM_179_B2_G01_T7	g342959	BLASTN	361	7e-10	60	paramecium species 4.51er mt dna dimer: replication init. region, clone 3.
12204	GM_179_B2_G03_MR	g480618	BLASTX	168	6e-12	49	ATAF1 protein - Arabidopsis thaliana (fragment) gi 1345506 gnl PID e85756 (X74755) ATAF1 gene product [Arabidopsis thaliana]
12205	GM_179_B2_G03_T7	g343788	BLASTN	337	4e-09	65	Yeast (S.cerevisiae) mitochondrial cytochrome oxi1 gene, 5' flank.
12206	GM_179_B2_G06_T7	g2760322	BLASTX	256	3e-21	50	(AC002130) F1N21.7 [Arabidopsis thaliana]
12207	GM_179_B2_G07_MR	g505129	BLASTN	394	7e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
12208	GM_179_B2_G09_T7	g3142328	BLASTN	548	8e-18	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12209	GM_179_B2_G10_T7	g2522228	BLASTX	256	6e-21	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
12210	GM_179_B2_H01_MR	g1769898	BLASTX	470	6e-44	74	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12211	GM_179_B2_H02_T7	g18559	BLASTN	459	9e-14	66	G.max gene for catalase
12212	GM_179_B2_H06_MR	g3378650	BLASTX	300	6e-26	81	(X97606) abscisic acid activated [Medicago sativa]
12213	GM_179_B2_H06_T7	g905361	BLASTX	373	5e-33	85	(U22103) gag-protease polyprotein [Glycine max]
12214	GM_179_B2_H08_T7	g2337888	BLASTN	331	6e-11	70	Genomic sequence for Arabidopsis thaliana BAC F14J16, complete sequence [Arabidopsis thaliana]
12215	GM_179_B2_H09_T7	g3142328	BLASTN	622	4e-21	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12216	GM_179_B2_H12_MR	g130582	BLASTX	220	6e-16	37	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
12217	GM_180_A1_A04_MR	g4063760	BLASTX	156	4e-09	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12218	GM_180_A1_A04_T7	g507910	BLASTN	473	9e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
12219	GM_180_A1_A05_T7	g4106408	BLASTN	384	1e-10	78	Oryza sativa subsp. indica dispersed centromeric repeat family RCS1
12220	GM_180_A1_A07_MR	g1732513	BLASTX	171	3e-12	67	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]
12221	GM_180_A1_A12_T7	g3094014	BLASTX	167	8e-12	57	(AF060862) unknown [Homo sapiens]
12222	GM_180_A1_B01_T7	g170606	BLASTN	558	2e-18	69	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
12223	GM_180_A1_B05_MR	g507910	BLASTN	525	4e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
12224	GM_180_A1_B07_MR	g4063756	BLASTN	448	3e-13	66	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12225	GM_180_A1_B07_T7	g507910	BLASTN	424	2e-12	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12226	GM_180_A1_B10_MR	g1076570	BLASTX	211	1e-16	78	homeotic protein CHB6 - carrot
12227	GM_180_A1_B12_T7	g4063760	BLASTX	100	1e-10	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12228	GM_180_A1_C01_MR	g2801423	BLASTN	450	3e-13	63	Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence [Homo sapiens]
12229	GM_180_A1_C07_MR	g130405	BLASTX	128	8e-11	50	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 17.6) gi 74642 pir GNFF17 retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) transposon 17.6 gi 1335613 gnl PID e1849 (X01472) ORF 2, pot. reverse transcriptase [Drosophila melanogaster] gi 224319 prf 1101404B ORF 2 [Drosophila melanogaster]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12230	GM_180_A1_C08_T7	g99922	BLASTX	187	1e-28	60	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
12231	GM_180_A1_D01_T7	g3273387	BLASTN	368	1e-09	61	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
12232	GM_180_A1_D02_T7	g4063760	BLASTX	104	2e-11	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12233	GM_180_A1_D03_MR	g3645899	BLASTX	369	5e-32	51	(U68408) 5' end not determined experimentally [Zea mays]
12234	GM_180_A1_D04_MR	g1045614	BLASTX	285	6e-28	57	(U37088) beta-ketoacyl-CoA synthase [Simmondsia chinensis]
12235	GM_180_A1_D05_MR	g3142302	BLASTX	236	1e-17	89	(AC002411) Strong similarity to myosin heavy chain gb Z34293 from A. thaliana. [Arabidopsis thaliana]
12236	GM_180_A1_E09_T7	g507910	BLASTN	479	5e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
12237	GM_180_A1_E10_MR	g1666236	BLASTX	172	7e-12	32	(U76261) unknown [Hordeum vulgare]
12238	GM_180_A1_F01_T7	g2618605	BLASTN	417	8e-12	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]
12239	GM_180_A1_F02_MR	g2522228	BLASTX	416	4e-38	64	(AB007466) reverse transcriptase-like protein [Vicia faba]
12240	GM_180_A1_F02_T7	g18559	BLASTN	755	3e-27	76	G.max gene for catalase
12241	GM_180_A1_F05_MR	g3511285	BLASTX	284	7e-24	87	(AF081534) cellulose synthase [Populus alba x Populus tremula]
12242	GM_180_A1_F05_T7	g1840106	BLASTN	388	4e-11	61	Human fragile site locus (FRA16B) minisatellite repeat
12243	GM_180_A1_F07_MR	g905360	BLASTN	640	4e-22	78	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
12244	GM_180_A1_F08_T7	g507910	BLASTN	566	6e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12245	GM_180_A1_G01_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12246	GM_180_A1_G04_MR	g2662469	BLASTX	142	1e-13	75	(AF034217) ribosomal protein S6 [Arabidopsis thaliana]
12247	GM_180_A1_G06_T7	g1040717	BLASTN	440	9e-14	62	D.polychroa microsatellite sequence (clone Dp ch1 F3)
12248	GM_180_A1_G08_MR	g861155	BLASTX	202	1e-14	67	(Z35162) beta-fructofuranosidase; cell wall invertase I; fructosidase [Vicia faba]
12249	GM_180_A1_H02_T7	g170080	BLASTN	399	4e-11	80	Soybean seed lectin gene transposable element tgm1.
12250	GM_180_A1_H05_MR	g3777527	BLASTX	170	1e-10	31	(AF053008) gag-pol polyprotein [Glycine max]
12251	GM_180_A1_H10_MR	g1769898	BLASTX	279	8e-23	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12252	GM_180_A1_H11_MR	g18695	BLASTN	435	8e-13	74	Soybean nodulin 22 gene
12253	GM_180_A2_A01_T7	g2982283	BLASTX	165	2e-11	63	(AF051226) PREG-like protein [Picea mariana]
12254	GM_180_A2_A08_T7	g507910	BLASTN	356	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12255	GM_180_A2_B01_T7	g4092470	BLASTN	394	9e-11	59	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
12256	GM_180_A2_B05_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12257	GM_180_A2_B06_T7	g3777527	BLASTX	301	2e-24	45	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12258	GM_180_A2_B07_T7	g13541	BLASTN	402	1e-11	62	Yeast mitochondrial HpaII-fragment 2.
12259	GM_180_A2_B08_T7	g3645899	BLASTX	228	6e-17	44	(U68408) 5' end not determined experimentally [Zea mays]
12260	GM_180_A2_B10_T7	g507910	BLASTN	342	7e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
12261	GM_180_A2_C08_T7	g3004563	BLASTX	230	2e-18	56	(AC003673) similar to APG (non proline-rich region) [Arabidopsis thaliana] gi 3176703 (AC002392) putative proline-rich protein APG [Arabidopsis thaliana]
12262	GM_180_A2_C09_T7	g3135969	BLASTN	386	2e-10	63	Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family prot...
12263	GM_180_A2_D02_T7	g4006831	BLASTX	147	1e-18	46	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
12264	GM_180_A2_D03_T7	g507910	BLASTN	624	1e-21	85	Glycine max BSR-101 satellite SB92 genomic sequence.
12265	GM_180_A2_D07_T7	g2522228	BLASTX	278	1e-23	55	(AB007466) reverse transcriptase-like protein [Vicia faba]
12266	GM_180_A2_E01_T7	g170605	BLASTN	648	7e-23	64	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
12267	GM_180_A2_E04_T7	g507910	BLASTN	348	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12268	GM_180_A2_E05_T7	g2879886	BLASTN	270	5e-11	71	Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes
12269	GM_180_A2_E10_T7	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
12270	GM_180_A2_F03_T7	g2190544	BLASTX	137	3e-13	96	(AC001229) Similar to Saccharomyces hypothetical protein P9642.2 (gb U40828). [Arabidopsis thaliana]
12271	GM_180_A2_F09_T7	g1666236	BLASTX	214	1e-16	31	(U76261) unknown [Hordeum vulgare]
12272	GM_180_A2_F10_T7	g4063760	BLASTX	153	7e-09	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12273	GM_180_A2_G01_T7	g100484	BLASTX	332	2e-28	41	hypothetical protein - garden snapdragon
12274	GM_180_A2_H04_T7	g3377855	BLASTX	240	2e-49	73	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
12275	GM_180_A2_H12_T7	g18683	BLASTN	659	6e-23	78	G.max N-20t gene
12276	GM_180_B1_A10_T7	g2522228	BLASTX	280	8e-24	40	(AB007466) reverse transcriptase-like protein [Vicia faba]
12277	GM_180_B1_B08_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12278	GM_180_B1_B08_T7	g3777527	BLASTX	689	7e-66	95	(AF053008) gag-pol polyprotein [Glycine max]
12279	GM_180_B1_B11_MR	g2982540	BLASTN	358	4e-09	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-30, complete sequence [Plasmodium falciparum]
12280	GM_180_B1_C08_MR	g1363051	BLASTX	206	4e-15	52	P58 protein - bovine gi 468012 (U04631) PKR inhibitor P58 [Bos taurus]
12281	GM_180_B1_C09_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12282	GM_180_B1_D11_MR	g3283026	BLASTX	152	5e-09	42	putative transposase [Arabidopsis thaliana]
12283	GM_180_B1_D12_MR	g3461846	BLASTX	486	3e-44	59	(AC005315) putative zinc-finger protein [Arabidopsis thaliana]
12284	GM_180_B1_E07_T7	g629693	BLASTX	195	3e-14	79	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
12285	GM_180_B1_E10_MR	g3097320	BLASTN	666	4e-23	76	Glycine max gene for Bd 30K, complete cds
12286	GM_180_B1_E10_T7	g1351239	BLASTX	119	2e-12	75	THIOREDOXIN M-TYPE PRECURSOR (TRX-M) gi 481594 pir S38909 thioredoxin m precursor - garden pea gi 431957 (X76269) thioredoxin m [Pisum sativum]
12287	GM_180_B1_F03_MR	g3142328	BLASTN	1691	7e-70	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12288	GM_180_B1_F04_MR	g3142328	BLASTN	842	4e-31	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12289	GM_180_B1_F08_MR	g3142328	BLASTN	1788	3e-74	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12290	GM_180_B1_F10_T7	g3142328	BLASTN	930	4e-35	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12291	GM_180_B1_F11_T7	g3777527	BLASTX	651	8e-62	92	(AF053008) gag-pol polyprotein [Glycine max]
12292	GM_180_B1_F12_MR	g507910	BLASTN	362	9e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12293	GM_180_B1_G09_T7	g3930515	BLASTX	117	1e-11	45	(AF059674) putative gag protein [Nicotiana tabacum]
12294	GM_180_B1_G10_MR	g3758836	BLASTN	351	8e-09	62	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
12295	GM_180_B1_H07_MR	g3845336	BLASTN	376	6e-10	63	Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence
12296	GM_180_B1_H08_T7	g4126312	BLASTN	364	2e-09	60	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
12297	GM_180_B2_A10_T7	g2995405	BLASTX	283	5e-23	52	(Y12432) polyprotein [Ananas comosus]
12298	GM_180_B2_B01_MR	g3097320	BLASTN	751	6e-27	77	Glycine max gene for Bd 30K, complete cds
12299	GM_180_B2_B04_T7	g3810595	BLASTX	204	3e-14	43	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
12300	GM_180_B2_C02_MR	g2982452	BLASTX	331	6e-28	58	(AL022223) receptor protein kinase - like protein [Arabidopsis thaliana]
12301	GM_180_B2_C03_T7	g3450889	BLASTX	496	1e-46	73	(AF083890) 19S proteosome subunit 9 [Arabidopsis thaliana]
12302	GM_180_B2_C08_MR	g4038056	BLASTX	214	1e-15	40	(AC005897) putative transposon [Arabidopsis thaliana]
12303	GM_180_B2_C08_T7	g3645899	BLASTX	225	1e-16	46	(U68408) 5' end not determined experimentally [Zea mays]
12304	GM_180_B2_C12_T7	g2462056	BLASTX	188	5e-14	44	(Y13388) reverse transcriptase [Antirrhinum majus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12305	GM_180_B2_D05_T7	g2462935	BLASTX	255	9e-20	40	(Y12321) open reading frame 1 [Brassica oleracea]
12306	GM_180_B2_D06_MR	g1769898	BLASTX	248	3e-22	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12307	GM_180_B2_E03_T7	g18559	BLASTN	445	4e-13	65	G.max gene for catalase
12308	GM_180_B2_E07_MR	g3142328	BLASTN	859	6e-32	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12309	GM_180_B2_F01_MR	g507910	BLASTN	603	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12310	GM_180_B2_F04_T7	g1805619	BLASTX	140	5e-09	76	(D49704) OSH42 transcript [Oryza sativa]
12311	GM_180_B2_F05_MR	g3845197	BLASTN	497	2e-15	65	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
12312	GM_180_B2_F05_T7	g2462134	BLASTX	218	2e-16	41	(Y13368) reverse transcriptase [Beta vulgaris]
12313	GM_180_B2_F06_MR	g4038056	BLASTX	302	6e-25	49	(AC005897) putative transposon [Arabidopsis thaliana]
12314	GM_180_B2_F06_T7	g13767	BLASTN	409	2e-12	66	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
12315	GM_180_B2_F07_MR	g4063760	BLASTX	464	5e-42	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12316	GM_180_B2_F07_T7	g4115365	BLASTX	170	1e-10	33	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
12317	GM_180_B2_F10_T7	g3142328	BLASTN	981	2e-37	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12318	GM_180_B2_G01_T7	g2292907	BLASTX	197	1e-13	35	(Y10099) P-glycoprotein homologue [Hordeum vulgare]
12319	GM_180_B2_H03_MR	g507910	BLASTN	352	3e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12320	GM_180_B2_H03_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12321	GM_180_B2_H04_T7	g100484	BLASTX	276	2e-22	53	hypothetical protein - garden snapdragon
12322	GM_180_B2_H07_MR	g3142328	BLASTN	580	3e-19	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12323	GM_180_B2_H09_MR	g2522228	BLASTX	292	4e-25	76	(AB007466) reverse transcriptase-like protein [Vicia faba]
12324	GM_181_A1_A07_T7	g3264565	BLASTN	450	3e-13	64	Homo sapiens chromosome 17, clone hRPC.1037_O_7, complete sequence [Homo sapiens]
12325	GM_181_A1_A08_MR	g4126312	BLASTN	356	5e-09	63	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
12326	GM_181_A1_B02_T7	g1326016	BLASTX	265	7e-21	47	TY3-2 orfB
12327	GM_181_A1_B05_MR	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12328	GM_181_A1_B08_MR	g507910	BLASTN	472	1e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
12329	GM_181_A1_B08_T7	g4063760	BLASTX	312	8e-26	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12330	GM_181_A1_B09_T7	g3873182	BLASTN	514	4e-16	64	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
12331	GM_181_A1_B11_MR	g3176783	BLASTN	349	2e-09	64	Homo sapiens allele 7 fragile site locus (FRA10B) minisatellite, 5' sequence
12332	GM_181_A1_C05_T7	g131289	BLASTX	703	1e-68	96	PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN) (CP43) gi 72709 pir F2NT44 photosystem II chlorophyll a-binding protein psbC - common tobacco chloroplast gi 225285 prf 1211235W photosystem II 44kD protein [Nicotiana tabacum]
12333	GM_181_A1_C10_MR	g3176795	BLASTN	418	2e-12	65	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
12334	GM_181_A1_D05_T7	g4063760	BLASTX	572	1e-53	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12335	GM_181_A1_D06_T7	g18730	BLASTN	2017	6e-85	96	Soybean 4.5 - 5S rRNA intergenic region
12336	GM_181_A1_D08_T7	g4063760	BLASTX	334	2e-33	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12337	GM_181_A1_E05_T7	g422418	BLASTX	241	3e-18	42	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
12338	GM_181_A1_E07_T7	g3645899	BLASTX	185	3e-14	42	(U68408) 5' end not determined experimentally [Zea mays]
12339	GM_181_A1_F02_T7	g507910	BLASTN	533	2e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
12340	GM_181_A1_F03_T7	g2245073	BLASTN	477	2e-14	65	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8
12341	GM_181_A1_F07_T7	g1633547	BLASTN	398	6e-11	69	Human chromosome 12p13 sequence, complete sequence [Homo sapiens]
12342	GM_181_A1_F08_T7	g3097320	BLASTN	401	4e-11	77	Glycine max gene for Bd 30K, complete cds
12343	GM_181_A1_F09_MR	g2462134	BLASTX	136	8e-09	40	(Y13368) reverse transcriptase [Beta vulgaris]
12344	GM_181_A1_G02_T7	g3510505	BLASTX	240	1e-25	49	(AF030881) pol polyprotein [Fugu rubripes]
12345	GM_181_A1_G04_MR	g3023281	BLASTX	315	4e-29	64	HIGH AFFINITY AMMONIUM TRANSPORTER gi 2065194 gnl PID e223603 (X95098) ammonium transporter [Lycopersicon esculentum]
12346	GM_181_A1_G09_MR	g665934	BLASTX	186	9e-13	40	(U20341) ORF III [Cassava vein mosaic virus] gi 1399884 (U59751) ORF 3 [Cassava vein mosaic virus]
12347	GM_181_A1_G10_MR	g507910	BLASTN	611	5e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12348	GM_181_A1_G10_T7	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
12349	GM_181_A1_H06_T7	g170080	BLASTN	390	1e-10	68	Soybean seed lectin gene transposable element tgm1.
12350	GM_181_A2_A01_MR	g3142328	BLASTN	899	9e-34	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12351	GM_181_A2_A04_T7	g4063760	BLASTX	372	3e-32	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12352	GM_181_A2_A09_MR	g3810596	BLASTX	274	6e-22	35	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
12353	GM_181_A2_A11_T7	g100484	BLASTX	369	4e-38	60	hypothetical protein - garden snapdragon
12354	GM_181_A2_B01_MR	g169363	BLASTX	266	2e-22	56	(M75856) PVPR3 [Phaseolus vulgaris]
12355	GM_181_A2_B01_T7	g3287696	BLASTX	390	1e-34	62	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]
12356	GM_181_A2_B02_MR	g18559	BLASTN	695	2e-24	77	G.max gene for catalase
12357	GM_181_A2_C04_MR	g2865424	BLASTX	143	1e-09	38	(AF039371) polyprotein [Arabidopsis thaliana]
12358	GM_181_A2_C06_T7	g2522228	BLASTX	629	9e-61	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
12359	GM_181_A2_C08_T7	g300517	BLASTN	453	2e-14	62	Apo(B) (HVE36)=Apolipoprotein B {3' region, AT rich minisatellite, VNTR} [human, caucasian, Genomic, 802 nt]
12360	GM_181_A2_C12_T7	g507910	BLASTN	619	2e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12361	GM_181_A2_D06_T7	g1495804	BLASTX	592	2e-58	76	(X96406) 13-lipoxygenase [Solanum tuberosum]
12362	GM_181_A2_D08_T7	g18559	BLASTN	529	6e-17	77	G.max gene for catalase
12363	GM_181_A2_D10_T7	g453514	BLASTN	402	4e-11	61	Tetrahymena pyriformis ribosomal RNA; tRNA-Trp; ORF 1-4; tRNA-Glu; cytochrome oxidase subunit 1; NADH dehydrogenase; ribosomal protein L14.
12364	GM_181_A2_E01_T7	g1769898	BLASTX	600	9e-58	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12365	GM_181_A2_E06_T7	g2245390	BLASTX	239	1e-18	53	(U89296) auxin response transcription factor 3; ARF3 [Arabidopsis thaliana]
12366	GM_181_A2_E08_T7	g3599418	BLASTN	354	5e-09	74	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
12367	GM_181_A2_E12_MR	g2642165	BLASTX	156	7e-10	61	(AC003000) hypothetical protein [Arabidopsis thaliana]
12368	GM_181_A2_F01_MR	g4063760	BLASTX	189	1e-26	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12369	GM_181_A2_F04_MR	g507910	BLASTN	371	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12370	GM_181_A2_F05_MR	g3193284	BLASTX	246	3e-28	67	(AF069298) No definition line found [Arabidopsis thaliana]
12371	GM_181_A2_F07_MR	g3777527	BLASTX	376	2e-32	93	(AF053008) gag-pol polyprotein [Glycine max]
12372	GM_181_A2_F07_T7	g3176777	BLASTN	462	7e-15	65	Homo sapiens allele 4 fragile site locus (FRA10B) minisatellite, 3' sequence
12373	GM_181_A2_F09_MR	g3097320	BLASTN	435	1e-12	68	Glycine max gene for Bd 30K, complete cds
12374	GM_181_A2_F12_MR	g3777527	BLASTX	396	1e-34	91	(AF053008) gag-pol polyprotein [Glycine max]
12375	GM_181_A2_F12_T7	g3142328	BLASTN	2487	4e-107	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12376	GM_181_A2_G03_MR	g1785744	BLASTX	99	4e-11	38	(Y08502) orf158 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12377	GM_181_A2_G08_MR	g2245044	BLASTX	185	2e-18	55	(Z97342) similarity to reverse transcriptase - Arabidopsis thaliana retrotransposon 2 (fragment) [Arabidopsis thaliana]
12378	GM_181_A2_G09_T7	g3142328	BLASTN	1828	4e-76	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12379	GM_181_A2_H08_MR	g4038056	BLASTX	149	1e-20	44	(AC005897) putative transposon [Arabidopsis thaliana]
12380	GM_181_A2_H12_T7	g1167523	BLASTX	455	5e-41	56	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
12381	GM_181_B1_A05_T7	g1619300	BLASTX	163	2e-11	33	(X95269) LRR protein [Lycopersicon esculentum]
12382	GM_181_B1_A06_T7	g1142701	BLASTN	1352	9e-55	90	Glycine max satellite STR120-A.3.
12383	GM_181_B1_A09_MR	g905361	BLASTX	191	3e-13	31	(U22103) gag-protease polyprotein [Glycine max]
12384	GM_181_B1_B08_MR	g3142328	BLASTN	1069	2e-41	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12385	GM_181_B1_C01_MR	g507910	BLASTN	348	4e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12386	GM_181_B1_C01_T7	g507910	BLASTN	409	7e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
12387	GM_181_B1_C03_MR	g2245104	BLASTX	320	2e-26	50	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
12388	GM_181_B1_C03_T7	g2088647	BLASTX	398	4e-36	66	(AF002109) hypothetical protein [Arabidopsis thaliana] gi 3158394 (AF036340) LRR-containing F-box protein [Arabidopsis thaliana]
12389	GM_181_B1_C06_MR	g4063760	BLASTX	213	3e-15	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12390	GM_181_B1_C07_MR	g3142328	BLASTN	1088	2e-42	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12391	GM_181_B1_C09_MR	g3550435	BLASTN	532	5e-17	62	Hordeum vulgare Hotr1 gene
12392	GM_181_B1_C09_T7	g2213599	BLASTX	315	6e-26	51	(AC000348) T7N9.19 [Arabidopsis thaliana]
12393	GM_181_B1_D04_T7	g3046704	BLASTX	285	6e-23	46	(AL022223) putative protein [Arabidopsis thaliana]
12394	GM_181_B1_D05_T7	g2429512	BLASTN	534	4e-17	64	Caenorhabditis elegans cosmid T27A1
12395	GM_181_B1_D07_MR	g3599418	BLASTN	381	3e-10	73	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
12396	GM_181_B1_D08_MR	g1167523	BLASTX	182	7e-12	33	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
12397	GM_181_B1_D09_T7	g1402881	BLASTX	216	1e-15	43	(X98130) non-ltr retrotransposon reverse transcriptase-like protein [Arabidopsis thaliana]
12398	GM_181_B1_E03_T7	g3287679	BLASTX	157	2e-09	54	(AC003979) T22J18.6 [Arabidopsis thaliana]
12399	GM_181_B1_E08_T7	g18559	BLASTN	449	2e-13	68	G.max gene for catalase
12400	GM_181_B1_E10_T7	g905361	BLASTX	586	3e-56	96	(U22103) gag-protease polyprotein [Glycine max]
12401	GM_181_B1_F02_T7	g905361	BLASTX	586	3e-56	95	(U22103) gag-protease polyprotein [Glycine max]
12402	GM_181_B1_F04_T7	g4063756	BLASTN	461	9e-14	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12403	GM_181_B1_F06_T7	g1732362	BLASTN	406	8e-12	82	Malus domestica pAFD103 mRNA, partial cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12404	GM_181_B1_F08_T7	g992916	BLASTN	422	5e-12	69	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
12405	GM_181_B1_F09_MR	g441205	BLASTN	485	6e-15	74	Soybean lox1gm4 gene encoding lipxygenase L-4
12406	GM_181_B1_F11_MR	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12407	GM_181_B1_G02_T7	g3319362	BLASTX	226	9e-17	42	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12408	GM_181_B1_G07_T7	g3695395	BLASTX	169	2e-13	43	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
12409	GM_181_B1_H05_T7	g4063760	BLASTX	252	2e-19	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12410	GM_181_B1_H06_MR	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12411	GM_181_B1_H07_MR	g3142328	BLASTN	796	2e-53	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12412	GM_181_B1_H09_T7	g3142328	BLASTN	887	3e-33	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12413	GM_181_B2_A02_MR	g2498731	BLASTX	310	6e-27	58	PROBABLE NADP-DEPENDENT OXIDOREDUCTASE P1 gi 1362013 pir S57611 zeta-crystallin homolog - Arabidopsis thaliana gi 886428 (Z49768) zeta-crystallin homologue [Arabidopsis thaliana]
12414	GM_181_B2_A08_MR	g507910	BLASTN	636	4e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
12415	GM_181_B2_A08_T7	g3930515	BLASTX	105	2e-11	44	(AF059674) putative gag protein [Nicotiana tabacum]
12416	GM_181_B2_A09_MR	g134646	BLASTX	291	7e-37	91	SUPEROXIDE DISMUTASE, CHLOROPLAST PRECURSOR (FE) gi 169955 (M64267) Fe-superoxide dismutase [Glycine max] gi 228415 prf 1803527A Fe superoxide dismutase [Glycine max]
12417	GM_181_B2_A09_T7	g3786004	BLASTX	180	3e-13	59	(AC005499) hypothetical protein [Arabidopsis thaliana]
12418	GM_181_B2_A10_T7	g4063756	BLASTN	469	4e-14	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12419	GM_181_B2_A11_MR	g507910	BLASTN	403	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
12420	GM_181_B2_B01_T7	g905361	BLASTX	118	4e-10	25	(U22103) gag-protease polyprotein [Glycine max]
12421	GM_181_B2_B02_T7	g3492857	BLASTN	356	5e-09	69	Homo sapiens 12q24.2 PAC RPCI1-157K6 (Roswell Park Cancer Institute Human PAC library) complete sequence [Homo sapiens]
12422	GM_181_B2_B03_MR	g507910	BLASTN	577	2e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12423	GM_181_B2_B03_T7	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12424	GM_181_B2_B09_MR	g1040717	BLASTN	372	1e-10	63	D.polychroa microsatellite sequence (clone Dp ch1 F3)
12425	GM_181_B2_C02_T7	g4063760	BLASTX	291	1e-23	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12426	GM_181_B2_C09_T7	g1040717	BLASTN	333	6e-09	62	D.polychroa microsatellite sequence (clone Dp ch1 F3)
12427	GM_181_B2_D01_MR	g1769898	BLASTX	422	1e-38	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12428	GM_181_B2_D02_MR	g507910	BLASTN	362	9e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
12429	GM_181_B2_D02_T7	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12430	GM_181_B2_D08_MR	g3482974	BLASTX	342	3e-29	76	(AL031369) ATP-dependent Clp proteinase - like protein [Arabidopsis thaliana]
12431	GM_181_B2_D11_MR	g3777527	BLASTX	701	4e-67	93	(AF053008) gag-pol polyprotein [Glycine max]
12432	GM_181_B2_D12_T7	g2443320	BLASTX	348	1e-29	52	(D85597) polyprotein [Oryza australiensis]
12433	GM_181_B2_E05_MR	g2462058	BLASTX	360	3e-32	52	(Y13389) reverse transcriptase [Antirrhinum majus]
12434	GM_181_B2_F03_MR	g505129	BLASTN	369	1e-09	74	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
12435	GM_181_B2_F04_MR	g3845197	BLASTN	410	2e-11	60	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
12436	GM_181_B2_F09_MR	g2522230	BLASTX	311	5e-27	39	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
12437	GM_181_B2_F12_MR	g507910	BLASTN	604	1e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12438	GM_181_B2_F12_T7	g507910	BLASTN	635	4e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12439	GM_181_B2_G02_MR	g3142379	BLASTX	119	7e-10	86	(AF053008) envelope-like [Glycine max]
12440	GM_181_B2_G09_MR	g2979574	BLASTN	357	4e-09	58	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence [Homo sapiens]
12441	GM_181_B2_H01_T7	g4150930	BLASTN	407	2e-11	63	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
12442	GM_182_A1_A01_MR	g3777527	BLASTX	167	3e-11	41	(AF053008) gag-pol polyprotein [Glycine max]
12443	GM_182_A1_A05_MR	g2522228	BLASTX	318	8e-28	56	(AB007466) reverse transcriptase-like protein [Vicia faba]
12444	GM_182_A1_A06_MR	g4063760	BLASTX	478	2e-43	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12445	GM_182_A1_A06_T7	g3243214	BLASTN	490	4e-15	67	Arabidopsis thaliana BAC T19B17 from chromsome IV, near 19.3 cM, complete sequence [Arabidopsis thaliana]
12446	GM_182_A1_A10_MR	g3688172	BLASTX	162	1e-11	50	(AL031804) putative protein [Arabidopsis thaliana]
12447	GM_182_A1_A12_MR	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
12448	GM_182_A1_B01_MR	g4104931	BLASTX	120	9e-10	78	(AF042196) auxin response factor 8 [Arabidopsis thaliana]
12449	GM_182_A1_B07_T7	g170606	BLASTN	554	3e-18	70	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
12450	GM_182_A1_B09_MR	g3142328	BLASTN	1112	2e-43	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12451	GM_182_A1_B10_T7	g905361	BLASTX	346	4e-30	96	(U22103) gag-protease polyprotein [Glycine max]
12452	GM_182_A1_B11_T7	g507910	BLASTN	588	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12453	GM_182_A1_B12_MR	g99922	BLASTX	381	4e-53	77	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12454	GM_182_A1_C02_MR	g4063760	BLASTX	551	2e-51	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12455	GM_182_A1_C03_MR	g905361	BLASTX	204	1e-14	35	(U22103) gag-protease polyprotein [Glycine max]
12456	GM_182_A1_C06_MR	g2995405	BLASTX	454	2e-41	66	(Y12432) polyprotein [Ananas comosus]
12457	GM_182_A1_C07_MR	g507910	BLASTN	361	1e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12458	GM_182_A1_C07_T7	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12459	GM_182_A1_C10_MR	g100484	BLASTX	137	1e-12	36	hypothetical protein - garden snapdragon
12460	GM_182_A1_D07_T7	g2244802	BLASTX	324	5e-27	50	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
12461	GM_182_A1_D08_MR	g3097320	BLASTN	896	2e-33	75	Glycine max gene for Bd 30K, complete cds
12462	GM_182_A1_D10_MR	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
12463	GM_182_A1_D10_T7	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12464	GM_182_A1_E02_T7	g3142328	BLASTN	1340	8e-54	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12465	GM_182_A1_E12_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
12466	GM_182_A1_F04_MR	g3777526	BLASTN	355	5e-09	64	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
12467	GM_182_A1_F09_MR	g505129	BLASTN	352	6e-09	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
12468	GM_182_A1_F09_T7	g4063760	BLASTX	153	7e-09	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12469	GM_182_A1_F10_MR	g170606	BLASTN	785	5e-29	71	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
12470	GM_182_A1_F12_MR	g4063760	BLASTX	520	5e-48	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12471	GM_182_A1_G03_T7	g18559	BLASTN	437	9e-13	73	G.max gene for catalase
12472	GM_182_A1_G07_T7	g18559	BLASTN	628	2e-21	78	G.max gene for catalase
12473	GM_182_A1_G12_T7	g3319362	BLASTX	209	6e-15	59	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12474	GM_182_A1_H02_T7	g3097320	BLASTN	354	5e-09	72	Glycine max gene for Bd 30K, complete cds
12475	GM_182_A1_H04_MR	g3142328	BLASTN	763	1e-27	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12476	GM_182_A1_H04_T7	g1000971	BLASTN	406	3e-11	63	Hansenula wingei mitochondrial DNA, complete sequence
12477	GM_182_A1_H05_T7	g507910	BLASTN	438	4e-13	84	Glycine max BSR-101 satellite SB92 genomic sequence.
12478	GM_182_A1_H06_MR	g4063760	BLASTX	178	2e-11	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12479	GM_182_A1_H06_T7	g507910	BLASTN	562	9e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12480	GM_182_A1_H07_T7	g18559	BLASTN	911	3e-34	77	G.max gene for catalase
12481	GM_182_A1_H09_T7	g4038056	BLASTX	290	1e-23	55	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12482	GM_182_A2_A03_MR	g505129	BLASTN	361	2e-09	73	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
12483	GM_182_A2_A05_T7	g505129	BLASTN	383	2e-10	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
12484	GM_182_A2_B07_T7	g507910	BLASTN	520	7e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
12485	GM_182_A2_B10_T7	g387902	BLASTX	191	8e-21	56	(L23524) ORF [Hordeum vulgare]
12486	GM_182_A2_C01_T7	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
12487	GM_182_A2_C03_T7	g3142328	BLASTN	426	3e-12	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12488	GM_182_A2_C10_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12489	GM_182_A2_C11_MR	g4092471	BLASTN	432	2e-12	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
12490	GM_182_A2_D03_T7	g3142328	BLASTN	2030	2e-85	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12491	GM_182_A2_D09_T7	g2586082	BLASTX	203	4e-14	54	(U72725) retrofit [Oryza longistaminata]
12492	GM_182_A2_D10_T7	g3395432	BLASTX	151	2e-20	93	(AC004683) unknown protein [Arabidopsis thaliana]
12493	GM_182_A2_E03_MR	g3097320	BLASTN	480	1e-14	72	Glycine max gene for Bd 30K, complete cds
12494	GM_182_A2_E05_T7	g3319362	BLASTX	310	9e-26	52	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12495	GM_182_A2_E06_T7	g3097320	BLASTN	480	1e-14	72	Glycine max gene for Bd 30K, complete cds
12496	GM_182_A2_E09_T7	g4160362	BLASTN	432	2e-12	63	Saccharomyces cerevisiae complete mitochondrial genome
12497	GM_182_A2_F02_T7	g100484	BLASTX	379	2e-33	53	hypothetical protein - garden snapdragon
12498	GM_182_A2_F04_MR	g1769899	BLASTX	170	4e-12	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12499	GM_182_A2_F04_T7	g93559	BLASTX	177	3e-11	34	ORF3 protein - rice tungro bacilliform virus gi 333967 (M65026) ORF3 [Rice tungro bacilliform virus]
12500	GM_182_A2_F08_T7	g2522230	BLASTX	303	3e-26	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
12501	GM_182_A2_F11_T7	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
12502	GM_182_A2_G06_MR	g507910	BLASTN	508	2e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
12503	GM_182_A2_G07_MR	g4063760	BLASTX	186	2e-12	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12504	GM_182_A2_H02_T7	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12505	GM_182_A2_H04_T7	g18702	BLASTN	410	2e-12	65	Soybean nodulin-24 gene 5' end
12506	GM_182_B1_A10_MR	g3142379	BLASTX	232	4e-18	58	(AF053008) envelope-like [Glycine max]
12507	GM_182_B1_A11_T7	g170603	BLASTN	387	6e-11	62	Broad bean (V.faba) BamHI repetitive element, 990 bp family.
12508	GM_182_B1_B05_MR	g4063760	BLASTX	260	3e-20	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12509	GM_182_B1_B05_T7	g3319362	BLASTX	197	1e-13	57	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12510	GM_182_B1_B07_MR	g507910	BLASTN	644	2e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
12511	GM_182_B1_B10_T7	g3319362	BLASTX	407	4e-36	52	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12512	GM_182_B1_C07_MR	g3834324	BLASTX	166	2e-11	81	(AC005679) Similar to gb X92762 tafazzins protein from Homo sapiens. [Arabidopsis thaliana]
12513	GM_182_B1_C08_MR	g3297823	BLASTX	223	7e-20	51	(AL031032) putative protein [Arabidopsis thaliana]
12514	GM_182_B1_C09_T7	g4063760	BLASTX	195	3e-14	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12515	GM_182_B1_C10_T7	g4063760	BLASTX	497	1e-45	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12516	GM_182_B1_D04_MR	g3695395	BLASTX	236	4e-18	47	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
12517	GM_182_B1_D04_T7	g2961349	BLASTX	181	6e-12	40	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
12518	GM_182_B1_D08_T7	g2961349	BLASTX	166	3e-10	35	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
12519	GM_182_B1_D09_T7	g1684913	BLASTX	311	9e-26	47	(U77888) receptor-like protein kinase [Ipomoea nil]
12520	GM_182_B1_D12_T7	g507910	BLASTN	584	9e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12521	GM_182_B1_E08_T7	g170065	BLASTN	451	2e-13	73	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds.
12522	GM_182_B1_E10_T7	g99922	BLASTX	227	6e-38	73	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
12523	GM_182_B1_E12_T7	g505129	BLASTN	365	1e-09	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
12524	GM_182_B1_F03_MR	g507910	BLASTN	711	2e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
12525	GM_182_B1_F05_T7	g99922	BLASTX	171	1e-26	68	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
12526	GM_182_B1_F12_MR	g2522228	BLASTX	315	2e-27	73	(AB007466) reverse transcriptase-like protein [Vicia faba]
12527	GM_182_B1_G07_MR	g4038056	BLASTX	170	9e-22	53	(AC005897) putative transposon [Arabidopsis thaliana]
12528	GM_182_B1_G07_T7	g4038056	BLASTX	288	2e-23	45	(AC005897) putative transposon [Arabidopsis thaliana]
12529	GM_182_B1_G08_MR	g3097320	BLASTN	457	1e-13	68	Glycine max gene for Bd 30K, complete cds
12530	GM_182_B1_G10_T7	g3540184	BLASTX	288	2e-23	56	(AC004122) Similar to endoxylanases [Arabidopsis thaliana]
12531	GM_182_B1_G12_T7	g905361	BLASTX	197	6e-14	31	(U22103) gag-protease polyprotein [Glycine max]
12532	GM_182_B1_H04_MR	g3283026	BLASTX	197	7e-14	42	putative transposase [Arabidopsis thaliana]
12533	GM_182_B1_H05_T7	g2522230	BLASTX	139	1e-08	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
12534	GM_182_B1_H08_T7	g2522226	BLASTN	562	2e-18	70	Vicia faba mRNA for reverse transcriptase-like protein, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12535	GM_182_B1_H12_MR	g3834307	BLASTX	233	4e-18	80	(AC005679) Strong similarity to gene T10I14.120 gi 2832679 putative protein from Arabidopsis thaliana BAC gb AL021712. ESTs gb N65887 and gb N65627 come from this gene. [Arabidopsis thaliana]
12536	GM_182_B2_A03_MR	g3548810	BLASTX	279	1e-27	48	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]
12537	GM_182_B2_A05_T7	g3645899	BLASTX	225	5e-29	50	(U68408) 5' end not determined experimentally [Zea mays]
12538	GM_182_B2_A10_T7	g3928116	BLASTN	399	6e-11	61	, complete sequence [Homo sapiens]
12539	GM_182_B2_B05_T7	g3777527	BLASTX	173	7e-11	37	(AF053008) gag-pol polyprotein [Glycine max]
12540	GM_182_B2_B09_T7	g2129618	BLASTX	175	2e-11	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
12541	GM_182_B2_C02_T7	g2346988	BLASTX	230	8e-18	54	(AB006606) ZPT4-4 [Petunia x hybrida]
12542	GM_182_B2_C04_MR	g2462058	BLASTX	192	2e-14	61	(Y13389) reverse transcriptase [Antirrhinum majus]
12543	GM_182_B2_C05_T7	g3810596	BLASTX	203	3e-14	43	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
12544	GM_182_B2_C08_MR	g2995405	BLASTX	306	2e-25	55	(Y12432) polyprotein [Ananas comosus]
12545	GM_182_B2_D03_T7	g3097320	BLASTN	488	5e-15	70	Glycine max gene for Bd 30K, complete cds
12546	GM_182_B2_D06_T7	g4063770	BLASTX	203	2e-14	38	(AB004906) transposase [Ipomoea purpurea]
12547	GM_182_B2_D08_T7	g2979574	BLASTN	373	8e-10	61	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence [Homo sapiens]
12548	GM_182_B2_E03_T7	g2085783	BLASTN	445	8e-14	68	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
12549	GM_182_B2_E06_T7	g2129618	BLASTX	211	3e-15	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
12550	GM_182_B2_F05_T7	g3097320	BLASTN	470	3e-14	73	Glycine max gene for Bd 30K, complete cds
12551	GM_182_B2_F06_MR	g2500724	BLASTX	142	4e-10	62	PREPROTEIN TRANSLOCASE SECA SUBUNIT PRECURSOR gi 2129894 pir S72453 secA protein precursor - garden pea gi 1122325 (X82404) chloroplast SecA protein [Pisum sativum]
12552	GM_182_B2_F08_T7	g507910	BLASTN	381	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12553	GM_182_B2_F09_T7	g507910	BLASTN	598	2e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12554	GM_182_B2_G03_MR	g3650039	BLASTX	142	7e-14	50	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
12555	GM_182_B2_G10_T7	g3777527	BLASTX	211	3e-20	44	(AF053008) gag-pol polyprotein [Glycine max]
12556	GM_182_B2_H02_MR	g507910	BLASTN	551	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
12557	GM_182_B2_H04_MR	g2129618	BLASTX	161	7e-10	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12558	GM_182_B2_H09_MR	g507910	BLASTN	358	1e-09	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12559	GM_183_A1_A03_MR	g4038056	BLASTX	265	5e-21	46	(AC005897) putative transposon [Arabidopsis thaliana]
12560	GM_183_A1_A07_MR	g18559	BLASTN	388	1e-10	68	G.max gene for catalase
12561	GM_183_A1_A12_T7	g3777527	BLASTX	633	7e-60	97	(AF053008) gag-pol polyprotein [Glycine max]
12562	GM_183_A1_B01_T7	g4063760	BLASTX	516	1e-47	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12563	GM_183_A1_B02_T7	g507910	BLASTN	641	2e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
12564	GM_183_A1_B06_MR	g2258469	BLASTX	126	8e-12	70	(AF009179) replication protein A1 [Oryza sativa]
12565	GM_183_A1_B06_T7	g530207	BLASTX	517	4e-48	85	(L35272) heat shock protein [Glycine max]
12566	GM_183_A1_B08_T7	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12567	GM_183_A1_B11_T7	g3337361	BLASTX	286	4e-33	81	(AC004481) ankyrin-like protein [Arabidopsis thaliana]
12568	GM_183_A1_C01_MR	g1769899	BLASTX	213	4e-20	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12569	GM_183_A1_C02_MR	g4063760	BLASTX	485	3e-44	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12570	GM_183_A1_C04_MR	g3142328	BLASTN	768	8e-28	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12571	GM_183_A1_C08_T7	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12572	GM_183_A1_C11_MR	g3142328	BLASTN	706	5e-25	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12573	GM_183_A1_C12_MR	g2564112	BLASTX	149	5e-09	45	(AF000371) UDP glucose:flavonoid 3-o-glucosyltransferase [Vitis vinifera]
12574	GM_183_A1_D01_T7	g320564	BLASTX	173	2e-12	44	transposon copia - Arabidopsis thaliana (fragment)
12575	GM_183_A1_D04_T7	g3097320	BLASTN	1212	7e-48	83	Glycine max gene for Bd 30K, complete cds
12576	GM_183_A1_D08_T7	g2781351	BLASTX	246	3e-20	70	(AC003113) F24O1.7 [Arabidopsis thaliana]
12577	GM_183_A1_E01_MR	g18559	BLASTN	896	1e-33	75	G.max gene for catalase
12578	GM_183_A1_E05_T7	g3695395	BLASTX	178	7e-12	42	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
12579	GM_183_A1_E06_MR	g2245104	BLASTX	189	1e-12	46	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
12580	GM_183_A1_E07_MR	g507910	BLASTN	389	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12581	GM_183_A1_E07_T7	g507910	BLASTN	379	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12582	GM_183_A1_E08_MR	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12583	GM_183_A1_E09_MR	g3097320	BLASTN	381	3e-10	72	Glycine max gene for Bd 30K, complete cds
12584	GM_183_A1_E10_MR	g100484	BLASTX	266	3e-21	41	hypothetical protein - garden snapdragon
12585	GM_183_A1_E12_T7	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12586	GM_183_A1_F02_T7	g905361	BLASTX	133	2e-14	36	(U22103) gag-protease polyprotein [Glycine max]
12587	GM_183_A1_F03_T7	g840618	BLASTN	345	9e-09	62	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
12588	GM_183_A1_F10_MR	g1769903	BLASTX	308	9e-27	74	(X95738) proline transporter 2 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12589	GM_183_A1_F11_MR	g4038056	BLASTX	185	2e-12	43	(AC005897) putative transposon [Arabidopsis thaliana]
12590	GM_183_A1_F12_T7	g1769898	BLASTX	329	3e-28	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12591	GM_183_A1_G04_T7	g18559	BLASTN	662	6e-23	73	G.max gene for catalase
12592	GM_183_A1_G05_T7	g2462058	BLASTX	269	1e-22	50	(Y13389) reverse transcriptase [Antirrhinum majus]
12593	GM_183_A1_G09_T7	g4038056	BLASTX	229	1e-27	52	(AC005897) putative transposon [Arabidopsis thaliana]
12594	GM_183_A1_G10_MR	g2642431	BLASTX	237	1e-17	56	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
12595	GM_183_A1_H02_MR	g3142328	BLASTN	1551	2e-63	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12596	GM_183_A1_H02_T7	g130582	BLASTX	166	3e-10	41	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
12597	GM_183_A1_H04_MR	g3702121	BLASTX	136	1e-16	68	(AJ011681) retinoblastoma-related protein [Chenopodium rubrum]
12598	GM_183_A1_H07_MR	g1167523	BLASTX	321	1e-26	55	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
12599	GM_183_A1_H09_MR	g100484	BLASTX	292	4e-24	50	hypothetical protein - garden snapdragon
12600	GM_183_A2_A01_MR	g2995405	BLASTX	444	3e-40	57	(Y12432) polyprotein [Ananas comosus]
12601	GM_183_A2_A06_MR	g4063760	BLASTX	385	1e-33	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12602	GM_183_A2_A09_MR	g3777527	BLASTX	614	7e-58	95	(AF053008) gag-pol polyprotein [Glycine max]
12603	GM_183_A2_A10_T7	g3337361	BLASTX	135	2e-12	73	(AC004481) ankyrin-like protein [Arabidopsis thaliana]
12604	GM_183_A2_B01_MR	g3142328	BLASTN	862	4e-32	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12605	GM_183_A2_B05_T7	g905361	BLASTX	752	8e-74	87	(U22103) gag-protease polyprotein [Glycine max]
12606	GM_183_A2_B07_MR	g2160128	BLASTN	380	4e-10	61	Genomic sequence from Human 17, complete sequence [Homo sapiens]
12607	GM_183_A2_B09_MR	g4063760	BLASTX	332	6e-28	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12608	GM_183_A2_B12_MR	g3426334	BLASTN	537	3e-17	63	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
12609	GM_183_A2_C01_T7	g3142328	BLASTN	949	5e-36	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12610	GM_183_A2_C04_MR	g4063760	BLASTX	359	7e-31	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12611	GM_183_A2_C04_T7	g905361	BLASTX	200	3e-14	31	(U22103) gag-protease polyprotein [Glycine max]
12612	GM_183_A2_C05_MR	g507910	BLASTN	485	3e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
12613	GM_183_A2_C06_T7	g2454214	BLASTN	445	3e-13	71	Glycine max nodule-specific phosphoribosylpyrophosphate amidotransferase (PRAT) gene, 5' upstream sequence and partial cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12614	GM_183_A2_C08_MR	g4092470	BLASTN	477	2e-14	62	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
12615	GM_183_A2_C12_T7	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12616	GM_183_A2_D01_MR	g1769897	BLASTX	220	1e-16	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12617	GM_183_A2_D02_MR	g18559	BLASTN	315	2e-10	70	G.max gene for catalase
12618	GM_183_A2_D03_MR	g1743251	BLASTN	406	3e-11	61	Human DNA sequence from PAC 293L6 on chromosome 22 Contains ESTs and STS, complete sequence [Homo sapiens]
12619	GM_183_A2_D03_T7	g99730	BLASTX	220	1e-16	34	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
12620	GM_183_A2_D09_MR	g3777527	BLASTX	591	2e-55	95	(AF053008) gag-pol polyprotein [Glycine max]
12621	GM_183_A2_E06_T7	g2980770	BLASTX	191	1e-13	48	(AL022198) putative protein kinase [Arabidopsis thaliana]
12622	GM_183_A2_E08_MR	g507910	BLASTN	349	4e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
12623	GM_183_A2_E08_T7	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12624	GM_183_A2_E10_MR	g4092471	BLASTN	508	7e-16	73	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
12625	GM_183_A2_E12_MR	g3046704	BLASTX	196	2e-13	41	(AL022223) putative protein [Arabidopsis thaliana]
12626	GM_183_A2_F07_MR	g507910	BLASTN	392	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12627	GM_183_A2_F09_T7	g3241925	BLASTN	833	1e-30	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK9, complete sequence [Arabidopsis thaliana]
12628	GM_183_A2_G01_T7	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12629	GM_183_A2_G02_MR	g507910	BLASTN	521	6e-17	76	Glycine max BSR-101 satellite SB92 genomic sequence.
12630	GM_183_A2_G02_T7	g4063756	BLASTN	405	3e-11	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12631	GM_183_A2_G04_MR	g995751	BLASTN	396	5e-11	61	Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence
12632	GM_183_A2_G04_T7	g2462058	BLASTX	131	1e-17	52	(Y13389) reverse transcriptase [Antirrhinum majus]
12633	GM_183_A2_G06_MR	g4050011	BLASTN	486	6e-15	67	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
12634	GM_183_A2_G08_T7	g2462058	BLASTX	310	6e-27	52	(Y13389) reverse transcriptase [Antirrhinum majus]
12635	GM_183_A2_G10_T7	g507910	BLASTN	597	2e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12636	GM_183_A2_G12_T7	g4063760	BLASTX	556	1e-52	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12637	GM_183_A2_H05_MR	g3319362	BLASTX	204	4e-27	50	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12638	GM_183_A2_H10_T7	g2129618	BLASTX	223	2e-16	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
12639	GM_183_A2_H11_MR	g2564051	BLASTN	450	3e-13	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MWD9, complete sequence [Arabidopsis thaliana]
12640	GM_183_B1_A05_T7	g3142328	BLASTN	862	3e-47	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12641	GM_183_B1_A07_T7	g3452139	BLASTN	351	1e-09	69	Glycine max mRNA for resistance protein, partial
12642	GM_183_B1_B04_T7	g4063760	BLASTX	387	8e-34	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12643	GM_183_B1_B05_T7	g3080426	BLASTX	198	7e-14	54	(AL022604) putative protein [Arabidopsis thaliana]
12644	GM_183_B1_B06_MR	g3193298	BLASTX	162	3e-11	43	(AF069298) T14P8.17 gene product [Arabidopsis thaliana]
12645	GM_183_B1_B06_T7	g3193287	BLASTX	449	1e-41	66	(AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]
12646	GM_183_B1_B07_MR	g3135251	BLASTX	351	3e-30	49	(AC003058) putative receptor protein kinase [Arabidopsis thaliana] gi 3176719 (AC002392) putative protein kinase [Arabidopsis thaliana]
12647	GM_183_B1_B09_MR	g18559	BLASTN	997	3e-38	74	G.max gene for catalase
12648	GM_183_B1_B09_T7	g3097320	BLASTN	444	5e-13	68	Glycine max gene for Bd 30K, complete cds
12649	GM_183_B1_B11_T7	g2911063	BLASTN	364	2e-09	74	Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSAII project)
12650	GM_183_B1_B12_MR	g3142328	BLASTN	729	5e-26	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12651	GM_183_B1_C01_MR	g18559	BLASTN	938	2e-35	73	G.max gene for catalase
12652	GM_183_B1_C02_MR	g2827718	BLASTX	313	5e-26	48	(AL021684) retrotransposon - like protein [Arabidopsis thaliana]
12653	GM_183_B1_C02_T7	g3845321	BLASTN	365	2e-09	65	Plasmodium falciparum chromosome 2, section 66 of 73 of the complete sequence
12654	GM_183_B1_C07_MR	g3860320	BLASTN	396	6e-11	88	Cicer arietinum mRNA for beta-galactosidase, clone CanBGal-5
12655	GM_183_B1_C09_MR	g2462134	BLASTX	346	1e-30	46	(Y13368) reverse transcriptase [Beta vulgaris]
12656	GM_183_B1_C10_T7	g1142703	BLASTN	301	4e-17	77	Glycine max satellite STR120-B.1.
12657	GM_183_B1_C12_T7	g3426334	BLASTN	361	3e-09	59	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
12658	GM_183_B1_D01_T7	g3142330	BLASTX	674	2e-65	94	(U96295) envelope-like [Glycine max]
12659	GM_183_B1_D02_T7	g3947735	BLASTX	374	9e-33	52	(AJ009720) NL27 [Solanum tuberosum]
12660	GM_183_B1_D07_MR	g18559	BLASTN	469	3e-14	69	G.max gene for catalase
12661	GM_183_B1_D08_T7	g3126935	BLASTN	361	1e-09	64	Neochanna diversus strain Kaimaumau14 mitochondrial D-loop, complete sequence
12662	GM_183_B1_D09_T7	g1769898	BLASTX	261	7e-21	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12663	GM_183_B1_D12_MR	g18768	BLASTN	525	2e-17	72	Soybean Tgm6 transposable element 3' end
12664	GM_183_B1_E03_T7	g3777527	BLASTX	110	5e-12	37	(AF053008) gag-pol polyprotein [Glycine max]
12665	GM_183_B1_E05_MR	g2522227	BLASTX	206	6e-16	54	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
12666	GM_183_B1_E06_MR	g99755	BLASTX	321	2e-27	52	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
12667	GM_183_B1_E07_MR	g2995405	BLASTX	323	3e-27	50	(Y12432) polyprotein [Ananas comosus]
12668	GM_183_B1_F01_MR	g3645899	BLASTX	277	7e-29	59	(U68408) 5' end not determined experimentally [Zea mays]
12669	GM_183_B1_F07_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12670	GM_183_B1_F07_T7	g4063756	BLASTN	541	2e-17	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12671	GM_183_B1_F10_MR	g1666236	BLASTX	153	9e-10	31	(U76261) unknown [Hordeum vulgare]
12672	GM_183_B1_F11_T7	g2244837	BLASTX	134	8e-19	80	(Z97337) proteasome chain protein [Arabidopsis thaliana] gi 2511572 gnl PID e1179970 (Y13175) multicatalytic endopeptidase [Arabidopsis thaliana] gi 3421114 (AF043535) 20S proteasome beta subunit PBD2 [Arabidopsis thaliana]
12673	GM_183_B1_G01_MR	g1184075	BLASTX	159	1e-09	37	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
12674	GM_183_B1_G04_T7	g2462134	BLASTX	153	2e-09	37	(Y13368) reverse transcriptase [Beta vulgaris]
12675	GM_183_B1_G05_T7	g4063756	BLASTN	387	2e-10	70	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12676	GM_183_B1_G06_MR	g3777527	BLASTX	146	3e-20	42	(AF053008) gag-pol polyprotein [Glycine max]
12677	GM_183_B1_G08_T7	g1769897	BLASTX	458	1e-42	67	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12678	GM_183_B1_G12_MR	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
12679	GM_183_B1_G12_T7	g507910	BLASTN	426	1e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
12680	GM_183_B1_H02_T7	g2462134	BLASTX	355	1e-31	50	(Y13368) reverse transcriptase [Beta vulgaris]
12681	GM_183_B1_H05_T7	g3643604	BLASTX	186	2e-12	43	(AC005395) receptor-like protein kinase [Arabidopsis thaliana]
12682	GM_183_B1_H09_T7	g3097320	BLASTN	448	3e-13	71	Glycine max gene for Bd 30K, complete cds
12683	GM_183_B1_H10_MR	g13533	BLASTN	299	4e-12	66	Yeast mitochondrial tRNA genes (several, map positions 3.5 to 8.6) encoding tRNAs for Lys, Arg, Gly, Asp, Ser, Arg, and Ala.
12684	GM_183_B1_H10_T7	g4056476	BLASTN	330	3e-09	64	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]
12685	GM_183_B2_A05_MR	g1321822	BLASTX	271	7e-23	66	(X96865) phosphoribosylglycinamide formyltransferase [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12686	GM_183_B2_A05_T7	g1588265	BLASTX	178	9e-12	82	100RNP protein [Spinacia oleracea]
12687	GM_183_B2_A08_MR	g1769898	BLASTX	176	1e-11	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12688	GM_183_B2_B03_T7	g1091678	BLASTX	179	3e-16	42	activator-like transposable element [Pennisetum glaucum]
12689	GM_183_B2_B05_MR	g4063756	BLASTN	365	2e-09	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12690	GM_183_B2_B10_MR	g3021268	BLASTX	298	3e-24	43	(AL022347) putative protein [Arabidopsis thaliana]
12691	GM_183_B2_C02_MR	g3097320	BLASTN	507	6e-16	84	Glycine max gene for Bd 30K, complete cds
12692	GM_183_B2_C03_MR	g99755	BLASTX	425	3e-39	50	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
12693	GM_183_B2_C04_MR	g3097320	BLASTN	636	9e-22	72	Glycine max gene for Bd 30K, complete cds
12694	GM_183_B2_C05_T7	g2522228	BLASTX	302	4e-26	49	(AB007466) reverse transcriptase-like protein [Vicia faba]
12695	GM_183_B2_C10_T7	g2522228	BLASTX	206	2e-15	49	(AB007466) reverse transcriptase-like protein [Vicia faba]
12696	GM_183_B2_C12_T7	g3097320	BLASTN	989	9e-38	74	Glycine max gene for Bd 30K, complete cds
12697	GM_183_B2_D01_MR	g3550044	BLASTN	392	1e-10	63	Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) ...
12698	GM_183_B2_D01_T7	g3142328	BLASTN	534	3e-17	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12699	GM_183_B2_D02_MR	g3738114	BLASTN	399	6e-11	61	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
12700	GM_183_B2_D02_T7	g4006828	BLASTX	183	3e-12	30	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
12701	GM_183_B2_D04_MR	g3319362	BLASTX	323	4e-27	50	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12702	GM_183_B2_D05_MR	g1142701	BLASTN	1253	3e-50	85	Glycine max satellite STR120-A.3.
12703	GM_183_B2_D07_T7	g862479	BLASTN	360	2e-17	92	Glycine max valosin-containing protein mRNA, complete cds.
12704	GM_183_B2_D11_MR	g3894391	BLASTX	192	5e-15	41	(AF053997) Hcr2-5B [Lycopersicon esculentum]
12705	GM_183_B2_E05_MR	g531389	BLASTX	134	7e-18	49	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
12706	GM_183_B2_E11_MR	g3142328	BLASTN	859	6e-32	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12707	GM_183_B2_F02_T7	g629693	BLASTX	405	5e-37	54	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12708	GM_183_B2_F06_MR	g3176798	BLASTN	351	4e-16	65	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite, 5' sequence
12709	GM_183_B2_F07_MR	g2462134	BLASTX	295	6e-25	39	(Y13368) reverse transcriptase [Beta vulgaris]
12710	GM_183_B2_F09_T7	g4150930	BLASTN	559	3e-18	64	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
12711	GM_183_B2_G01_MR	g507910	BLASTN	398	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12712	GM_183_B2_G01_T7	g507910	BLASTN	369	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12713	GM_183_B2_G02_MR	g2583130	BLASTX	177	2e-11	35	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
12714	GM_183_B2_G02_T7	g3810596	BLASTX	271	1e-21	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
12715	GM_183_B2_G03_MR	g454847	BLASTN	449	2e-13	72	Glycine max ribosomal protein S11 gene, complete cds
12716	GM_183_B2_G06_MR	g3142328	BLASTN	608	7e-34	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12717	GM_183_B2_G06_T7	g2995405	BLASTX	183	3e-12	41	(Y12432) polyprotein [Ananas comosus]
12718	GM_183_B2_G10_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12719	GM_183_B2_G10_T7	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12720	GM_183_B2_H01_MR	g3482979	BLASTX	392	1e-35	71	(AL031369) putative protein [Arabidopsis thaliana]
12721	GM_183_B2_H04_T7	g2244915	BLASTX	233	3e-19	46	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
12722	GM_183_B2_H08_MR	g3126783	BLASTN	395	8e-11	60	Homo sapiens chromosome 17, clone hCIT529I10, complete sequence [Homo sapiens]
12723	GM_183_B2_H09_MR	g4063760	BLASTX	451	1e-40	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12724	GM_183_B2_H10_MR	g3142328	BLASTN	676	1e-23	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12725	GM_183_B2_H12_MR	g3097320	BLASTN	529	6e-17	67	Glycine max gene for Bd 30K, complete cds
12726	GM_184_A1_A01_MR	g3097320	BLASTN	467	4e-14	77	Glycine max gene for Bd 30K, complete cds
12727	GM_184_A1_A02_T7	g3142328	BLASTN	431	2e-12	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12728	GM_184_A1_A05_T7	g3645899	BLASTX	284	2e-24	52	(U68408) 5' end not determined experimentally [Zea mays]
12729	GM_184_A1_A06_MR	g2760330	BLASTX	153	3e-10	75	(AC002130) F1N21.15 [Arabidopsis thaliana]
12730	GM_184_A1_A11_MR	g507910	BLASTN	461	3e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
12731	GM_184_A1_A11_T7	g507910	BLASTN	577	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12732	GM_184_A1_B01_T7	g3142330	BLASTX	616	2e-59	92	(U96295) envelope-like [Glycine max]
12733	GM_184_A1_B07_T7	g4006885	BLASTN	351	8e-09	71	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No. 2
12734	GM_184_A1_B09_MR	g3885339	BLASTX	258	2e-20	46	(AC005623) putative bzip protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12735	GM_184_A1_B11_MR	g4140712	BLASTX	208	4e-16	42	(AF110183) putative integrase [Oryza sativa]
12736	GM_184_A1_B12_T7	g587603	BLASTN	375	5e-10	64	P.falciparum gene for beta subunit RNA polymerase
12737	GM_184_A1_C04_MR	g3599418	BLASTN	953	3e-36	91	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
12738	GM_184_A1_C05_MR	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
12739	GM_184_A1_C08_MR	g99711	BLASTX	211	2e-16	61	hypothetical protein H1.2flk - Arabidopsis thaliana (fragment) gi 16322 (X62460) H1-2flk [Arabidopsis thaliana]
12740	GM_184_A1_C10_MR	g3033398	BLASTX	165	7e-25	85	(AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [Arabidopsis thaliana]
12741	GM_184_A1_D03_MR	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12742	GM_184_A1_D03_T7	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12743	GM_184_A1_D04_MR	g84801	BLASTX	245	1e-18	37	hypothetical protein 2 - silkworm transposon mag
12744	GM_184_A1_D06_T7	g2995405	BLASTX	223	2e-16	51	(Y12432) polyprotein [Ananas comosus]
12745	GM_184_A1_D09_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12746	GM_184_A1_D10_MR	g1142701	BLASTN	1355	6e-55	87	Glycine max satellite STR120-A.3.
12747	GM_184_A1_E03_T7	g18559	BLASTN	390	1e-10	70	G.max gene for catalase
12748	GM_184_A1_E04_MR	g3769670	BLASTN	575	9e-20	72	Pisum sativum Tic22 mRNA, nuclear mRNA encoding chloroplast protein, complete cds
12749	GM_184_A1_F06_MR	g1142703	BLASTN	295	3e-17	77	Glycine max satellite STR120-B.1.
12750	GM_184_A1_F07_MR	g1769898	BLASTX	277	1e-32	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12751	GM_184_A1_F11_T7	g3947433	BLASTN	447	4e-13	66	Homo sapiens BAC clone RG060P12 from 7q21, complete sequence [Homo sapiens]
12752	GM_184_A1_G02_MR	g3135965	BLASTN	363	2e-09	62	Homo sapiens DNA sequence from PAC 164C20 on chromosome 6q16.1-22.1. Contains ESTs and GSSs (BAC end sequences), complete sequence [Homo sapiens]
12753	GM_184_A1_G06_T7	g4063760	BLASTX	179	1e-12	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12754	GM_184_A1_G07_T7	g4063760	BLASTX	186	2e-12	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12755	GM_184_A1_G09_T7	g3142330	BLASTX	645	2e-62	90	(U96295) envelope-like [Glycine max]
12756	GM_184_A1_H02_MR	g507910	BLASTN	602	1e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12757	GM_184_A1_H02_T7	g18559	BLASTN	453	2e-13	66	G.max gene for catalase
12758	GM_184_A1_H03_MR	g3319362	BLASTX	162	5e-10	37	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12759	GM_184_A1_H07_T7	g3599418	BLASTN	612	2e-28	77	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
12760	GM_184_A1_H10_T7	g3777527	BLASTX	582	2e-54	94	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12761	GM_184_A2_A09_MR	g507910	BLASTN	653	7e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
12762	GM_184_A2_A11_MR	g3142328	BLASTN	856	8e-32	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12763	GM_184_A2_A12_MR	g3152938	BLASTX	130	3e-09	37	(AF065482) sorting nexin 2 [Homo sapiens]
12764	GM_184_A2_B07_MR	g12708	BLASTN	357	4e-09	59	Aspergillus nidlans mitochondrial DNA for L-rRNA
12765	GM_184_A2_C01_MR	g2196878	BLASTX	298	2e-28	80	(Y08292) NADH glutamate dehydrogenase [Nicotiana plumbaginifolia]
12766	GM_184_A2_C03_MR	g507910	BLASTN	368	5e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12767	GM_184_A2_C04_MR	g4038056	BLASTX	247	2e-33	56	(AC005897) putative transposon [Arabidopsis thaliana]
12768	GM_184_A2_C08_MR	g3777527	BLASTX	927	2e-91	96	(AF053008) gag-pol polyprotein [Glycine max]
12769	GM_184_A2_D07_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12770	GM_184_A2_D09_MR	g3097320	BLASTN	529	6e-17	79	Glycine max gene for Bd 30K, complete cds
12771	GM_184_A2_E10_MR	g3377831	BLASTX	183	3e-12	29	(AF075598) similar to maize transposon MuDR mudrA (GB:M76978) [Arabidopsis thaliana]
12772	GM_184_A2_F01_MR	g4160362	BLASTN	410	5e-15	66	Saccharomyces cerevisiae complete mitochondrial genome
12773	GM_184_A2_F06_MR	g3645899	BLASTX	192	9e-25	39	(U68408) 5' end not determined experimentally [Zea mays]
12774	GM_184_A2_F09_MR	g3319362	BLASTX	287	3e-23	39	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
12775	GM_184_A2_F11_MR	g2194124	BLASTX	194	4e-14	62	(AC002062) Similar to Glycine metalloendoproteinase (gb U63725). [Arabidopsis thaliana]
12776	GM_184_A2_G04_MR	g1045614	BLASTX	335	3e-29	51	(U37088) beta-ketoacyl-CoA synthase [Simmondsia chinensis]
12777	GM_184_A2_G06_MR	g4098244	BLASTX	241	3e-37	97	(U76409) homeobox 1 protein [Lycopersicon esculentum]
12778	GM_184_A2_G08_MR	g3264544	BLASTN	700	1e-24	64	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
12779	GM_184_A2_G09_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12780	GM_184_A2_G12_MR	g2129618	BLASTX	179	8e-12	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
12781	GM_184_A2_H01_MR	g3645899	BLASTX	449	1e-42	59	(U68408) 5' end not determined experimentally [Zea mays]
12782	GM_184_A2_H04_MR	g3097320	BLASTN	1116	2e-43	75	Glycine max gene for Bd 30K, complete cds
12783	GM_184_A2_H12_MR	g170080	BLASTN	474	2e-14	67	Soybean seed lectin gene transposable element tgm1.
12784	GM_184_B1_A02_MR	g905361	BLASTX	334	9e-29	80	(U22103) gag-protease polyprotein [Glycine max]
12785	GM_184_B1_A03_MR	g1769898	BLASTX	326	7e-42	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12786	GM_184_B1_A10_T7	g2244959	BLASTX	154	1e-08	41	(Z97340) similar to B.vulgaris CMS-associated mitochondrial ... (reverse transcriptase) [Arabidopsis thaliana]
12787	GM_184_B1_A12_T7	g3097320	BLASTN	388	2e-10	73	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12788	GM_184_B1_B03_MR	g905361	BLASTX	329	3e-28	77	(U22103) gag-protease polyprotein [Glycine max]
12789	GM_184_B1_B05_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12790	GM_184_B1_B06_MR	g4063760	BLASTX	232	2e-17	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12791	GM_184_B1_B07_MR	g3645899	BLASTX	235	6e-23	45	(U68408) 5' end not determined experimentally [Zea mays]
12792	GM_184_B1_B10_T7	g343799	BLASTN	411	4e-12	62	S.cerevisiae mitochondrial cytochrome c oxidase subunit 2 (COX2) gene, 5' end.
12793	GM_184_B1_C02_T7	g629693	BLASTX	442	6e-41	59	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
12794	GM_184_B1_C07_T7	g4063760	BLASTX	352	8e-45	76	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12795	GM_184_B1_C10_T7	g507910	BLASTN	500	6e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
12796	GM_184_B1_D01_MR	g3021278	BLASTX	134	2e-14	54	(AL022347) putative protein [Arabidopsis thaliana]
12797	GM_184_B1_D05_MR	g3810596	BLASTX	198	8e-14	52	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
12798	GM_184_B1_D05_T7	g2586082	BLASTX	286	6e-23	45	(U72725) retrofit [Oryza longistaminata]
12799	GM_184_B1_D06_T7	g3894385	BLASTX	240	2e-18	50	(AF053994) Hcr2-0A [Lycopersicon esculentum]
12800	GM_184_B1_D09_MR	g4063760	BLASTX	296	4e-24	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12801	GM_184_B1_D10_T7	g3513745	BLASTX	249	7e-19	39	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
12802	GM_184_B1_D12_MR	g507910	BLASTN	388	6e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
12803	GM_184_B1_E01_MR	g4150930	BLASTN	407	2e-11	61	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
12804	GM_184_B1_E04_MR	g99922	BLASTX	188	4e-20	43	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
12805	GM_184_B1_E04_T7	g507910	BLASTN	546	5e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
12806	GM_184_B1_E05_T7	g507910	BLASTN	415	4e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12807	GM_184_B1_E06_T7	g3777527	BLASTX	623	8e-59	93	(AF053008) gag-pol polyprotein [Glycine max]
12808	GM_184_B1_E08_MR	g3882356	BLASTX	217	9e-17	67	(U92460) pdr2 [Arabidopsis thaliana]
12809	GM_184_B1_E08_T7	g3097320	BLASTN	513	3e-16	83	Glycine max gene for Bd 30K, complete cds
12810	GM_184_B1_E09_T7	g2462936	BLASTX	329	5e-29	54	(Y12321) open reading frame 2 [Brassica oleracea]
12811	GM_184_B1_F02_MR	g3493214	BLASTX	217	1e-15	35	(AF056940) pol polyprotein [Drosophila virilis]
12812	GM_184_B1_F02_T7	g18559	BLASTN	1120	9e-44	77	G.max gene for catalase
12813	GM_184_B1_F03_MR	g4063760	BLASTX	387	7e-34	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12814	GM_184_B1_G02_MR	g1431738	BLASTN	412	1e-11	92	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
12815	GM_184_B1_G07_MR	g3152618	BLASTX	218	5e-23	53	(AC004482) putative pectinesterase [Arabidopsis thaliana] gi 3242724 (AC003040) putative pectinesterase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12816	GM_184_B1_G07_T7	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
12817	GM_184_B1_G08_T7	g507910	BLASTN	368	5e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
12818	GM_184_B1_H02_MR	g99922	BLASTX	453	2e-54	84	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
12819	GM_184_B2_A02_T7	g2462134	BLASTX	259	7e-21	50	(Y13368) reverse transcriptase [Beta vulgaris]
12820	GM_184_B2_A04_MR	g3176795	BLASTN	400	1e-11	61	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
12821	GM_184_B2_A05_MR	g4126312	BLASTN	390	1e-10	63	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
12822	GM_184_B2_A07_T7	g1769901	BLASTX	213	5e-16	78	(X95737) proline transporter 1 [Arabidopsis thaliana] gi 2088642 (AF002109) proline transporter 1 [Arabidopsis thaliana]
12823	GM_184_B2_A09_T7	g507910	BLASTN	394	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12824	GM_184_B2_B01_T7	g507910	BLASTN	417	3e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
12825	GM_184_B2_B03_T7	g4063760	BLASTX	165	1e-11	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12826	GM_184_B2_B05_T7	g507910	BLASTN	357	2e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12827	GM_184_B2_B09_T7	g3928116	BLASTN	442	6e-13	65	, complete sequence [Homo sapiens]
12828	GM_184_B2_B10_T7	g2522230	BLASTX	163	2e-11	35	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
12829	GM_184_B2_B12_MR	g3097320	BLASTN	441	6e-13	74	Glycine max gene for Bd 30K, complete cds
12830	GM_184_B2_B12_T7	g2462134	BLASTX	149	6e-09	36	(Y13368) reverse transcriptase [Beta vulgaris]
12831	GM_184_B2_C01_T7	g2522228	BLASTX	175	6e-12	57	(AB007466) reverse transcriptase-like protein [Vicia faba]
12832	GM_184_B2_C02_T7	g1091678	BLASTX	171	5e-11	44	activator-like transposable element [Pennisetum glaucum]
12833	GM_184_B2_C05_MR	g2522227	BLASTX	191	2e-14	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
12834	GM_184_B2_C09_T7	g99721	BLASTX	173	2e-17	53	retrovirus-related polyprotein - Arabidopsis thaliana retrotransposon Ta1-3 gi 16534 (X13291) polyprotein [Arabidopsis thaliana]
12835	GM_184_B2_D02_T7	g1435021	BLASTX	144	5e-09	56	(D26575) DNA-binding protein [Daucus carota]
12836	GM_184_B2_D04_T7	g1680686	BLASTX	369	1e-32	55	(U51330) rust resistance kinase Lr10 [Triticum aestivum]
12837	GM_184_B2_D10_MR	g4063760	BLASTX	280	2e-22	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12838	GM_184_B2_D10_T7	g507910	BLASTN	661	3e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
12839	GM_184_B2_E01_T7	g3645899	BLASTX	347	1e-29	48	(U68408) 5' end not determined experimentally [Zea mays]
12840	GM_184_B2_E04_T7	g3947433	BLASTN	364	2e-09	65	Homo sapiens BAC clone RG060P12 from 7q21, complete sequence [Homo sapiens]
12841	GM_184_B2_E09_T7	g1769898	BLASTX	208	4e-15	36	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12842	GM_184_B2_F03_MR	g4063756	BLASTN	389	1e-10	74	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12843	GM_184_B2_F12_MR	g1142701	BLASTN	1285	9e-52	85	Glycine max satellite STR120-A.3.
12844	GM_184_B2_G01_MR	g905361	BLASTX	153	3e-09	83	(U22103) gag-protease polyprotein [Glycine max]
12845	GM_184_B2_G04_MR	g507910	BLASTN	347	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12846	GM_184_B2_G04_T7	g507910	BLASTN	414	4e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12847	GM_184_B2_G08_T7	g3097320	BLASTN	553	5e-18	79	Glycine max gene for Bd 30K, complete cds
12848	GM_184_B2_H01_T7	g130582	BLASTX	172	9e-12	36	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
12849	GM_184_B2_H03_MR	g507910	BLASTN	484	3e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
12850	GM_184_B2_H03_T7	g507910	BLASTN	480	4e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
12851	GM_184_B2_H10_MR	g1769898	BLASTX	401	3e-36	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12852	GM_185_A1_A01_MR	g629693	BLASTX	278	1e-23	42	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
12853	GM_185_A1_A01_T7	g1946279	BLASTX	242	8e-20	47	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
12854	GM_185_A1_A02_T7	g136125	BLASTX	194	2e-13	42	PUTATIVE AC TRANSPOSASE (ORFA) gi 22113 (X05424) ORFa [Zea mays]
12855	GM_185_A1_A04_T7	g507910	BLASTN	358	1e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12856	GM_185_A1_A05_MR	g507910	BLASTN	434	5e-13	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12857	GM_185_A1_A05_T7	g507910	BLASTN	385	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12858	GM_185_A1_A08_T7	g343950	BLASTN	347	1e-09	63	S.cerevisiae mitochondrion Tyr-tRNA gene.
12859	GM_185_A1_B01_T7	g1785729	BLASTN	400	5e-11	66	A.thaliana mitochondrial genome, part B
12860	GM_185_A1_B07_T7	g3097322	BLASTN	1638	3e-67	99	Glycine max pseudogene for Bd 30K
12861	GM_185_A1_B08_MR	g99755	BLASTX	290	4e-24	55	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
12862	GM_185_A1_B11_MR	g3402758	BLASTX	288	1e-24	73	(AL031187) serine/threonine kinase - like protein [Arabidopsis thaliana]
12863	GM_185_A1_B11_T7	g18559	BLASTN	948	6e-36	83	G.max gene for catalase
12864	GM_185_A1_C06_MR	g4092470	BLASTN	351	8e-09	63	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12865	GM_185_A1_C08_T7	g507910	BLASTN	367	6e-10	69	Glycine max BSR-101 satellite SB92 genomic sequence.
12866	GM_185_A1_C10_T7	g2995405	BLASTX	241	5e-20	52	(Y12432) polyprotein [Ananas comosus]
12867	GM_185_A1_D03_MR	g3935157	BLASTX	147	7e-13	66	(AC005106) T25N20.21 [Arabidopsis thaliana]
12868	GM_185_A1_E04_MR	g3142328	BLASTN	1563	5e-64	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12869	GM_185_A1_E05_MR	g2367675	BLASTX	202	3e-14	34	(AF017040) Pol [Dictyostelium discoideum]
12870	GM_185_A1_E06_MR	g3097320	BLASTN	874	2e-32	79	Glycine max gene for Bd 30K, complete cds
12871	GM_185_A1_E10_MR	g2522228	BLASTX	266	3e-22	54	(AB007466) reverse transcriptase-like protein [Vicia faba]
12872	GM_185_A1_F09_T7	g1326016	BLASTX	205	2e-14	44	TY3-2 orfB
12873	GM_185_A1_G01_T7	g1045530	BLASTN	358	3e-09	63	Magnaporthe grisea host-species specificity (Pwl1) gene, complete cds.
12874	GM_185_A1_G04_MR	g4063760	BLASTX	181	7e-12	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12875	GM_185_A1_G06_MR	g3097320	BLASTN	363	2e-09	74	Glycine max gene for Bd 30K, complete cds
12876	GM_185_A1_G06_T7	g3142328	BLASTN	1258	4e-50	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12877	GM_185_A1_G08_MR	g4063760	BLASTX	243	2e-18	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12878	GM_185_A1_G09_MR	g1431738	BLASTN	357	3e-09	74	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
12879	GM_185_A1_H01_T7	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
12880	GM_185_A1_H03_T7	g130582	BLASTX	121	3e-14	47	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
12881	GM_185_A1_H06_T7	g4050011	BLASTN	359	3e-09	62	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
12882	GM_185_A2_A03_MR	g2995405	BLASTX	244	9e-19	37	(Y12432) polyprotein [Ananas comosus]
12883	GM_185_A2_A04_MR	g4115365	BLASTX	290	2e-23	38	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
12884	GM_185_A2_A05_MR	g2583106	BLASTN	388	2e-10	68	Arabidopsis thaliana chromosome II BAC F4L23 genomic sequence, complete sequence [Arabidopsis thaliana]
12885	GM_185_A2_A12_MR	g3935200	BLASTN	523	1e-16	71	Homo sapiens Chromosome 22q11.2 PAC Clone p201m18 In DGCR Region, complete sequence [Homo sapiens]
12886	GM_185_A2_B02_T7	g2981494	BLASTX	116	7e-09	62	(AF053473) kinesin heavy chain [Mus musculus]
12887	GM_185_A2_B04_T7	g2462134	BLASTX	172	7e-13	39	(Y13368) reverse transcriptase [Beta vulgaris]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12888	GM_185_A2_B05_MR	g4049609	BLASTN	358	4e-09	61	Oryzias latipes gene for membrane guanylyl cyclase OlGC1, complete cds
12889	GM_185_A2_B05_T7	g3645899	BLASTX	222	3e-35	60	(U68408) 5' end not determined experimentally [Zea mays]
12890	GM_185_A2_B07_MR	g3845197	BLASTN	448	3e-13	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
12891	GM_185_A2_B08_T7	g3650378	BLASTX	125	1e-14	52	(AL031740) putative rRNA biogenesis protein; rrp5 homolog; multiple S1 rna binding domain protein [Schizosaccharomyces pombe]
12892	GM_185_A2_B09_T7	g4063760	BLASTX	389	5e-34	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12893	GM_185_A2_B12_T7	g2443320	BLASTX	301	1e-24	44	(D85597) polyprotein [Oryza australiensis]
12894	GM_185_A2_C03_MR	g4115365	BLASTX	154	6e-09	30	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
12895	GM_185_A2_C04_T7	g1666236	BLASTX	209	4e-16	34	(U76261) unknown [Hordeum vulgare]
12896	GM_185_A2_C06_T7	g2995405	BLASTX	324	2e-54	60	(Y12432) polyprotein [Ananas comosus]
12897	GM_185_A2_C08_MR	g100484	BLASTX	430	5e-39	49	hypothetical protein - garden snapdragon
12898	GM_185_A2_C10_MR	g2995405	BLASTX	558	1e-52	53	(Y12432) polyprotein [Ananas comosus]
12899	GM_185_A2_C11_T7	g3142328	BLASTN	1240	3e-49	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12900	GM_185_A2_D03_MR	g4115365	BLASTX	137	3e-13	28	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
12901	GM_185_A2_D03_T7	g18559	BLASTN	1256	6e-50	76	G.max gene for catalase
12902	GM_185_A2_D06_MR	g3097320	BLASTN	442	6e-13	79	Glycine max gene for Bd 30K, complete cds
12903	GM_185_A2_D07_MR	g1666236	BLASTX	288	1e-24	34	(U76261) unknown [Hordeum vulgare]
12904	GM_185_A2_D08_T7	g3283026	BLASTX	210	3e-15	33	putative transposase [Arabidopsis thaliana]
12905	GM_185_A2_D09_MR	g4063760	BLASTX	130	2e-10	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12906	GM_185_A2_D09_T7	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12907	GM_185_A2_D11_MR	g2462134	BLASTX	237	3e-26	52	(Y13368) reverse transcriptase [Beta vulgaris]
12908	GM_185_A2_D11_T7	g4050011	BLASTN	565	1e-18	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
12909	GM_185_A2_E01_T7	g4050011	BLASTN	395	8e-11	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
12910	GM_185_A2_E04_T7	g535454	BLASTX	146	6e-09	50	(U13940) cysteine proteinase [Alnus glutinosa]
12911	GM_185_A2_E08_T7	g3599418	BLASTN	652	1e-22	75	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
12912	GM_185_A2_E09_MR	g1769897	BLASTX	200	8e-20	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12913	GM_185_A2_E10_MR	g4038056	BLASTX	425	4e-38	55	(AC005897) putative transposon [Arabidopsis thaliana]
12914	GM_185_A2_E10_T7	g535454	BLASTX	179	2e-29	55	(U13940) cysteine proteinase [Alnus glutinosa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12915	GM_185_A2_E12_MR	g3142328	BLASTN	797	4e-29	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12916	GM_185_A2_F02_MR	g3810596	BLASTX	206	1e-14	38	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
12917	GM_185_A2_F02_T7	g345511	BLASTX	193	2e-18	33	retrovirus-related copia polyprotein - fruit fly (Drosophila simulans) (fragments)
12918	GM_185_A2_F04_MR	g1666236	BLASTX	174	4e-12	30	(U76261) unknown [Hordeum vulgare]
12919	GM_185_A2_F07_T7	g2565011	BLASTX	235	7e-18	34	(AC002983) putative mudrA-like retrotransposon-associated protein [Arabidopsis thaliana]
12920	GM_185_A2_F11_T7	g728905	BLASTX	180	1e-11	45	PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC RETICULUM CA2+-ATPASE) gi 1078206 pir S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) gi 171114 (L01795) ATPase [Saccharomyces cerevisiae] gi 595560 (U12980) Drs2p: Membrane spanning Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae]
12921	GM_185_A2_F12_MR	g3599418	BLASTN	315	2e-17	80	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
12922	GM_185_A2_G10_T7	g3097320	BLASTN	552	6e-18	74	Glycine max gene for Bd 30K, complete cds
12923	GM_185_A2_H03_T7	g3153101	BLASTN	384	3e-10	64	Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22; segment 1/3
12924	GM_185_A2_H05_MR	g2522230	BLASTX	361	2e-32	41	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
12925	GM_185_A2_H08_T7	g3097322	BLASTN	2448	3e-104	94	Glycine max pseudogene for Bd 30K
12926	GM_185_A2_H10_MR	g99755	BLASTX	339	2e-42	55	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
12927	GM_185_B2_A07_T7	g3080376	BLASTX	170	6e-11	70	(AL022580) putative protein [Arabidopsis thaliana]
12928	GM_185_B2_A09_MR	g507910	BLASTN	358	1e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12929	GM_185_B2_A11_MR	g342964	BLASTN	386	2e-11	63	paramecium species 5,311 mt dna dimer: replication init. region.
12930	GM_185_B2_A12_T7	g3319351	BLASTX	341	8e-29	52	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
12931	GM_185_B2_B04_MR	g3777527	BLASTX	629	2e-59	94	(AF053008) gag-pol polyprotein [Glycine max]
12932	GM_185_B2_B04_T7	g507910	BLASTN	357	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
12933	GM_185_B2_B07_MR	g4063760	BLASTX	105	1e-09	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12934	GM_185_B2_B09_T7	g2522230	BLASTX	193	1e-14	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
12935	GM_185_B2_B10_T7	g507910	BLASTN	356	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
12936	GM_185_B2_B11_MR	g4038056	BLASTX	200	5e-14	44	(AC005897) putative transposon [Arabidopsis thaliana]
12937	GM_185_B2_B11_T7	g3413522	BLASTX	71	5e-09	33	(AB016585) unnamed protein product [Tricholoma matsutake]
12938	GM_185_B2_B12_T7	g3645899	BLASTX	319	1e-26	51	(U68408) 5' end not determined experimentally [Zea mays]
12939	GM_185_B2_C02_MR	g3122784	BLASTX	110	2e-09	50	PROBABLE 40S RIBOSOMAL PROTEIN S12 gi 2370511 gnl PID e339198 (Z98887) putative 40s ribosomal protein [Schizosaccharomyces pombe] gi 3451319 gnl PID e1316718 (AL031323) 40s ribosomal protein s12 [Schizosaccharomyces pombe]
12940	GM_185_B2_C10_T7	g3184283	BLASTX	323	4e-29	79	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]
12941	GM_185_B2_C11_T7	g22490	BLASTX	174	1e-12	40	(X01380) ORF1 [Zea mays]
12942	GM_185_B2_D01_MR	g2264309	BLASTN	452	2e-13	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJJ3, complete sequence [Arabidopsis thaliana]
12943	GM_185_B2_D04_T7	g3930515	BLASTX	115	7e-10	46	(AF059674) putative gag protein [Nicotiana tabacum]
12944	GM_185_B2_D08_T7	g3777527	BLASTX	529	9e-49	89	(AF053008) gag-pol polyprotein [Glycine max]
12945	GM_185_B2_D09_T7	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12946	GM_185_B2_D10_T7	g507910	BLASTN	622	2e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
12947	GM_185_B2_E03_T7	g2245104	BLASTX	155	5e-09	33	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
12948	GM_185_B2_E08_MR	g507910	BLASTN	411	6e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12949	GM_185_B2_E08_T7	g3142328	BLASTN	956	2e-36	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12950	GM_185_B2_E10_T7	g4063760	BLASTX	211	5e-15	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12951	GM_185_B2_F03_MR	g3645899	BLASTX	195	2e-13	37	(U68408) 5' end not determined experimentally [Zea mays]
12952	GM_185_B2_F08_MR	g3135969	BLASTN	418	8e-12	61	Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family prot...
12953	GM_185_B2_F09_MR	g130582	BLASTX	168	2e-10	35	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
12954	GM_185_B2_F12_MR	g3645899	BLASTX	348	9e-30	60	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12955	GM_185_B2_G04_MR	g3550044	BLASTN	369	1e-09	62	Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SW1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) ...
12956	GM_185_B2_G05_T7	g507910	BLASTN	569	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
12957	GM_185_B2_G06_MR	g1666236	BLASTX	187	1e-13	34	(U76261) unknown [Hordeum vulgare]
12958	GM_185_B2_H07_T7	g3599418	BLASTN	469	3e-14	77	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
12959	GM_185_B2_H08_T7	g322663	BLASTX	275	3e-23	58	S-receptor kinase-related protein - Chinese kale gi 17917 (Z18884) S-receptor kinase related protein [Brassica oleracea]
12960	GM_186_A2_A01_MR	g507910	BLASTN	444	2e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
12961	GM_186_A2_A04_MR	g99755	BLASTX	383	2e-34	53	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
12962	GM_186_A2_A10_MR	g3645899	BLASTX	239	4e-18	44	(U68408) 5' end not determined experimentally [Zea mays]
12963	GM_186_A2_B01_T7	g3935164	BLASTX	97	8e-10	38	(AC004557) F17L21.7 [Arabidopsis thaliana]
12964	GM_186_A2_B09_MR	g4063756	BLASTN	535	4e-17	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
12965	GM_186_A2_C11_MR	g3142328	BLASTN	405	3e-11	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12966	GM_186_A2_C12_MR	g507910	BLASTN	653	7e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
12967	GM_186_A2_C12_T7	g507910	BLASTN	343	7e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
12968	GM_186_A2_D01_MR	g3142328	BLASTN	694	2e-24	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12969	GM_186_A2_D03_MR	g421954	BLASTX	199	4e-14	37	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
12970	GM_186_A2_D07_MR	g2982291	BLASTX	142	3e-09	59	(AF051230) heat shock protein [Picea mariana]
12971	GM_186_A2_D09_MR	g421955	BLASTX	388	2e-39	63	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
12972	GM_186_A2_E01_T7	g3645899	BLASTX	322	1e-29	65	(U68408) 5' end not determined experimentally [Zea mays]
12973	GM_186_A2_E08_MR	g3142328	BLASTN	667	3e-23	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12974	GM_186_A2_E11_MR	g18559	BLASTN	715	2e-25	78	G.max gene for catalase
12975	GM_186_A2_F04_MR	g3142328	BLASTN	841	4e-31	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12976	GM_186_A2_F12_MR	g3097320	BLASTN	445	4e-13	70	Glycine max gene for Bd 30K, complete cds
12977	GM_186_A2_G01_T7	g507910	BLASTN	582	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
12978	GM_186_A2_G04_MR	g267055	BLASTX	146	1e-09	65	SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) gi 66572 pir YUMU sucrose synthase (EC 2.4.1.13) - Arabidopsis thaliana gi 16526 (X60987) sucrose synthase [Arabidopsis thaliana]
12979	GM_186_A2_G04_T7	g1769899	BLASTX	177	7e-13	72	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
12980	GM_186_A2_G05_MR	g1666236	BLASTX	149	3e-09	29	(U76261) unknown [Hordeum vulgare]
12981	GM_186_A2_G07_MR	g3135252	BLASTX	159	4e-10	29	(AC003058) hypothetical protein [Arabidopsis thaliana] gi 3176720 (AC002392) hypothetical protein [Arabidopsis thaliana]
12982	GM_186_A2_G11_T7	g1346113	BLASTX	334	2e-29	92	GTP CYCLOHYDROLASE II gi 1084339 pir JC4209 GTP cyclohydrolase II (EC 3.5.4.25) - Arabidopsis thaliana gi 940383 gnl PID d1008704 (D45165) GTP cyclohydrolase II [Arabidopsis thaliana]
12983	GM_186_A2_H05_MR	g3142330	BLASTX	720	2e-70	98	(U96295) envelope-like [Glycine max]
12984	GM_186_A2_H10_T7	g2642431	BLASTX	188	2e-12	60	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
12985	GM_186_A2_H12_MR	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
12986	GM_186_B2_A08_T7	g3142328	BLASTN	834	8e-31	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
12987	GM_186_B2_A10_T7	g507910	BLASTN	341	8e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12988	GM_186_B2_B03_T7	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
12989	GM_186_B2_B09_T7	g3777527	BLASTX	265	1e-20	52	(AF053008) gag-pol polyprotein [Glycine max]
12990	GM_186_B2_B11_MR	g507910	BLASTN	503	4e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
12991	GM_186_B2_B12_T7	g2642431	BLASTX	145	1e-10	46	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
12992	GM_186_B2_C01_MR	g4063760	BLASTX	268	4e-21	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12993	GM_186_B2_C03_T7	g3513747	BLASTX	364	4e-31	52	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
12994	GM_186_B2_C04_MR	g3510251	BLASTX	150	6e-09	46	(AC005310) unknown protein [Arabidopsis thaliana]
12995	GM_186_B2_C04_T7	g3979928	BLASTN	430	2e-12	63	Caenorhabditis elegans cosmid Y18D10A, complete sequence [Caenorhabditis elegans]
12996	GM_186_B2_C10_MR	g4063760	BLASTX	209	8e-15	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
12997	GM_186_B2_D01_T7	g3645899	BLASTX	276	5e-22	38	(U68408) 5' end not determined experimentally [Zea mays]
12998	GM_186_B2_D03_MR	g3928083	BLASTX	141	6e-10	87	(AC005770) unknown protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
12999	GM_186_B2_E02_MR	g2264312	BLASTN	384	5e-12	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]
13000	GM_186_B2_E10_T7	g3790154	BLASTN	441	7e-13	66	Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs ...
13001	GM_186_B2_E11_T7	g3695408	BLASTX	189	4e-14	51	(AF096373) contains similarity to Solanum lycopersicum (tomato) wound-induced protein (GB:X59882) [Arabidopsis thaliana]
13002	GM_186_B2_F01_MR	g3645899	BLASTX	281	1e-22	42	(U68408) 5' end not determined experimentally [Zea mays]
13003	GM_186_B2_F03_T7	g170029	BLASTN	419	6e-12	83	Glycine max cv. Dare nodulin 26 gene fragment.
13004	GM_186_B2_F04_MR	g2832608	BLASTX	183	3e-13	35	(AL021637) leucine rich repeat-like protein (fragment) [Arabidopsis thaliana]
13005	GM_186_B2_F10_MR	g629693	BLASTX	127	5e-16	41	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
13006	GM_186_B2_G02_T7	g3650039	BLASTX	237	3e-18	38	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
13007	GM_186_B2_G03_MR	g2792161	BLASTX	249	2e-20	55	(AJ223558) reverse transcriptase [Alstroemeria ligtu]
13008	GM_186_B2_G08_MR	g3650039	BLASTX	225	6e-17	40	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
13009	GM_186_B2_G10_MR	g905361	BLASTX	214	9e-16	31	(U22103) gag-protease polyprotein [Glycine max]
13010	GM_186_B2_G11_MR	g4063760	BLASTX	290	2e-23	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13011	GM_186_B2_G12_MR	g3641845	BLASTX	247	1e-22	57	(AJ223358) stelar K+ outward rectifying channel [Arabidopsis thaliana]
13012	GM_186_B2_H02_T7	g507910	BLASTN	609	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
13013	GM_186_B2_H03_MR	g2209031	BLASTX	134	1e-13	30	(AB001569) ORF of 1.56 kb [Daucus carota]
13014	GM_186_B2_H04_MR	g507910	BLASTN	527	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
13015	GM_186_B2_H09_T7	g2264312	BLASTN	373	8e-10	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOK16, complete sequence [Arabidopsis thaliana]
13016	GM_186_B2_H12_MR	g905361	BLASTX	186	9e-13	28	(U22103) gag-protease polyprotein [Glycine max]
13017	GM_187_A1_A10_MR	g2970556	BLASTX	142	2e-16	81	(AF049708) aspartokinase-homoserine dehydrogenase [Glycine max]
13018	GM_187_A1_B02_MR	g507910	BLASTN	557	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
13019	GM_187_A1_B03_MR	g1743410	BLASTX	150	7e-11	46	(Y09825) amino acid transporter [Solanum tuberosum]
13020	GM_187_A1_B05_MR	g1685003	BLASTX	310	9e-27	39	(U32643) immediate-early salicylate-induced glucosyltransferase [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13021	GM_187_A1_B10_MR	g3193221	BLASTN	465	5e-14	79	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
13022	GM_187_A1_C08_MR	g3777527	BLASTX	559	5e-52	92	(AF053008) gag-pol polyprotein [Glycine max]
13023	GM_187_A1_D03_MR	g905360	BLASTN	353	5e-09	77	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
13024	GM_187_A1_E03_MR	g3287696	BLASTX	258	2e-20	53	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]
13025	GM_187_A1_F08_MR	g3337395	BLASTN	410	2e-11	68	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
13026	GM_187_A1_F10_MR	g2522228	BLASTX	226	6e-38	70	(AB007466) reverse transcriptase-like protein [Vicia faba]
13027	GM_187_A1_F12_MR	g507910	BLASTN	395	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13028	GM_187_A1_G06_MR	g3402755	BLASTX	298	3e-24	45	(AL031187) putative transposable element [Arabidopsis thaliana]
13029	GM_187_A1_G08_MR	g4063760	BLASTX	196	2e-13	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13030	GM_187_A1_G09_MR	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
13031	GM_187_A1_G10_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13032	GM_187_A2_A03_MR	g2522228	BLASTX	337	8e-30	47	(AB007466) reverse transcriptase-like protein [Vicia faba]
13033	GM_187_A2_A05_T7	g2827644	BLASTN	363	2e-09	63	Arabidopsis thaliana DNA chromosome 4, BAC clone F18F4 (ESSAII project).
13034	GM_187_A2_B03_MR	g507910	BLASTN	628	9e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
13035	GM_187_A2_B03_T7	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
13036	GM_187_A2_B04_T7	g4098966	BLASTN	1539	1e-63	83	Glycine max putative reistance gene analog genomic sequence
13037	GM_187_A2_B10_MR	g1666236	BLASTX	168	2e-11	32	(U76261) unknown [Hordeum vulgare]
13038	GM_187_A2_B11_MR	g122106	BLASTX	385	6e-35	100	HISTONE H4 gi 70771 pir HSZM4 histone H4 - maize gi 81642 pir S06904 histone H4 - Arabidopsis thaliana gi 2119028 pir S60475 histone H4 - garden pea gi 21795 (X00043) histone H4 [Triticum aestivum] gi 166740 (M17132) histone H4 [Arabidopsis thaliana] gi 166742 (M17133) histone H4 [Arabidopsis thaliana] gi 168499 (M36659) histone H4 (H4C13) [Zea mays] gi 168501 (M13370) histone H4 [Zea mays] gi 168503 (M13377) histone H4 [Zea mays] gi 498898 (U10042) histone H4 homolog [Pisum sativum] gi 1806285 gnl PID e263432 (Z79638) histone H4 homologue [Sesbania rostrata] gi 225838 prf 1314298A histone H4 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13039	GM_187_A2_B11_T7	g421955	BLASTX	167	3e-18	42	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
13040	GM_187_A2_C01_T7	g170080	BLASTN	361	2e-09	68	Soybean seed lectin gene transposable element tgm1.
13041	GM_187_A2_C02_MR	g1633547	BLASTN	416	9e-12	63	Human chromosome 12p13 sequence, complete sequence [Homo sapiens]
13042	GM_187_A2_C05_T7	g3142328	BLASTN	1067	2e-41	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13043	GM_187_A2_C08_T7	g3337395	BLASTN	370	1e-09	63	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
13044	GM_187_A2_C10_MR	g18559	BLASTN	424	3e-12	69	G.max gene for catalase
13045	GM_187_A2_C12_T7	g2191126	BLASTN	238	9e-10	64	Arabidopsis thaliana BAC IG002N01
13046	GM_187_A2_D02_MR	g1666236	BLASTX	149	3e-09	28	(U76261) unknown [Hordeum vulgare]
13047	GM_187_A2_D07_MR	g505129	BLASTN	380	5e-13	71	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
13048	GM_187_A2_D07_T7	g2462936	BLASTX	136	2e-20	40	(Y12321) open reading frame 2 [Brassica oleracea]
13049	GM_187_A2_D10_MR	g3907448	BLASTN	349	1e-08	62	Homo sapiens chromosome 18, clone hRPK.24_A_23, complete sequence [Homo sapiens]
13050	GM_187_A2_D11_MR	g3645899	BLASTX	213	2e-19	57	(U68408) 5' end not determined experimentally [Zea mays]
13051	GM_187_A2_D11_T7	g2586082	BLASTX	185	4e-12	32	(U72725) retrofit [Oryza longistaminata]
13052	GM_187_A2_D12_MR	g3777527	BLASTX	469	2e-42	94	(AF053008) gag-pol polyprotein [Glycine max]
13053	GM_187_A2_E03_MR	g2764526	BLASTN	544	1e-17	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
13054	GM_187_A2_E08_MR	g4056486	BLASTX	182	2e-12	43	(AC005896) hypothetical protein [Arabidopsis thaliana]
13055	GM_187_A2_E10_T7	g4006831	BLASTX	216	1e-15	35	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
13056	GM_187_A2_F01_T7	g2501460	BLASTX	168	4e-19	69	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) gi 1545952 gnl PID e244584 (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]
13057	GM_187_A2_F03_T7	g1769897	BLASTX	172	2e-11	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13058	GM_187_A2_F08_MR	g2764526	BLASTN	401	4e-11	61	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
13059	GM_187_A2_F11_T7	g18559	BLASTN	963	1e-36	80	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13060	GM_187_A2_G01_MR	g170605	BLASTN	597	2e-20	63	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
13061	GM_187_A2_G03_T7	g3142328	BLASTN	1623	9e-67	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13062	GM_187_A2_G11_T7	g4038056	BLASTX	111	2e-09	41	(AC005897) putative transposon [Arabidopsis thaliana]
13063	GM_187_A2_H01_MR	g1666236	BLASTX	212	2e-16	32	(U76261) unknown [Hordeum vulgare]
13064	GM_187_A2_H01_T7	g3930515	BLASTX	164	1e-10	33	(AF059674) putative gag protein [Nicotiana tabacum]
13065	GM_187_A2_H02_T7	g840618	BLASTN	362	1e-09	61	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
13066	GM_187_A2_H04_T7	g4063760	BLASTX	340	8e-29	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13067	GM_187_A2_H05_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13068	GM_187_A2_H08_MR	g4063760	BLASTX	313	6e-26	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13069	GM_187_A2_H11_MR	g3810596	BLASTX	351	4e-30	51	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
13070	GM_187_A2_H11_T7	g1769897	BLASTX	207	4e-15	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13071	GM_187_B2_A12_MR	g4063760	BLASTX	359	8e-31	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13072	GM_187_B2_B04_MR	g629693	BLASTX	250	2e-20	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
13073	GM_187_B2_B07_MR	g1086249	BLASTX	206	8e-15	38	subtilisin-like protease - Alnus glutinosa gi 757522 (X85975) subtilisin-like protease [Alnus glutinosa]
13074	GM_187_B2_B12_MR	g2459406	BLASTN	446	4e-13	69	Arabidopsis thaliana chromosome II BAC F4P9 genomic sequence, complete sequence [Arabidopsis thaliana]
13075	GM_187_B2_F08_MR	g100484	BLASTX	279	1e-22	50	hypothetical protein - garden snapdragon
13076	GM_187_B2_F10_MR	g4063760	BLASTX	155	4e-09	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13077	GM_187_B2_G02_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
13078	GM_187_B2_G03_MR	g4115365	BLASTX	176	3e-11	32	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
13079	GM_187_B2_G12_MR	g3273127	BLASTN	370	1e-09	64	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-54, complete sequence [Plasmodium falciparum]
13080	GM_187_B2_H01_MR	g3142379	BLASTX	273	1e-22	64	(AF053008) envelope-like [Glycine max]
13081	GM_187_B2_H07_MR	g507910	BLASTN	615	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
13082	GM_188_A2_A01_T7	g170606	BLASTN	649	1e-22	64	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
13083	GM_188_A2_A02_MR	g2522228	BLASTX	404	6e-37	78	(AB007466) reverse transcriptase-like protein [Vicia faba]
13084	GM_188_A2_A07_MR	g3860321	BLASTX	178	1e-24	84	(AJ012687) beta-galactosidase [Cicer arietinum]
13085	GM_188_A2_A12_MR	g3687234	BLASTX	166	8e-22	55	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
13086	GM_188_A2_B01_T7	g3047060	BLASTN	378	5e-10	64	Arabidopsis thaliana BAC F7N22
13087	GM_188_A2_B04_T7	g2244916	BLASTX	153	3e-09	29	(Z97339) hypothetical protein [Arabidopsis thaliana]
13088	GM_188_A2_B08_T7	g3885341	BLASTX	369	3e-32	51	(AC005623) unknown protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13089	GM_188_A2_B10_MR	g2921211	BLASTX	176	1e-19	100	(AF026149) beta-ketoacyl-ACP synthase II [Perilla frutescens]
13090	GM_188_A2_C11_T7	g2121303	BLASTN	427	3e-12	65	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
13091	GM_188_A2_D01_T7	g4063760	BLASTX	294	3e-26	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13092	GM_188_A2_D04_T7	g4160362	BLASTN	378	5e-10	60	Saccharomyces cerevisiae complete mitochondrial genome
13093	GM_188_A2_D09_MR	g1736642	BLASTX	567	2e-52	86	(D90836) Invasin. [Escherichia coli]
13094	GM_188_A2_D10_T7	g1772985	BLASTX	160	3e-14	53	(Z83835) zeaxanthin epoxidase [Lycopersicon esculentum]
13095	GM_188_A2_D12_MR	g1518540	BLASTX	704	1e-68	95	(U53418) UDP-glucose dehydrogenase [Glycine max]
13096	GM_188_A2_D12_T7	g2642438	BLASTX	149	5e-09	36	(AC002391) putative indole-3-acetate beta-glucosyltransferase [Arabidopsis thaliana]
13097	GM_188_A2_E01_MR	g2618689	BLASTX	382	1e-34	85	(AC002510) unknown protein [Arabidopsis thaliana]
13098	GM_188_A2_E01_T7	g905361	BLASTX	119	2e-13	47	(U22103) gag-protease polyprotein [Glycine max]
13099	GM_188_A2_E02_T7	g507910	BLASTN	671	1e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
13100	GM_188_A2_E03_T7	g4038056	BLASTX	258	3e-20	44	(AC005897) putative transposon [Arabidopsis thaliana]
13101	GM_188_A2_E05_T7	g507910	BLASTN	585	8e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
13102	GM_188_A2_E08_MR	g507910	BLASTN	662	3e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
13103	GM_188_A2_E08_T7	g507910	BLASTN	518	8e-17	81	Glycine max BSR-101 satellite SB92 genomic sequence.
13104	GM_188_A2_E12_MR	g2276452	BLASTN	362	3e-09	62	Homo sapiens shox gene, alternatively spliced products, complete cds
13105	GM_188_A2_F03_T7	g3377848	BLASTX	202	2e-21	53	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
13106	GM_188_A2_F04_T7	g4140712	BLASTX	412	8e-45	53	(AF110183) putative integrase [Oryza sativa]
13107	GM_188_A2_F07_T7	g507910	BLASTN	472	1e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
13108	GM_188_A2_F09_MR	g507910	BLASTN	538	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
13109	GM_188_A2_F10_T7	g507910	BLASTN	538	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
13110	GM_188_A2_F12_MR	g3650035	BLASTX	154	4e-09	41	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
13111	GM_188_A2_G03_T7	g1531760	BLASTX	183	1e-12	62	(X97075) proline oxidase [Arabidopsis thaliana]
13112	GM_188_A2_G09_MR	g3097320	BLASTN	546	1e-17	66	Glycine max gene for Bd 30K, complete cds
13113	GM_188_A2_H01_MR	g3947433	BLASTN	412	1e-11	63	Homo sapiens BAC clone RG060P12 from 7q21, complete sequence [Homo sapiens]
13114	GM_188_A2_H04_MR	g3746069	BLASTX	176	3e-11	31	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
13115	GM_188_A2_H06_T7	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
13116	GM_188_A2_H09_T7	g791097	BLASTN	348	8e-09	68	P.vulgaris plsB mRNA.
13117	GM_188_A2_H11_MR	g1165321	BLASTN	714	2e-25	81	Glycine max extensin (SbHRGP3) gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13118	GM_188_A2_H11_T7	g113363	BLASTX	153	1e-12	59	ALCOHOL DEHYDROGENASE 1 gi 279445 pir DEPJA1 alcohol dehydrogenase (EC 1.1.1.1) 1 - garden petunia gi 20506 (X54106) alcohol dehydrogenase [Petunia hybrida]
13119	GM_188_B1_A01_T7	g507910	BLASTN	419	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13120	GM_188_B1_A05_T7	g3845184	BLASTN	247	8e-10	62	Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence
13121	GM_188_B1_A06_T7	g507910	BLASTN	370	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13122	GM_188_B1_B04_T7	g3810596	BLASTX	255	2e-22	48	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
13123	GM_188_B1_B06_T7	g3894156	BLASTN	364	2e-09	67	Arabidopsis thaliana chromosome II BAC T16F16 genomic sequence, complete sequence [Arabidopsis thaliana]
13124	GM_188_B1_B09_T7	g2276452	BLASTN	361	3e-09	61	Homo sapiens shox gene, alternatively spliced products, complete cds
13125	GM_188_B1_C02_T7	g587603	BLASTN	383	2e-10	60	P.falciparum gene for beta subunit RNA polymerase
13126	GM_188_B1_C04_T7	g2665376	BLASTN	354	6e-09	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-15, complete sequence [Plasmodium falciparum]
13127	GM_188_B1_C09_T7	g3142328	BLASTN	1100	7e-43	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13128	GM_188_B1_E02_T7	g3142328	BLASTN	584	2e-19	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13129	GM_188_B1_E06_T7	g507910	BLASTN	340	9e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13130	GM_188_B1_E11_T7	g905361	BLASTX	437	3e-40	96	(U22103) gag-protease polyprotein [Glycine max]
13131	GM_188_B1_F05_T7	g2708743	BLASTX	188	2e-12	32	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
13132	GM_188_B1_F09_T7	g2194136	BLASTX	106	3e-09	31	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
13133	GM_188_B2_A11_MR	g100484	BLASTX	195	1e-13	48	hypothetical protein - garden snapdragon
13134	GM_188_B2_B06_MR	g3142328	BLASTN	894	2e-33	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13135	GM_188_B2_B06_T7	g13767	BLASTN	344	2e-09	65	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
13136	GM_188_B2_B07_T7	g2522228	BLASTX	177	3e-22	81	(AB007466) reverse transcriptase-like protein [Vicia faba]
13137	GM_188_B2_B09_MR	g2995405	BLASTX	186	1e-12	37	(Y12432) polyprotein [Ananas comosus]
13138	GM_188_B2_B12_T7	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13139	GM_188_B2_D10_T7	g2970554	BLASTN	2009	7e-84	98	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
13140	GM_188_B2_E04_T7	g507910	BLASTN	463	3e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
13141	GM_188_B2_E12_MR	g3142328	BLASTN	1166	7e-46	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13142	GM_188_B2_F05_MR	g2708743	BLASTX	217	1e-15	41	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
13143	GM_188_B2_F07_MR	g2522230	BLASTX	178	6e-13	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13144	GM_188_B2_F08_MR	g3097320	BLASTN	967	9e-37	78	Glycine max gene for Bd 30K, complete cds
13145	GM_188_B2_F10_T7	g1769897	BLASTX	270	2e-36	71	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13146	GM_188_B2_F12_T7	g3142328	BLASTN	1033	7e-40	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13147	GM_188_B2_G06_T7	g2225930	BLASTN	355	5e-09	66	Human DNA sequence from PAC 522O2 on chromosome 6q21 contains ESTs, STSs and polymorphic CA repeat
13148	GM_188_B2_H03_T7	g905361	BLASTX	189	4e-13	32	(U22103) gag-protease polyprotein [Glycine max]
13149	GM_188_B2_H06_T7	g99755	BLASTX	165	1e-18	46	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
13150	GM_188_B2_H07_MR	g1769897	BLASTX	108	1e-08	36	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13151	GM_188_B2_H10_MR	g2129618	BLASTX	243	1e-18	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
13152	GM_188_B2_H12_T7	g3142328	BLASTN	669	3e-23	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13153	GM_189_A2_A02_MR	g507910	BLASTN	415	4e-12	79	Glycine max BSR-101 satellite SB92 genomic sequence.
13154	GM_189_A2_A02_T7	g507910	BLASTN	368	5e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13155	GM_189_A2_A03_T7	g18559	BLASTN	517	2e-16	66	G.max gene for catalase
13156	GM_189_A2_A07_T7	g2522228	BLASTX	329	6e-29	65	(AB007466) reverse transcriptase-like protein [Vicia faba]
13157	GM_189_A2_A08_T7	g2982303	BLASTX	361	9e-55	87	(AF051236) hypothetical protein [Picea mariana]
13158	GM_189_A2_A09_MR	g507910	BLASTN	516	1e-16	83	Glycine max BSR-101 satellite SB92 genomic sequence.
13159	GM_189_A2_A10_MR	g4038056	BLASTX	191	4e-13	48	(AC005897) putative transposon [Arabidopsis thaliana]
13160	GM_189_A2_A12_MR	g3450842	BLASTX	241	1e-18	71	(AF080436) mitogen activated protein kinase kinase [Oryza sativa]
13161	GM_189_A2_A12_T7	g18559	BLASTN	886	4e-33	74	G.max gene for catalase
13162	GM_189_A2_B02_T7	g507910	BLASTN	413	5e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13163	GM_189_A2_B03_T7	g4063760	BLASTX	409	8e-51	76	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13164	GM_189_A2_B04_T7	g3283026	BLASTX	142	3e-14	59	putative transposase [Arabidopsis thaliana]
13165	GM_189_A2_C06_MR	g505129	BLASTN	367	1e-09	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
13166	GM_189_A2_C08_MR	g2443320	BLASTX	276	2e-27	44	(D85597) polyprotein [Oryza australiensis]
13167	GM_189_A2_C10_MR	g507910	BLASTN	412	5e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13168	GM_189_A2_C11_T7	g2443320	BLASTX	181	9e-16	47	(D85597) polyprotein [Oryza australiensis]
13169	GM_189_A2_D06_MR	g18559	BLASTN	383	3e-10	73	G.max gene for catalase
13170	GM_189_A2_D10_T7	g3142328	BLASTN	1654	4e-68	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13171	GM_189_A2_D11_MR	g3777527	BLASTX	589	2e-59	95	(AF053008) gag-pol polyprotein [Glycine max]
13172	GM_189_A2_D12_T7	g3426334	BLASTN	473	2e-14	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
13173	GM_189_A2_E03_MR	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13174	GM_189_A2_E08_MR	g2443320	BLASTX	297	1e-28	44	(D85597) polyprotein [Oryza australiensis]
13175	GM_189_A2_E08_T7	g507910	BLASTN	498	7e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
13176	GM_189_A2_E09_T7	g2864621	BLASTX	153	2e-09	38	hypothetical protein [Arabidopsis thaliana]
13177	GM_189_A2_E11_MR	g4008006	BLASTX	182	2e-12	58	(AF084034) receptor-like protein kinase [Arabidopsis thaliana]
13178	GM_189_A2_F01_MR	g2522227	BLASTX	184	2e-13	51	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
13179	GM_189_A2_F04_T7	g3142328	BLASTN	1422	1e-57	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13180	GM_189_A2_F09_MR	g1769898	BLASTX	188	2e-28	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13181	GM_189_A2_F10_MR	g2316016	BLASTX	157	1e-10	55	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
13182	GM_189_A2_F12_MR	g3395431	BLASTX	132	7e-11	86	(AC004683) unknown protein [Arabidopsis thaliana]
13183	GM_189_A2_G01_MR	g3777527	BLASTX	610	8e-64	92	(AF053008) gag-pol polyprotein [Glycine max]
13184	GM_189_A2_G06_MR	g3319362	BLASTX	183	7e-18	44	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
13185	GM_189_A2_G07_T7	g2129618	BLASTX	154	4e-09	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
13186	GM_189_A2_G10_T7	g3695387	BLASTX	153	9e-11	46	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
13187	GM_189_A2_G11_MR	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13188	GM_189_A2_H02_MR	g20613	BLASTN	576	4e-20	70	Phaseolus vulgaris tRNA-Pro(UGG2) gene
13189	GM_189_A2_H05_MR	g3183979	BLASTX	193	2e-13	46	(AJ005171) P69C protein [Lycopersicon esculentum]
13190	GM_189_A2_H06_T7	g1171499	BLASTX	308	9e-27	64	(Z68913) reverse transcriptase [Beta vulgaris]
13191	GM_189_A2_H11_T7	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13192	GM_189_A2_H12_MR	g1840106	BLASTN	404	6e-12	67	Human fragile site locus (FRA16B) minisatellite repeat
13193	GM_189_B1_C12_T7	g2970554	BLASTN	892	3e-33	83	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
13194	GM_189_B1_D09_T7	g170605	BLASTN	369	7e-10	63	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
13195	GM_189_B2_A04_MR	g4063760	BLASTX	171	8e-11	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13196	GM_189_B2_B03_T7	g169940	BLASTN	388	1e-10	71	Glycine max chalcone synthase (chs6) gene, complete cds.
13197	GM_189_B2_B08_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13198	GM_189_B2_B10_T7	g4140691	BLASTX	567	3e-54	78	(AF101972) zeatin O-glucosyltransferase [Phaseolus lunatus]
13199	GM_189_B2_B11_T7	g629693	BLASTX	145	9e-09	69	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
13200	GM_189_B2_C04_MR	g4063756	BLASTN	660	9e-23	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
13201	GM_189_B2_C04_T7	g1666236	BLASTX	229	2e-18	31	(U76261) unknown [Hordeum vulgare]
13202	GM_189_B2_C10_MR	g4063760	BLASTX	270	7e-42	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13203	GM_189_B2_C10_T7	g1769897	BLASTX	189	3e-13	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13204	GM_189_B2_C11_T7	g2129618	BLASTX	243	1e-18	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
13205	GM_189_B2_D01_T7	g2764526	BLASTN	631	2e-21	63	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
13206	GM_189_B2_D04_MR	g13767	BLASTN	453	3e-14	62	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
13207	GM_189_B2_D07_MR	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13208	GM_189_B2_E02_T7	g3746069	BLASTX	129	3e-10	35	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
13209	GM_189_B2_E08_T7	g3142328	BLASTN	552	5e-18	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13210	GM_189_B2_E12_T7	g3142379	BLASTX	236	1e-18	57	(AF053008) envelope-like [Glycine max]
13211	GM_189_B2_G01_MR	g3599418	BLASTN	509	5e-16	90	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
13212	GM_189_B2_G02_T7	g4063760	BLASTX	240	4e-18	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13213	GM_189_B2_G05_MR	g2826450	BLASTN	356	5e-09	61	Human Chromosome X, complete sequence [Homo sapiens]
13214	GM_189_B2_G05_T7	g2564750	BLASTN	617	8e-21	67	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13215	GM_189_B2_G07_T7	g3171154	BLASTN	354	6e-09	66	Homo sapiens PAC 128M19 derived from chromosome 21q22.3, containing the HMG-14 and CHD5 genes, complete cds, complete sequence [Homo sapiens]
13216	GM_189_B2_G10_MR	g4063760	BLASTX	512	4e-47	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13217	GM_189_B2_G11_MR	g1142703	BLASTN	292	4e-15	78	Glycine max satellite STR120-B.1.
13218	GM_189_B2_H02_T7	g1931647	BLASTX	199	3e-14	64	(U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]
13219	GM_189_B2_H05_MR	g2865437	BLASTX	131	3e-12	49	(AF039376) polyprotein [Arabidopsis arenosa]
13220	GM_189_B2_H08_MR	g507910	BLASTN	451	9e-14	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13221	GM_189_B2_H08_T7	g4063760	BLASTX	185	3e-12	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13222	GM_190_A1_A01_T7	g2772557	BLASTN	374	7e-10	63	Homo sapiens BAC clone RG437L15 from 8q21, complete sequence [Homo sapiens]
13223	GM_190_A1_A08_MR	g3777527	BLASTX	584	7e-62	94	(AF053008) gag-pol polyprotein [Glycine max]
13224	GM_190_A1_A09_T7	g3250687	BLASTX	275	3e-23	38	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
13225	GM_190_A1_B01_MR	g2443320	BLASTX	209	9e-15	46	(D85597) polyprotein [Oryza australiensis]
13226	GM_190_A1_B07_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13227	GM_190_A1_B07_T7	g507910	BLASTN	395	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13228	GM_190_A1_B08_MR	g4140712	BLASTX	305	1e-28	52	(AF110183) putative integrase [Oryza sativa]
13229	GM_190_A1_B12_MR	g3810596	BLASTX	163	5e-10	43	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
13230	GM_190_A1_C01_T7	g130582	BLASTX	239	5e-18	36	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
13231	GM_190_A1_C03_MR	g1617268	BLASTX	308	3e-33	67	(Z72153) acyl CoA synthetase [Brassica napus]
13232	GM_190_A1_C07_T7	g3097320	BLASTN	857	9e-32	69	Glycine max gene for Bd 30K, complete cds
13233	GM_190_A1_D04_MR	g3319351	BLASTX	208	1e-14	37	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
13234	GM_190_A1_D04_T7	g3935152	BLASTX	161	6e-10	75	(AC005106) T25N20.16 [Arabidopsis thaliana]
13235	GM_190_A1_D07_T7	g2654440	BLASTX	212	1e-16	52	(U70076) Lemir [Lycopersicon esculentum]
13236	GM_190_A1_D08_MR	g3142328	BLASTN	1169	5e-46	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13237	GM_190_A1_E01_MR	g4063756	BLASTN	443	6e-13	72	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13238	GM_190_A1_E01_T7	g3810596	BLASTX	134	1e-11	31	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
13239	GM_190_A1_E05_T7	g4102691	BLASTN	353	7e-10	81	Glycine max late-embryogenesis abundant protein mRNA, complete cds
13240	GM_190_A1_E06_MR	g507910	BLASTN	502	4e-16	81	Glycine max BSR-101 satellite SB92 genomic sequence.
13241	GM_190_A1_E07_MR	g4006828	BLASTX	174	2e-14	48	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
13242	GM_190_A1_F02_MR	g2462134	BLASTX	197	4e-14	35	(Y13368) reverse transcriptase [Beta vulgaris]
13243	GM_190_A1_G02_MR	g507910	BLASTN	388	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13244	GM_190_A1_G08_T7	g3046856	BLASTN	457	1e-13	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXI22, complete sequence [Arabidopsis thaliana]
13245	GM_190_A1_G10_MR	g4063760	BLASTX	178	1e-11	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13246	GM_190_A1_H01_MR	g3777527	BLASTX	394	2e-34	78	(AF053008) gag-pol polyprotein [Glycine max]
13247	GM_190_A1_H01_T7	g2995405	BLASTX	478	6e-44	59	(Y12432) polyprotein [Ananas comosus]
13248	GM_190_A1_H08_T7	g1769898	BLASTX	399	5e-36	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13249	GM_190_A1_H11_MR	g507910	BLASTN	349	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13250	GM_190_A2_A03_MR	g1184075	BLASTX	226	1e-16	43	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
13251	GM_190_A2_A10_MR	g4063756	BLASTN	534	4e-17	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
13252	GM_190_A2_B01_MR	g2764526	BLASTN	710	5e-25	66	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
13253	GM_190_A2_B07_MR	g507910	BLASTN	375	2e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
13254	GM_190_A2_B07_T7	g507910	BLASTN	394	3e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
13255	GM_190_A2_B08_T7	g1769899	BLASTX	140	6e-09	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13256	GM_190_A2_B11_T7	g2522227	BLASTX	228	3e-18	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
13257	GM_190_A2_C01_T7	g2462134	BLASTX	381	2e-34	53	(Y13368) reverse transcriptase [Beta vulgaris]
13258	GM_190_A2_C02_MR	g2245082	BLASTX	247	3e-20	45	(Z97343) SCARECROW homolog [Arabidopsis thaliana]
13259	GM_190_A2_C04_MR	g975703	BLASTN	876	1e-32	80	P.sativum GR gene
13260	GM_190_A2_C05_T7	g3142379	BLASTX	242	3e-19	66	(AF053008) envelope-like [Glycine max]
13261	GM_190_A2_C09_MR	g1769898	BLASTX	191	2e-13	33	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13262	GM_190_A2_C09_T7	g4063760	BLASTX	280	2e-22	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13263	GM_190_A2_D01_T7	g1666236	BLASTX	220	2e-17	31	(U76261) unknown [Hordeum vulgare]
13264	GM_190_A2_D04_T7	g1313926	BLASTX	152	3e-10	46	(X97677) non intermediate filament IFA binding protein [Brassica oleracea]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13265	GM_190_A2_D08_MR	g3142328	BLASTN	724	7e-40	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13266	GM_190_A2_D10_MR	g3513747	BLASTX	175	5e-11	29	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
13267	GM_190_A2_E03_MR	g18559	BLASTN	934	3e-35	72	G.max gene for catalase
13268	GM_190_A2_E05_MR	g507910	BLASTN	413	5e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13269	GM_190_A2_E05_T7	g507910	BLASTN	348	4e-09	68	Glycine max BSR-101 satellite SB92 genomic sequence.
13270	GM_190_A2_E10_T7	g905361	BLASTX	634	3e-61	94	(U22103) gag-protease polyprotein [Glycine max]
13271	GM_190_A2_F02_MR	g2462058	BLASTX	137	2e-17	46	(Y13389) reverse transcriptase [Antirrhinum majus]
13272	GM_190_A2_F05_MR	g99755	BLASTX	279	3e-25	44	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
13273	GM_190_A2_F07_T7	g2564046	BLASTN	352	7e-09	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]
13274	GM_190_A2_F12_MR	g629693	BLASTX	360	3e-32	49	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
13275	GM_190_A2_G02_MR	g3142328	BLASTN	1402	1e-56	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13276	GM_190_A2_G04_MR	g3426334	BLASTN	429	2e-12	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
13277	GM_190_A2_G07_T7	g3860271	BLASTX	276	3e-22	45	(AC005824) putative selenium-binding protein [Arabidopsis thaliana]
13278	GM_190_A2_G09_T7	g170080	BLASTN	408	2e-11	81	Soybean seed lectin gene transposable element tgm1.
13279	GM_190_A2_G12_T7	g530207	BLASTX	227	6e-17	70	(L35272) heat shock protein [Glycine max]
13280	GM_190_A2_H01_MR	g2760171	BLASTN	351	8e-09	77	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPA24, complete sequence [Arabidopsis thaliana]
13281	GM_190_A2_H10_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13282	GM_190_A2_H12_T7	g3810596	BLASTX	162	6e-10	50	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
13283	GM_190_B1_A08_T7	g4063760	BLASTX	180	2e-13	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13284	GM_190_B1_B01_T7	g507910	BLASTN	446	1e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
13285	GM_190_B1_B03_T7	g4063760	BLASTX	337	1e-38	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13286	GM_190_B1_B04_T7	g3645899	BLASTX	236	1e-23	46	(U68408) 5' end not determined experimentally [Zea mays]
13287	GM_190_B1_B05_T7	g3056580	BLASTX	176	1e-11	51	(AC004255) T1F9.1 [Arabidopsis thaliana]
13288	GM_190_B1_C03_T7	g1806140	BLASTX	217	1e-26	97	(X97314) cdc2MsC [Medicago sativa]
13289	GM_190_B1_C11_T7	g3510347	BLASTN	583	3e-19	73	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13290	GM_190_B1_D02_T7	g3142328	BLASTN	452	2e-13	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13291	GM_190_B1_D11_T7	g507910	BLASTN	395	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13292	GM_190_B1_E09_T7	g3869065	BLASTN	365	2e-09	64	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]
13293	GM_190_B1_E10_T7	g2129709	BLASTX	169	2e-10	38	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
13294	GM_190_B1_E11_T7	g3097320	BLASTN	871	2e-32	76	Glycine max gene for Bd 30K, complete cds
13295	GM_190_B1_E12_T7	g2462058	BLASTX	301	5e-26	56	(Y13389) reverse transcriptase [Antirrhinum majus]
13296	GM_190_B1_F11_T7	g4050011	BLASTN	352	7e-09	70	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
13297	GM_190_B1_G07_T7	g255572	BLASTN	471	2e-19	78	small auxin up RNA gene cluster: orf 15A [Glycine max=soybeans, cv. Wayne, Genomic, 637 nt]
13298	GM_190_B1_G10_T7	g2997694	BLASTX	142	9e-16	48	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
13299	GM_190_B1_H01_T7	g3777527	BLASTX	286	7e-23	84	(AF053008) gag-pol polyprotein [Glycine max]
13300	GM_190_B1_H02_T7	g422418	BLASTX	154	4e-09	39	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
13301	GM_190_B1_H07_T7	g3142328	BLASTN	1249	1e-49	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13302	GM_190_B1_H10_T7	g3133272	BLASTN	429	2e-12	68	Genomic sequence for Arabidopsis thaliana BAC T17H7, complete sequence.
13303	GM_190_B2_A03_T7	g3859610	BLASTN	513	4e-16	66	Arabidopsis thaliana BAC T9E19
13304	GM_190_B2_A06_T7	g507910	BLASTN	482	4e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13305	GM_190_B2_B10_T7	g507910	BLASTN	356	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13306	GM_190_B2_D01_T7	g4156152	BLASTN	407	2e-11	62	Homo sapiens clone DJ56J10, complete sequence [Homo sapiens]
13307	GM_190_B2_D12_T7	g2315153	BLASTX	233	3e-22	74	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
13308	GM_190_B2_E04_T7	g3859610	BLASTN	478	1e-14	64	Arabidopsis thaliana BAC T9E19
13309	GM_190_B2_E05_T7	g507910	BLASTN	518	8e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
13310	GM_190_B2_F01_T7	g995751	BLASTN	444	3e-13	63	Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence
13311	GM_190_B2_F04_T7	g2769655	BLASTN	353	7e-09	61	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13312	GM_190_B2_F08_T7	g3860247	BLASTX	131	6e-11	81	(AC005824) unknown protein [Arabidopsis thaliana]
13313	GM_190_B2_F11_T7	g3907448	BLASTN	394	9e-11	68	Homo sapiens chromosome 18, clone hRPK.24_A_23, complete sequence [Homo sapiens]
13314	GM_190_B2_G01_T7	g2129618	BLASTX	233	2e-17	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
13315	GM_190_B2_G02_T7	g3687234	BLASTX	299	2e-24	53	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
13316	GM_190_B2_H04_T7	g2443321	BLASTN	385	8e-11	61	Oryza australiensis retrotransposon RIRE1, LTR sequence.
13317	GM_190_B2_H06_T7	g507910	BLASTN	439	3e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13318	GM_191_A1_A01_MR	g507910	BLASTN	405	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13319	GM_191_A1_A01_T7	g3142328	BLASTN	728	5e-26	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13320	GM_191_A1_A05_MR	g507910	BLASTN	411	6e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13321	GM_191_A1_A05_T7	g4063760	BLASTX	433	1e-38	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13322	GM_191_A1_A10_MR	g3419855	BLASTN	441	7e-13	64	Homo sapiens PAC clone DJ0755G17 from 7p21-p22, complete sequence [Homo sapiens]
13323	GM_191_A1_B09_T7	g4063756	BLASTN	420	6e-12	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
13324	GM_191_A1_B12_T7	g342965	BLASTN	487	5e-16	66	paramecium species 7,227 mt dna dimer: replication init. region.
13325	GM_191_A1_C02_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13326	GM_191_A1_C02_T7	g1871190	BLASTX	310	6e-27	50	(U90439) Ser/Thr kinase isolog [Arabidopsis thaliana]
13327	GM_191_A1_C08_MR	g282965	BLASTX	251	6e-20	77	transforming protein (myb) homolog (clone myb.Ph3) - garden petunia gi 20565 (Z13998) protein 3 [Petunia hybrida]
13328	GM_191_A1_C11_MR	g18559	BLASTN	771	6e-28	75	G.max gene for catalase
13329	GM_191_A1_D03_T7	g3142330	BLASTX	570	2e-54	94	(U96295) envelope-like [Glycine max]
13330	GM_191_A1_D04_T7	g3281847	BLASTN	311	1e-11	69	Arabidopsis thaliana DNA chromosome 4, BAC clone F28M20 (ESSAII project)
13331	GM_191_A1_D08_T7	g2982459	BLASTX	225	6e-18	81	(AL022223) putative protein [Arabidopsis thaliana]
13332	GM_191_A1_D09_T7	g1778375	BLASTN	366	1e-09	88	Pisum sativum PsRT17-1 mRNA, complete cds
13333	GM_191_A1_E02_T7	g4063760	BLASTX	178	1e-11	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13334	GM_191_A1_E04_T7	g3687301	BLASTX	279	1e-22	50	(AJ006376) subtilisin-like protease [Lycopersicon esculentum] gi 3687309 gnl PID e1299614 (AJ006380) subtilisin-like protease [Lycopersicon esculentum]
13335	GM_191_A1_E08_MR	g507910	BLASTN	370	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13336	GM_191_A1_F02_MR	g2129965	BLASTX	206	6e-16	86	Sar1 homolog GTP-binding protein NTGB2 - common tobacco (fragment) gi 1184989 (U46928) NTGB2 [Nicotiana tabacum]
13337	GM_191_A1_F02_T7	g2950210	BLASTX	159	5e-10	84	(Y14615) Importin alpha-like protein [Arabidopsis thaliana]
13338	GM_191_A1_F03_T7	g4063760	BLASTX	448	3e-40	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13339	GM_191_A1_F08_T7	g2459412	BLASTX	273	4e-22	51	(AC002332) putative G9a protein [Arabidopsis thaliana]
13340	GM_191_A1_G06_MR	g507910	BLASTN	611	5e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
13341	GM_191_A1_G08_MR	g3142328	BLASTN	621	4e-21	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13342	GM_191_A1_G10_T7	g3176795	BLASTN	404	7e-12	67	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
13343	GM_191_A1_H06_T7	g3599418	BLASTN	969	6e-37	78	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
13344	GM_191_A1_H09_T7	g1399164	BLASTN	377	7e-11	67	Oenothera elata subsp. hookeri chloroplast spacer between (trnG) and (trnH) genes
13345	GM_191_A1_H12_MR	g507910	BLASTN	594	3e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
13346	GM_191_A1_H12_T7	g507910	BLASTN	621	2e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
13347	GM_191_A2_A04_T7	g421954	BLASTX	306	2e-27	47	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
13348	GM_191_A2_A10_T7	g1167523	BLASTX	367	1e-31	47	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
13349	GM_191_A2_B01_T7	g18559	BLASTN	1178	2e-46	88	G.max gene for catalase
13350	GM_191_A2_C01_T7	g3777527	BLASTX	764	7e-74	94	(AF053008) gag-pol polyprotein [Glycine max]
13351	GM_191_A2_C02_T7	g2642431	BLASTX	184	5e-12	43	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
13352	GM_191_A2_C08_T7	g3645899	BLASTX	166	9e-18	43	(U68408) 5' end not determined experimentally [Zea mays]
13353	GM_191_A2_C11_T7	g4050011	BLASTN	688	4e-24	68	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
13354	GM_191_A2_C12_T7	g4063760	BLASTX	369	6e-32	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13355	GM_191_A2_D02_T7	g170605	BLASTN	625	8e-22	63	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
13356	GM_191_A2_D06_T7	g100484	BLASTX	370	2e-32	55	hypothetical protein - garden snapdragon
13357	GM_191_A2_D10_T7	g4296	BLASTN	777	2e-28	98	S. carlsbergensis rDNA not transcribed spacer (NTS) sequence
13358	GM_191_A2_E11_T7	g3142328	BLASTN	803	2e-29	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13359	GM_191_A2_F09_T7	g3096935	BLASTX	121	6e-16	92	(AL023094) putative protein [Arabidopsis thaliana]
13360	GM_191_A2_F10_T7	g342967	BLASTN	258	3e-12	68	paramecium species 8,299 mt dna dimer: replication init. region.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13361	GM_191_A2_G01_T7	g3142328	BLASTN	894	2e-33	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13362	GM_191_A2_G02_T7	g3645899	BLASTX	197	1e-13	34	(U68408) 5' end not determined experimentally [Zea mays]
13363	GM_191_A2_G06_T7	g507910	BLASTN	396	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13364	GM_191_A2_H07_T7	g2244801	BLASTX	188	5e-14	66	(Z97336) hypothetical protein [Arabidopsis thaliana]
13365	GM_191_B1_A04_MR	g99922	BLASTX	299	2e-52	81	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13366	GM_191_B1_A04_T7	g3152618	BLASTX	235	3e-18	74	(AC004482) putative pectinesterase [Arabidopsis thaliana] gi 3242724 (AC003040) putative pectinesterase [Arabidopsis thaliana]
13367	GM_191_B1_A05_MR	g169992	BLASTN	1860	2e-78	96	soybean leghemoglobin lba gene.
13368	GM_191_B1_A07_MR	g3645899	BLASTX	166	2e-20	42	(U68408) 5' end not determined experimentally [Zea mays]
13369	GM_191_B1_A07_T7	g1142701	BLASTN	861	1e-32	83	Glycine max satellite STR120-A.3.
13370	GM_191_B1_A08_MR	g2335061	BLASTN	386	2e-10	61	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence [Homo sapiens]
13371	GM_191_B1_A10_T7	g3046854	BLASTN	403	4e-11	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRG7, complete sequence [Arabidopsis thaliana]
13372	GM_191_B1_B02_MR	g3128170	BLASTX	232	7e-18	55	(AC004521) hypothetical protein [Arabidopsis thaliana]
13373	GM_191_B1_B04_MR	g2586082	BLASTX	339	1e-28	50	(U72725) retrofit [Oryza longistaminata]
13374	GM_191_B1_B10_T7	g507910	BLASTN	355	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
13375	GM_191_B1_B12_T7	g2244802	BLASTX	320	2e-26	51	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
13376	GM_191_B1_C09_T7	g4006828	BLASTX	152	7e-09	31	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
13377	GM_191_B1_C10_MR	g2443320	BLASTX	158	5e-11	33	(D85597) polyprotein [Oryza australiensis]
13378	GM_191_B1_C10_T7	g3777527	BLASTX	258	6e-20	44	(AF053008) gag-pol polyprotein [Glycine max]
13379	GM_191_B1_D02_T7	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
13380	GM_191_B1_D05_MR	g2073400	BLASTN	384	3e-10	63	Caenorhabditis elegans cosmid Y6G8, complete sequence [Caenorhabditis elegans]
13381	GM_191_B1_E02_MR	g18559	BLASTN	350	8e-09	67	G.max gene for catalase
13382	GM_191_B1_E03_MR	g226407	BLASTX	240	5e-18	43	retrotransposon del1-46 [Lilium henryi]
13383	GM_191_B1_E05_MR	g3645899	BLASTX	468	1e-42	60	(U68408) 5' end not determined experimentally [Zea mays]
13384	GM_191_B1_F02_MR	g2244802	BLASTX	295	6e-24	37	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
13385	GM_191_B1_F02_T7	g3985957	BLASTN	358	4e-09	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence [Arabidopsis thaliana]
13386	GM_191_B1_F03_MR	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13387	GM_191_B1_F07_T7	g130582	BLASTX	157	4e-16	65	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
13388	GM_191_B1_F10_MR	g3941520	BLASTX	104	2e-10	57	(AF062914) putative transcription factor [Arabidopsis thaliana]
13389	GM_191_B1_G02_T7	g4063760	BLASTX	270	2e-21	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13390	GM_191_B1_G04_MR	g507910	BLASTN	402	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13391	GM_191_B1_G04_T7	g3075397	BLASTX	374	2e-33	61	(AC004484) hypothetical protein [Arabidopsis thaliana]
13392	GM_191_B1_G05_MR	g2262105	BLASTX	332	2e-28	71	(AC002343) unknown protein [Arabidopsis thaliana]
13393	GM_191_B1_G08_T7	g421954	BLASTX	234	4e-20	47	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
13394	GM_191_B1_G12_T7	g2828280	BLASTX	172	9e-11	86	(AL021687) putative protein [Arabidopsis thaliana] gi 2832633 gnl PID e1249651 (AL021711) putative protein [Arabidopsis thaliana]
13395	GM_191_B1_H05_T7	g2618701	BLASTX	189	4e-14	70	(AC002510) hypothetical protein [Arabidopsis thaliana]
13396	GM_191_B1_H07_MR	g3283026	BLASTX	176	7e-20	41	putative transposase [Arabidopsis thaliana]
13397	GM_191_B1_H07_T7	g531389	BLASTX	185	6e-15	47	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
13398	GM_191_B1_H10_T7	g531389	BLASTX	153	4e-10	41	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
13399	GM_191_B2_A04_MR	g100484	BLASTX	179	5e-12	39	hypothetical protein - garden snapdragon
13400	GM_191_B2_A05_MR	g1871192	BLASTX	179	6e-12	80	(U90439) Cys3His zinc finger protein isolog [Arabidopsis thaliana]
13401	GM_191_B2_B01_MR	g1087073	BLASTX	204	4e-15	56	(S79243) calmodulin-binding heat-shock protein, CaMBP [Nicotiana tabacum=tobacco, Wisconsin-38, Peptide, 449 aa] [Nicotiana tabacum]
13402	GM_191_B2_B02_MR	g4038056	BLASTX	340	5e-29	46	(AC005897) putative transposon [Arabidopsis thaliana]
13403	GM_191_B2_B10_MR	g507910	BLASTN	362	9e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13404	GM_191_B2_C01_MR	g976284	BLASTX	203	1e-15	39	reverse transcriptase [Arabidopsis thaliana]
13405	GM_191_B2_C02_MR	g18768	BLASTN	485	1e-15	72	Soybean Tgm6 transposable element 3' end
13406	GM_191_B2_C10_MR	g2245104	BLASTX	327	3e-29	73	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
13407	GM_191_B2_D01_MR	g3047066	BLASTX	163	3e-19	54	(AF058825) contains similarity to retrovirus-related POL polyproteins [Arabidopsis thaliana]
13408	GM_191_B2_E12_MR	g343819	BLASTN	378	6e-11	67	Saccharomyces exiguus mitochondrial Metf-tRNA, Pro-tRNA and putative ribonuclease P subunit.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13409	GM_191_B2_F02_MR	g2769655	BLASTN	430	2e-12	64	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
13410	GM_191_B2_G02_MR	g507910	BLASTN	513	1e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
13411	GM_191_B2_G04_MR	g3873182	BLASTN	361	3e-09	61	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
13412	GM_191_B2_G06_MR	g18559	BLASTN	522	1e-16	75	G.max gene for catalase
13413	GM_191_B2_G10_MR	g3513745	BLASTX	205	3e-14	38	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
13414	GM_191_B2_H02_MR	g3599418	BLASTN	361	2e-09	87	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
13415	GM_191_B2_H06_MR	g1769898	BLASTX	137	1e-14	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13416	GM_191_B2_H12_MR	g2997694	BLASTX	169	7e-17	48	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
13417	GM_192_A2_A01_MR	g3142328	BLASTN	729	5e-26	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13418	GM_192_A2_A02_T7	g13774	BLASTN	346	7e-09	64	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
13419	GM_192_A2_A03_MR	g4140712	BLASTX	238	5e-24	36	(AF110183) putative integrase [Oryza sativa]
13420	GM_192_A2_A05_MR	g18695	BLASTN	370	7e-10	68	Soybean nodulin 22 gene
13421	GM_192_A2_A07_T7	g505129	BLASTN	393	8e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
13422	GM_192_A2_A09_MR	g4063760	BLASTX	561	2e-52	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13423	GM_192_A2_A12_MR	g3377834	BLASTX	207	6e-15	33	(AF075598) No definition line found [Arabidopsis thaliana]
13424	GM_192_A2_A12_T7	g4160362	BLASTN	413	1e-11	59	Saccharomyces cerevisiae complete mitochondrial genome
13425	GM_192_A2_B01_T7	g3097320	BLASTN	501	1e-15	69	Glycine max gene for Bd 30K, complete cds
13426	GM_192_A2_B02_MR	g905361	BLASTX	708	4e-69	95	(U22103) gag-protease polyprotein [Glycine max]
13427	GM_192_A2_B04_MR	g1142699	BLASTN	914	5e-35	83	Glycine max satellite STR120-A.1.
13428	GM_192_A2_B05_T7	g3097320	BLASTN	437	9e-13	73	Glycine max gene for Bd 30K, complete cds
13429	GM_192_A2_B09_T7	g3319362	BLASTX	96	7e-10	42	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
13430	GM_192_A2_B12_MR	g18559	BLASTN	545	1e-17	83	G.max gene for catalase
13431	GM_192_A2_C02_MR	g507910	BLASTN	413	5e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13432	GM_192_A2_C04_T7	g4092470	BLASTN	680	1e-23	65	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
13433	GM_192_A2_C07_T7	g4063760	BLASTX	484	3e-44	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13434	GM_192_A2_C08_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13435	GM_192_A2_C08_T7	g507910	BLASTN	385	9e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13436	GM_192_A2_C10_MR	g2760170	BLASTN	457	1e-13	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIO24, complete sequence [Arabidopsis thaliana]
13437	GM_192_A2_C12_MR	g4038056	BLASTX	353	2e-30	51	(AC005897) putative transposon [Arabidopsis thaliana]
13438	GM_192_A2_D04_T7	g2832623	BLASTX	255	5e-23	74	(AL021711) protein kinase - like protein [Arabidopsis thaliana]
13439	GM_192_A2_D07_T7	g507910	BLASTN	558	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
13440	GM_192_A2_D08_T7	g3786000	BLASTX	151	4e-09	55	(AC005499) hypothetical protein [Arabidopsis thaliana]
13441	GM_192_A2_E02_MR	g505129	BLASTN	396	6e-11	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
13442	GM_192_A2_E04_T7	g1370140	BLASTX	215	6e-17	67	(X98308) myb-related transcription factor [Lycopersicon esculentum]
13443	GM_192_A2_E05_MR	g2462134	BLASTX	373	1e-33	43	(Y13368) reverse transcriptase [Beta vulgaris]
13444	GM_192_A2_E05_T7	g3777527	BLASTX	386	2e-41	76	(AF053008) gag-pol polyprotein [Glycine max]
13445	GM_192_A2_E06_MR	g1773014	BLASTX	350	3e-30	55	(Y10338) chloride channel Stclc1 [Solanum tuberosum]
13446	GM_192_A2_E10_T7	g3193317	BLASTX	429	1e-39	62	(AF069299) similar to plant chalcone and stilbene synthases [Arabidopsis thaliana]
13447	GM_192_A2_F02_MR	g3777527	BLASTX	773	7e-75	98	(AF053008) gag-pol polyprotein [Glycine max]
13448	GM_192_A2_F02_T7	g507910	BLASTN	579	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
13449	GM_192_A2_F03_MR	g4063760	BLASTX	365	2e-31	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13450	GM_192_A2_F03_T7	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
13451	GM_192_A2_F08_MR	g1666236	BLASTX	156	4e-10	29	(U76261) unknown [Hordeum vulgare]
13452	GM_192_A2_F12_MR	g3319351	BLASTX	220	6e-16	40	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
13453	GM_192_A2_G03_MR	g2462058	BLASTX	317	1e-27	53	(Y13389) reverse transcriptase [Antirrhinum majus]
13454	GM_192_A2_G04_T7	g18559	BLASTN	1086	3e-42	75	G.max gene for catalase
13455	GM_192_A2_G07_MR	g226407	BLASTX	393	2e-34	47	retrotransposon del1-46 [Lilium henryi]
13456	GM_192_A2_G07_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13457	GM_192_A2_G12_T7	g1710401	BLASTX	167	2e-11	75	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE SMALL CHAIN (RIBONUCLEOTIDE REDUCTASE) (R2 SUBUNIT) gi 1044912 (X92443) ribonucleotide reductase R2 [Nicotiana tabacum]
13458	GM_192_A2_H02_T7	g2811226	BLASTX	265	3e-21	91	(AF042669) fimbrin 2 [Arabidopsis thaliana] gi 2811232 (AF042671) fimbrin 2 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13459	GM_192_A2_H06_MR	g3097320	BLASTN	1177	3e-46	80	Glycine max gene for Bd 30K, complete cds
13460	GM_192_A2_H08_MR	g3097320	BLASTN	664	5e-23	79	Glycine max gene for Bd 30K, complete cds
13461	GM_192_A2_H10_T7	g703220	BLASTN	546	3e-18	74	Pisum sativum (clone HW16-26) gene fragment.
13462	GM_192_B2_A08_T7	g507910	BLASTN	403	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13463	GM_192_B2_B04_T7	g507910	BLASTN	363	8e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13464	GM_192_B2_B10_MR	g1658457	BLASTX	174	2e-12	75	(U75248) reverse transcriptase [Gossypium barbadense]
13465	GM_192_B2_C05_T7	g507910	BLASTN	352	3e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13466	GM_192_B2_C07_T7	g3650039	BLASTX	203	1e-14	38	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
13467	GM_192_B2_C11_T7	g99922	BLASTX	278	2e-23	59	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13468	GM_192_B2_D10_T7	g1360633	BLASTN	386	2e-10	69	V.sativa mRNA for protein binding to ENOD12B promoter.
13469	GM_192_B2_E01_T7	g2085783	BLASTN	371	1e-09	64	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
13470	GM_192_B2_F06_MR	g3142328	BLASTN	355	5e-09	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13471	GM_192_B2_F12_T7	g507910	BLASTN	514	1e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
13472	GM_192_B2_G08_T7	g1785739	BLASTX	161	3e-11	42	(Y08502) orf240b [Arabidopsis thaliana]
13473	GM_192_B2_G09_T7	g3377848	BLASTX	152	2e-09	46	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
13474	GM_192_B2_H03_T7	g3777527	BLASTX	375	2e-32	84	(AF053008) gag-pol polyprotein [Glycine max]
13475	GM_192_B2_H11_T7	g4063760	BLASTX	184	3e-12	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13476	GM_193_A1_A01_T7	g4063760	BLASTX	336	2e-28	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13477	GM_193_A1_A03_T7	g507910	BLASTN	436	4e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13478	GM_193_A1_A04_T7	g2995405	BLASTX	320	6e-27	52	(Y12432) polyprotein [Ananas comosus]
13479	GM_193_A1_A10_T7	g2196878	BLASTX	192	1e-17	87	(Y08292) NADH glutamate dehydrogenase [Nicotiana plumbaginifolia]
13480	GM_193_A1_B04_T7	g2462749	BLASTX	221	1e-16	44	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]
13481	GM_193_A1_B05_MR	g507910	BLASTN	534	2e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
13482	GM_193_A1_B05_T7	g4063760	BLASTX	409	3e-36	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13483	GM_193_A1_B06_MR	g2129618	BLASTX	229	4e-17	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
13484	GM_193_A1_B12_MR	g2244915	BLASTX	185	2e-12	38	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13485	GM_193_A1_C02_T7	g1769899	BLASTX	217	4e-17	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13486	GM_193_A1_C03_T7	g99922	BLASTX	373	2e-48	72	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13487	GM_193_A1_C06_T7	g2129618	BLASTX	203	2e-14	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
13488	GM_193_A1_C07_MR	g2462936	BLASTX	162	4e-15	40	(Y12321) open reading frame 2 [Brassica oleracea]
13489	GM_193_A1_D06_T7	g18767	BLASTN	374	2e-22	79	Soybean Tgm6 transposable element 5' end
13490	GM_193_A1_D07_MR	g417154	BLASTX	260	1e-20	61	HEAT SHOCK PROTEIN 82 gi 100685 pir S25541 heat shock protein 82 - rice (strain Taichung Native One) gi 20256 (Z11920) heat shock protein 82 (HSP82) [Oryza sativa]
13491	GM_193_A1_D08_MR	g507910	BLASTN	403	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13492	GM_193_A1_D08_T7	g507910	BLASTN	380	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13493	GM_193_A1_D12_MR	g2764526	BLASTN	455	1e-13	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
13494	GM_193_A1_D12_T7	g4063756	BLASTN	492	3e-15	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
13495	GM_193_A1_E07_MR	g3513745	BLASTX	238	9e-18	42	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
13496	GM_193_A1_E10_T7	g3097320	BLASTN	1363	1e-54	82	Glycine max gene for Bd 30K, complete cds
13497	GM_193_A1_E12_MR	g4063760	BLASTX	209	7e-15	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13498	GM_193_A1_F08_MR	g3645899	BLASTX	231	2e-23	56	(U68408) 5' end not determined experimentally [Zea mays]
13499	GM_193_A1_F09_T7	g1345644	BLASTX	189	3e-13	50	CYTOCHROME P450 LXXXVI gi 940446 (X90458) cytochrome p450 [Arabidopsis thaliana]
13500	GM_193_A1_G02_T7	g1167523	BLASTX	206	2e-14	42	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
13501	GM_193_A1_G06_T7	g549056	BLASTX	446	2e-41	71	T-COMPLEX PROTEIN 1, BETA SUBUNIT (TCP-1-BETA) (CCT-BETA) gi 631651 pir S43059 CCT (chaperonin containing TCP-1) beta chain - mouse gi 468546 (Z31553) CCT (chaperonin containing TCP-1) beta subunit [Mus musculus]
13502	GM_193_A1_G08_T7	g2245044	BLASTX	197	3e-13	49	(Z97342) similarity to reverse transcriptase - Arabidopsis thaliana retrotransposon 2 (fragment) [Arabidopsis thaliana]
13503	GM_193_A1_H06_T7	g1899158	BLASTN	526	4e-17	64	Saccharomyces cerevisiae synthetic green fluorescent protein (cox3::GFPm) gene, mitochondrial gene construct, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13504	GM_193_A1_H07_T7	g13773	BLASTN	347	4e-09	62	Torulopsis glabrata mitochondrial genes for tRNAs -Tyr, -Asn, -Ala, -Ile -Trp (from Var1-LrRNA intergenic region) >gi 343959 gb M11906 YSLMTIG09 Yeast (T.glabrata) mitochondrial DNA between var1 and L rRNA genes.
13505	GM_193_A2_A03_T7	g1840106	BLASTN	429	3e-13	63	Human fragile site locus (FRA16B) minisatellite repeat
13506	GM_193_A2_A04_T7	g2842542	BLASTN	383	3e-10	61	Ipomoea purpurea DNA, LTR retrotransposon RTip1
13507	GM_193_A2_A05_T7	g3914402	BLASTX	226	3e-28	81	PROTOPORPHYRINOGEN OXIDASE, CHLOROPLAST PRECURSOR (PPO I) (PROTOPORPHYRINOGEN IX OXIDASE ISOZYME I) (PPX I) >gi 2370333 gnl PID e337830 (Y13465) protoporphyrinogen oxidase [Nicotiana tabacum]
13508	GM_193_A2_A06_MR	g11748	BLASTN	1247	6e-60	91	Nicotiana debneyi chloroplast DNA for tRNA-Ile and ribosomal protein L2
13509	GM_193_A2_A06_T7	g133917	BLASTX	288	1e-24	92	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 gi 70856 pir R3NT2 ribosomal protein S2 - common tobacco chloroplast gi 11814 (Z00044) ribosomal protein S2 [Nicotiana tabacum] gi 225274 prf 1211235J ribosomal protein S2 [Nicotiana tabacum]
13510	GM_193_A2_B02_MR	g2914758	BLASTN	428	3e-12	67	Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds
13511	GM_193_A2_B02_T7	g3075400	BLASTX	166	9e-11	47	(AC004484) putative thromboxane-A synthase [Arabidopsis thaliana] gi 3413720 (AC004747) putative thromboxin-A synthase [Arabidopsis thaliana]
13512	GM_193_A2_B03_MR	g1399302	BLASTN	783	7e-29	99	Glycine max phosphoinositide-specific phospholipase C P12 mRNA, complete cds.
13513	GM_193_A2_B06_MR	g3650039	BLASTX	235	5e-18	34	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
13514	GM_193_A2_B06_T7	g1666236	BLASTX	213	1e-16	31	(U76261) unknown [Hordeum vulgare]
13515	GM_193_A2_B07_T7	g4092471	BLASTN	441	7e-13	67	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
13516	GM_193_A2_B08_T7	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13517	GM_193_A2_B10_T7	g3695395	BLASTX	130	2e-12	63	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
13518	GM_193_A2_C02_MR	g3250687	BLASTX	246	3e-20	40	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
13519	GM_193_A2_C03_MR	g18559	BLASTN	418	7e-12	73	G.max gene for catalase
13520	GM_193_A2_C04_MR	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13521	GM_193_A2_C05_T7	g3142328	BLASTN	990	7e-38	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13522	GM_193_A2_C09_MR	g3645899	BLASTX	350	6e-31	59	(U68408) 5' end not determined experimentally [Zea mays]
13523	GM_193_A2_C09_T7	g4038062	BLASTX	194	2e-13	40	(AC005897) putative transposon MuDR [Arabidopsis thaliana]
13524	GM_193_A2_C10_MR	g3777527	BLASTX	148	2e-14	45	(AF053008) gag-pol polyprotein [Glycine max]
13525	GM_193_A2_D05_T7	g4160362	BLASTN	341	1e-10	62	Saccharomyces cerevisiae complete mitochondrial genome
13526	GM_193_A2_D07_MR	g3033389	BLASTX	168	1e-10	39	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
13527	GM_193_A2_D08_MR	g170029	BLASTN	362	2e-09	77	Glycine max cv. Dare nodulin 26 gene fragment.
13528	GM_193_A2_D12_T7	g2995405	BLASTX	315	1e-28	49	(Y12432) polyprotein [Ananas comosus]
13529	GM_193_A2_E01_T7	g4063756	BLASTN	546	1e-17	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
13530	GM_193_A2_E06_MR	g3142328	BLASTN	1458	3e-59	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13531	GM_193_A2_E06_T7	g2462058	BLASTX	257	2e-21	42	(Y13389) reverse transcriptase [Antirrhinum majus]
13532	GM_193_A2_E07_MR	g3142328	BLASTN	773	5e-28	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13533	GM_193_A2_E09_MR	g2462936	BLASTX	150	7e-13	41	(Y12321) open reading frame 2 [Brassica oleracea]
13534	GM_193_A2_F04_MR	g3777527	BLASTX	574	1e-53	83	(AF053008) gag-pol polyprotein [Glycine max]
13535	GM_193_A2_F04_T7	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13536	GM_193_A2_F05_MR	g1236949	BLASTX	222	2e-16	93	(U50075) lipoxygenase L-5 [Glycine max]
13537	GM_193_A2_F07_MR	g4038056	BLASTX	352	3e-30	51	(AC005897) putative transposon [Arabidopsis thaliana]
13538	GM_193_A2_F08_MR	g2129618	BLASTX	264	7e-21	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
13539	GM_193_A2_F12_T7	g21595	BLASTN	699	2e-25	70	S. tuberosum U2-22 gene for U2 snRNA
13540	GM_193_A2_G02_T7	g2792208	BLASTX	141	9e-09	35	(AF032682) NBS-LRR type resistance protein [Hordeum vulgare]
13541	GM_193_A2_G04_MR	g3947735	BLASTX	323	3e-27	51	(AJ009720) NL27 [Solanum tuberosum]
13542	GM_193_A2_G04_T7	g2934885	BLASTX	187	1e-13	94	(L28004) TGACG-motif-binding factor [Glycine max]
13543	GM_193_A2_G07_MR	g3080426	BLASTX	194	2e-13	53	(AL022604) putative protein [Arabidopsis thaliana]
13544	GM_193_A2_H02_T7	g3337361	BLASTX	297	1e-37	65	(AC004481) ankyrin-like protein [Arabidopsis thaliana]
13545	GM_193_A2_H04_T7	g3097320	BLASTN	438	9e-13	70	Glycine max gene for Bd 30K, complete cds
13546	GM_193_A2_H05_MR	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13547	GM_193_A2_H05_T7	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13548	GM_193_A2_H06_MR	g343938	BLASTN	292	2e-14	69	Yeast (S.cerevisiae) mitochondrial Ser-tRNA and ATPase proteolipid genes.
13549	GM_193_A2_H07_MR	g2864621	BLASTX	142	8e-21	38	hypothetical protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13550	GM_193_A2_H08_MR	g2462134	BLASTX	379	3e-34	53	(Y13368) reverse transcriptase [Beta vulgaris]
13551	GM_193_B1_F03_MR	g559263	BLASTN	269	7e-09	58	Saccharomyces cerevisiae mitochondrion transfer RNA- Leu, Gln, Lys, Arg, Gly, Asp, Ser2, Arg2, Ala, Ile, Tyr, Asn genes.
13552	GM_193_B1_F08_MR	g226407	BLASTX	174	6e-19	47	retrotransposon del1-46 [Lilium henryi]
13553	GM_193_B1_G03_MR	g976178	BLASTX	167	8e-12	44	(L47183) reverse transcriptase [Arabidopsis thaliana]
13554	GM_193_B1_G09_MR	g507910	BLASTN	440	3e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13555	GM_193_B2_A01_MR	g2501353	BLASTX	337	1e-29	59	TRANSKETOLASE, CHLOROPLAST (TK) gi 1084440 pir S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) gi 664901 (Z46646) transketolase [Craterostigma plantagineum]
13556	GM_193_B2_A06_MR	g2501353	BLASTX	431	8e-40	66	TRANSKETOLASE, CHLOROPLAST (TK) gi 1084440 pir S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) gi 664901 (Z46646) transketolase [Craterostigma plantagineum]
13557	GM_193_B2_B04_MR	g507910	BLASTN	360	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13558	GM_193_B2_B04_T7	g507910	BLASTN	378	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13559	GM_193_B2_B07_T7	g99922	BLASTX	486	3e-50	72	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13560	GM_193_B2_B10_MR	g3645899	BLASTX	415	6e-37	51	(U68408) 5' end not determined experimentally [Zea mays]
13561	GM_193_B2_C01_T7	g1769898	BLASTX	179	3e-14	37	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13562	GM_193_B2_C02_T7	g18559	BLASTN	362	2e-09	69	G.max gene for catalase
13563	GM_193_B2_C03_T7	g507910	BLASTN	406	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13564	GM_193_B2_C08_T7	g3176811	BLASTN	374	8e-11	63	Homo sapiens allele 18 fragile site locus (FRA10B) minisatellite, 3' sequence
13565	GM_193_B2_D02_MR	g905361	BLASTX	195	9e-14	30	(U22103) gag-protease polyprotein [Glycine max]
13566	GM_193_B2_D04_T7	g2832629	BLASTX	172	2e-11	32	(AL021711) 4-coumarate-CoA ligase - like [Arabidopsis thaliana]
13567	GM_193_B2_D05_T7	g3645899	BLASTX	203	1e-16	44	(U68408) 5' end not determined experimentally [Zea mays]
13568	GM_193_B2_D11_T7	g507910	BLASTN	573	3e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
13569	GM_193_B2_D12_T7	g3319345	BLASTX	179	9e-12	35	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
13570	GM_193_B2_E04_T7	g130582	BLASTX	175	3e-11	33	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
13571	GM_193_B2_E07_T7	g4063760	BLASTX	453	7e-41	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13572	GM_193_B2_E08_MR	g1431738	BLASTN	441	5e-13	87	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
13573	GM_193_B2_E08_T7	g2522230	BLASTX	151	4e-10	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13574	GM_193_B2_E09_T7	g2995405	BLASTX	244	8e-19	44	(Y12432) polyprotein [Ananas comosus]
13575	GM_193_B2_E12_T7	g3645899	BLASTX	397	5e-35	60	(U68408) 5' end not determined experimentally [Zea mays]
13576	GM_193_B2_F04_T7	g2244915	BLASTX	121	6e-11	31	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
13577	GM_193_B2_F05_T7	g3097320	BLASTN	1393	4e-56	79	Glycine max gene for Bd 30K, complete cds
13578	GM_193_B2_F08_T7	g3941729	BLASTN	506	8e-16	62	Homo sapiens chromosome 7 BAC clone F5, complete sequence [Homo sapiens]
13579	GM_193_B2_G02_MR	g130582	BLASTX	350	8e-30	46	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
13580	GM_193_B2_G12_T7	g1769898	BLASTX	256	7e-24	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13581	GM_193_B2_H01_MR	g3777527	BLASTX	275	1e-21	51	(AF053008) gag-pol polyprotein [Glycine max]
13582	GM_193_B2_H01_T7	g100484	BLASTX	398	2e-35	53	hypothetical protein - garden snapdragon
13583	GM_193_B2_H02_MR	g18559	BLASTN	851	2e-38	73	G.max gene for catalase
13584	GM_193_B2_H07_MR	g3777527	BLASTX	456	5e-41	91	(AF053008) gag-pol polyprotein [Glycine max]
13585	GM_193_B2_H10_MR	g905361	BLASTX	247	2e-19	33	(U22103) gag-protease polyprotein [Glycine max]
13586	GM_194_A1_A01_MR	g4102181	BLASTN	367	1e-09	63	Mus musculus phosphoenolpyruvate carboxykinase (PEPCK) gene, complete cds
13587	GM_194_A1_A01_T7	g3645899	BLASTX	199	4e-23	48	(U68408) 5' end not determined experimentally [Zea mays]
13588	GM_194_A1_A11_MR	g130582	BLASTX	129	6e-09	63	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
13589	GM_194_A1_B02_MR	g2995405	BLASTX	220	3e-33	53	(Y12432) polyprotein [Ananas comosus]
13590	GM_194_A1_B08_T7	g4063756	BLASTN	440	8e-13	61	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
13591	GM_194_A1_B09_T7	g4063756	BLASTN	502	1e-15	71	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13592	GM_194_A1_B10_MR	g3377813	BLASTX	254	4e-21	56	(AF076275) No definition line found [Arabidopsis thaliana]
13593	GM_194_A1_C01_T7	g507910	BLASTN	704	3e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
13594	GM_194_A1_C02_T7	g3599418	BLASTN	659	7e-23	73	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
13595	GM_194_A1_C03_MR	g1769897	BLASTX	159	3e-12	35	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13596	GM_194_A1_C04_T7	g1769897	BLASTX	173	6e-36	74	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13597	GM_194_A1_C10_T7	g4063760	BLASTX	203	3e-14	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13598	GM_194_A1_C12_T7	g1172441	BLASTX	284	3e-24	52	POSSIBLE TRANSCRIPTION FACTOR POSF21 gi 99685 pir S21883 DNA-binding protein POSF21 - Arabidopsis thaliana gi 16429 (X61031) posF21 gene product [Arabidopsis thaliana]
13599	GM_194_A1_D01_MR	g1000971	BLASTN	234	4e-10	62	Hansenula wingei mitochondrial DNA, complete sequence
13600	GM_194_A1_D01_T7	g3845197	BLASTN	352	7e-09	60	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
13601	GM_194_A1_D04_MR	g3264544	BLASTN	351	8e-09	61	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
13602	GM_194_A1_D04_T7	g3810596	BLASTX	151	9e-09	40	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
13603	GM_194_A1_D10_MR	g2443320	BLASTX	191	8e-21	40	(D85597) polyprotein [Oryza australiensis]
13604	GM_194_A1_E01_MR	g4038056	BLASTX	321	5e-27	52	(AC005897) putative transposon [Arabidopsis thaliana]
13605	GM_194_A1_E01_T7	g1906603	BLASTN	744	1e-26	66	Zea mays ACCase gene, intron containing colonist1 and colonist2 retrotransposons and reverse transcriptase pseudogene, complete sequence
13606	GM_194_A1_E02_T7	g3777527	BLASTX	773	7e-75	92	(AF053008) gag-pol polyprotein [Glycine max]
13607	GM_194_A1_E04_T7	g2443320	BLASTX	179	2e-16	36	(D85597) polyprotein [Oryza australiensis]
13608	GM_194_A1_E12_MR	g2522230	BLASTX	143	3e-09	29	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13609	GM_194_A1_F01_T7	g3097320	BLASTN	494	2e-15	70	Glycine max gene for Bd 30K, complete cds
13610	GM_194_A1_F07_MR	g507910	BLASTN	406	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13611	GM_194_A1_G02_MR	g1666236	BLASTX	146	6e-09	26	(U76261) unknown [Hordeum vulgare]
13612	GM_194_A1_H02_MR	g13373	BLASTN	472	4e-15	65	Terminal inverted repeat from Paramecium mitochondrion >gi 342968 gb J01432 PARMTDIN1 paramecium species 1 mitochondria dimer initiation region dna.
13613	GM_194_A1_H03_MR	g905361	BLASTX	404	2e-36	97	(U22103) gag-protease polyprotein [Glycine max]
13614	GM_194_A1_H04_MR	g3695395	BLASTX	163	2e-12	53	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
13615	GM_194_A1_H07_MR	g18559	BLASTN	625	3e-21	73	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13616	GM_194_A1_H08_MR	g2522227	BLASTX	200	2e-15	51	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
13617	GM_194_A2_A05_MR	g3097320	BLASTN	1001	3e-38	79	Glycine max gene for Bd 30K, complete cds
13618	GM_194_A2_A05_T7	g2808682	BLASTX	155	3e-09	39	(AJ002235) Hcr9-4C [Lycopersicon hirsutum]
13619	GM_194_A2_A06_MR	g4150930	BLASTN	441	7e-13	60	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
13620	GM_194_A2_A08_MR	g2522229	BLASTN	585	2e-19	64	Vicia faba mRNA expressed from retrotransposon-like gene
13621	GM_194_A2_A12_T7	g3319372	BLASTX	243	2e-18	37	(AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]
13622	GM_194_A2_B01_MR	g336279	BLASTN	368	1e-09	61	Apis mellifera ligustica complete mitochondrial genome
13623	GM_194_A2_B01_T7	g3810596	BLASTX	275	5e-22	41	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
13624	GM_194_A2_B02_T7	g3777527	BLASTX	167	3e-10	32	(AF053008) gag-pol polyprotein [Glycine max]
13625	GM_194_A2_B04_MR	g3319362	BLASTX	306	3e-25	47	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
13626	GM_194_A2_B06_T7	g1666236	BLASTX	228	3e-18	34	(U76261) unknown [Hordeum vulgare]
13627	GM_194_A2_B07_MR	g1644291	BLASTX	170	8e-18	69	(Z73295) receptor-like protein kinase [Catharanthus roseus]
13628	GM_194_A2_B11_T7	g3142328	BLASTN	2096	2e-88	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13629	GM_194_A2_C02_MR	g2264315	BLASTN	355	5e-09	74	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana]
13630	GM_194_A2_C04_MR	g3777527	BLASTX	202	6e-29	50	(AF053008) gag-pol polyprotein [Glycine max]
13631	GM_194_A2_C05_MR	g3097320	BLASTN	387	2e-10	73	Glycine max gene for Bd 30K, complete cds
13632	GM_194_A2_C06_T7	g3097320	BLASTN	528	7e-17	69	Glycine max gene for Bd 30K, complete cds
13633	GM_194_A2_D02_MR	g170065	BLASTN	393	8e-11	75	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds.
13634	GM_194_A2_D04_MR	g507910	BLASTN	342	7e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13635	GM_194_A2_D04_T7	g507910	BLASTN	590	5e-20	86	Glycine max BSR-101 satellite SB92 genomic sequence.
13636	GM_194_A2_D05_MR	g3171875	BLASTN	372	9e-10	60	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.1...
13637	GM_194_A2_D07_MR	g2522228	BLASTX	632	4e-61	71	(AB007466) reverse transcriptase-like protein [Vicia faba]
13638	GM_194_A2_D09_MR	g507910	BLASTN	580	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
13639	GM_194_A2_E01_MR	g3777527	BLASTX	236	3e-21	41	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13640	GM_194_A2_E04_MR	g421955	BLASTX	223	1e-31	63	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
13641	GM_194_A2_E06_MR	g18695	BLASTN	354	4e-09	67	Soybean nodulin 22 gene
13642	GM_194_A2_E10_MR	g4063760	BLASTX	242	2e-18	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13643	GM_194_A2_F02_MR	g18559	BLASTN	740	2e-52	74	G.max gene for catalase
13644	GM_194_A2_F03_MR	g905361	BLASTX	437	3e-40	97	(U22103) gag-protease polyprotein [Glycine max]
13645	GM_194_A2_F03_T7	g507910	BLASTN	411	6e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13646	GM_194_A2_F08_T7	g4063760	BLASTX	448	2e-40	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13647	GM_194_A2_F09_MR	g1769898	BLASTX	348	7e-43	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13648	GM_194_A2_G02_MR	g1246823	BLASTX	162	4e-14	84	(X89865) unknown gene product [Phoenix dactylifera]
13649	GM_194_A2_G04_MR	g4140712	BLASTX	208	4e-16	62	(AF110183) putative integrase [Oryza sativa]
13650	GM_194_A2_G11_MR	g18559	BLASTN	1053	1e-40	74	G.max gene for catalase
13651	GM_194_A2_H12_MR	g507910	BLASTN	484	3e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
13652	GM_194_B1_A01_MR	g3947719	BLASTX	237	3e-19	92	(AJ012653) ribosomal protein S28 [Prunus persica] >gi 3947721 gnl PID e1356377 (AJ012654) ribosomal protein S28 [Prunus persica] >gi 3947723 gnl PID e1356379 (AJ012655) ribosomal protein S28 [Prunus persica]
13653	GM_194_B1_A05_MR	g2522230	BLASTX	157	9e-11	34	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13654	GM_194_B1_A08_MR	g2462834	BLASTX	333	2e-29	47	(AF000657) hypothetical protein [Arabidopsis thaliana]
13655	GM_194_B1_B02_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13656	GM_194_B1_B02_T7	g507910	BLASTN	381	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13657	GM_194_B1_B04_T7	g1931642	BLASTX	316	8e-27	56	(U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]
13658	GM_194_B1_B06_MR	g905361	BLASTX	276	2e-22	66	(U22103) gag-protease polyprotein [Glycine max]
13659	GM_194_B1_B08_T7	g3097320	BLASTN	940	2e-35	74	Glycine max gene for Bd 30K, complete cds
13660	GM_194_B1_B09_T7	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
13661	GM_194_B1_C01_MR	g3097320	BLASTN	1125	6e-44	79	Glycine max gene for Bd 30K, complete cds
13662	GM_194_B1_C02_T7	g3426334	BLASTN	548	8e-18	64	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
13663	GM_194_B1_C06_T7	g2245073	BLASTN	353	2e-10	61	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8
13664	GM_194_B1_C11_MR	g2462935	BLASTX	307	3e-25	45	(Y12321) open reading frame 1 [Brassica oleracea]
13665	GM_194_B1_C11_T7	g343840	BLASTN	427	1e-12	62	Yeast (S.cerevisiae) strain B mitochondrial petite mutant b-1 ori1 region.
13666	GM_194_B1_D01_MR	g2586082	BLASTX	305	6e-25	50	(U72725) retrofit [Oryza longistaminata]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13667	GM_194_B1_D09_T7	g99729	BLASTX	363	1e-32	46	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
13668	GM_194_B1_D12_MR	g4006828	BLASTX	219	4e-16	31	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
13669	GM_194_B1_D12_T7	g629693	BLASTX	150	3e-09	26	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
13670	GM_194_B1_E03_MR	g99922	BLASTX	392	1e-35	58	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13671	GM_194_B1_E04_T7	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
13672	GM_194_B1_E10_MR	g3033400	BLASTX	221	5e-16	79	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]
13673	GM_194_B1_F02_MR	g322660	BLASTX	123	6e-19	48	S-receptor kinase-related protein - Chinese kale gi 17913 (Z18861) S-receptor kinase related protein [Brassica oleracea]
13674	GM_194_B1_F02_T7	g1666236	BLASTX	192	4e-14	32	(U76261) unknown [Hordeum vulgare]
13675	GM_194_B1_F03_MR	g3777527	BLASTX	228	9e-17	41	(AF053008) gag-pol polyprotein [Glycine max]
13676	GM_194_B1_F07_MR	g3282521	BLASTX	390	2e-39	53	tyrosine/dopa decarboxylase [Papaver somniferum]
13677	GM_194_B1_F10_T7	g905361	BLASTX	567	4e-57	90	(U22103) gag-protease polyprotein [Glycine max]
13678	GM_194_B1_F11_T7	g3142328	BLASTN	839	3e-36	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13679	GM_194_B1_G03_MR	g1769899	BLASTX	282	2e-34	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13680	GM_194_B1_G03_T7	g99922	BLASTX	466	2e-43	68	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13681	GM_194_B1_G05_T7	g2995405	BLASTX	223	1e-16	41	(Y12432) polyprotein [Ananas comosus]
13682	GM_194_B1_G09_MR	g2765093	BLASTX	159	5e-10	63	(Y10983) putative cytochrome P450 [Glycine max]
13683	GM_194_B1_G12_MR	g4063760	BLASTX	304	6e-25	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13684	GM_194_B1_H03_T7	g3142328	BLASTN	766	1e-27	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13685	GM_194_B1_H04_MR	g2911052	BLASTX	156	3e-21	56	(AL021961) putative protein [Arabidopsis thaliana]
13686	GM_194_B1_H12_T7	g3142328	BLASTN	633	1e-21	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13687	GM_195_A1_A03_MR	g2995405	BLASTX	226	8e-17	46	(Y12432) polyprotein [Ananas comosus]
13688	GM_195_A1_A04_MR	g1769897	BLASTX	126	2e-12	30	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13689	GM_195_A1_A05_MR	g507910	BLASTN	446	1e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13690	GM_195_A1_A09_MR	g2995405	BLASTX	223	1e-23	49	(Y12432) polyprotein [Ananas comosus]
13691	GM_195_A1_A10_MR	g2129618	BLASTX	193	3e-13	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13692	GM_195_A1_B01_MR	g507910	BLASTN	423	2e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13693	GM_195_A1_B08_MR	g99922	BLASTX	717	4e-70	86	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13694	GM_195_A1_B08_T7	g1167523	BLASTX	241	9e-22	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
13695	GM_195_A1_B09_MR	g3142328	BLASTN	1715	6e-71	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13696	GM_195_A1_B10_MR	g531389	BLASTX	173	7e-11	41	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
13697	GM_195_A1_B11_MR	g3021268	BLASTX	384	2e-33	52	(AL022347) putative protein [Arabidopsis thaliana]
13698	GM_195_A1_B12_MR	g3264544	BLASTN	440	8e-13	64	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
13699	GM_195_A1_C01_T7	g1769898	BLASTX	274	3e-22	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13700	GM_195_A1_C08_MR	g99688	BLASTX	461	6e-43	93	translation elongation factor eEF-1 alpha chain (gene A4) - Arabidopsis thaliana gi 295789 (X16432) elongation factor 1-alpha [Arabidopsis thaliana]
13701	GM_195_A1_C09_MR	g905361	BLASTX	667	9e-65	97	(U22103) gag-protease polyprotein [Glycine max]
13702	GM_195_A1_D02_MR	g2822134	BLASTN	386	2e-10	61	Human Chromosome X, complete sequence [Homo sapiens]
13703	GM_195_A1_D04_T7	g507910	BLASTN	481	4e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
13704	GM_195_A1_D06_MR	g3777527	BLASTX	559	1e-52	97	(AF053008) gag-pol polyprotein [Glycine max]
13705	GM_195_A1_D06_T7	g507910	BLASTN	659	4e-23	84	Glycine max BSR-101 satellite SB92 genomic sequence.
13706	GM_195_A1_D08_T7	g507910	BLASTN	522	6e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
13707	GM_195_A1_D09_T7	g1061420	BLASTX	466	2e-43	87	(U38965) p-type H+-ATPase [Vicia faba]
13708	GM_195_A1_E02_MR	g100484	BLASTX	250	8e-22	44	hypothetical protein - garden snapdragon
13709	GM_195_A1_F02_T7	g1658455	BLASTX	129	2e-12	38	(U75247) reverse transcriptase [Gossypium barbadense]
13710	GM_195_A1_F05_T7	g99922	BLASTX	349	4e-31	69	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13711	GM_195_A1_G02_MR	g3080375	BLASTX	244	3e-19	42	(AL022580) putative protein [Arabidopsis thaliana]
13712	GM_195_A1_G04_MR	g4063760	BLASTX	292	1e-23	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13713	GM_195_A1_G04_T7	g3449326	BLASTN	616	9e-21	67	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]
13714	GM_195_A1_G08_MR	g1076758	BLASTX	176	1e-11	59	heat-shock protein precursor - rye gi 2130093 pir S65776 heat-shock protein, 82K, precursor - rye gi 556673 (Z30243) heat-shock protein [Secale cereale]
13715	GM_195_A1_G10_MR	g3273150	BLASTN	366	1e-09	64	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-81, complete sequence [Plasmodium falciparum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13716	GM_195_A1_G11_T7	g3142328	BLASTN	628	2e-21	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13717	GM_195_A1_H12_MR	g507910	BLASTN	697	7e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
13718	GM_195_A2_A04_MR	g4063760	BLASTX	472	7e-43	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13719	GM_195_A2_B04_MR	g905361	BLASTX	104	2e-10	28	(U22103) gag-protease polyprotein [Glycine max]
13720	GM_195_A2_C03_MR	g1167523	BLASTX	419	4e-37	54	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
13721	GM_195_A2_C05_MR	g3319362	BLASTX	163	5e-10	43	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
13722	GM_195_A2_D01_MR	g2288997	BLASTX	318	1e-26	63	(AC002335) hypothetical protein [Arabidopsis thaliana]
13723	GM_195_A2_D04_MR	g3377855	BLASTX	145	6e-09	38	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
13724	GM_195_A2_D05_MR	g507910	BLASTN	500	6e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
13725	GM_195_A2_D11_MR	g2522228	BLASTX	451	7e-42	65	(AB007466) reverse transcriptase-like protein [Vicia faba]
13726	GM_195_A2_E02_MR	g3820757	BLASTN	359	2e-09	60	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
13727	GM_195_A2_E11_MR	g3097320	BLASTN	450	2e-13	73	Glycine max gene for Bd 30K, complete cds
13728	GM_195_A2_F01_MR	g507910	BLASTN	386	8e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13729	GM_195_A2_G04_MR	g18559	BLASTN	547	9e-18	74	G.max gene for catalase
13730	GM_195_A2_H05_MR	g507910	BLASTN	384	9e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13731	GM_196_A1_A03_MR	g2828780	BLASTN	393	1e-10	62	Homo sapiens chromosome 17, clone 289A8, complete sequence [Homo sapiens]
13732	GM_196_A1_A04_MR	g3386534	BLASTX	263	1e-21	42	(AF078934) mariner transposase [Glycine max]
13733	GM_196_A1_A07_MR	g1666236	BLASTX	227	3e-18	34	(U76261) unknown [Hordeum vulgare]
13734	GM_196_A1_A10_MR	g3287269	BLASTN	509	5e-16	67	S.tuberosum mRNA for protein involved in starch metabolism
13735	GM_196_A1_B02_T7	g3171879	BLASTN	361	3e-09	65	Homo sapiens DNA sequence from PAC 357I16 on chromosome 1p36.13. Contains GSSs, genomic marker D1S449 and a CA repeat polymorphism, complete sequence [Homo sapiens]
13736	GM_196_A1_B03_MR	g3097320	BLASTN	481	1e-14	69	Glycine max gene for Bd 30K, complete cds
13737	GM_196_A1_B03_T7	g18559	BLASTN	1081	5e-42	74	G.max gene for catalase
13738	GM_196_A1_C04_T7	g3142328	BLASTN	864	4e-32	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13739	GM_196_A1_C06_MR	g3097320	BLASTN	866	3e-32	79	Glycine max gene for Bd 30K, complete cds
13740	GM_196_A1_C11_MR	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
13741	GM_196_A1_C12_MR	g507910	BLASTN	385	9e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13742	GM_196_A1_D06_T7	g2522228	BLASTX	83	6e-10	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
13743	GM_196_A1_D07_T7	g18700	BLASTN	1105	1e-43	80	Soybean nodulin-23 gene
13744	GM_196_A1_D12_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13745	GM_196_A1_D12_T7	g507910	BLASTN	373	3e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13746	GM_196_A1_E05_MR	g3097320	BLASTN	466	5e-14	73	Glycine max gene for Bd 30K, complete cds
13747	GM_196_A1_E07_T7	g3687234	BLASTX	229	5e-17	44	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
13748	GM_196_A1_F01_MR	g170606	BLASTN	417	5e-12	68	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
13749	GM_196_A1_F05_MR	g3776559	BLASTX	393	1e-35	75	(AC005388) Strong similarity to gene F14J9.26 gi 3482933 cdc2 protein kinase homolog from A. thaliana BAC gb AC003970. ESTs gb Z35332 and gb F19907 come from this gene. [Arabidopsis thaliana]
13750	GM_196_A1_F06_MR	g3599418	BLASTN	979	2e-37	79	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
13751	GM_196_A1_F11_MR	g3395432	BLASTX	146	1e-21	80	(AC004683) unknown protein [Arabidopsis thaliana]
13752	GM_196_A1_G11_T7	g3142328	BLASTN	1112	2e-43	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13753	GM_196_A1_G12_MR	g4063756	BLASTN	707	7e-25	70	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
13754	GM_196_A1_H01_MR	g507910	BLASTN	488	2e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
13755	GM_196_A1_H07_T7	g2522230	BLASTX	209	3e-20	36	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13756	GM_196_A1_H08_MR	g1669680	BLASTN	391	1e-10	65	Human DNA sequence from PAC 293E14 contains ESTs, STS
13757	GM_196_A2_A04_MR	g3659406	BLASTN	375	7e-10	65	Homo sapiens Xp22 bins 29-30 BAC GSHB-227L7 (Genome Systems Human BAC Library) complete sequence [Homo sapiens]
13758	GM_196_A2_A05_MR	g3645899	BLASTX	402	1e-35	61	(U68408) 5' end not determined experimentally [Zea mays]
13759	GM_196_A2_A07_T7	g2827635	BLASTX	243	7e-19	52	(AL021636) predicted protein [Arabidopsis thaliana]
13760	GM_196_A2_A10_T7	g22491	BLASTX	128	2e-14	39	(X01380) ORF2 [Zea mays]
13761	GM_196_A2_B02_MR	g905361	BLASTX	206	6e-15	31	(U22103) gag-protease polyprotein [Glycine max]
13762	GM_196_A2_B02_T7	g169157	BLASTN	367	1e-09	64	Pisum sativum serine hydroxymethyltransferase mRNA, complete cds.
13763	GM_196_A2_B08_MR	g1705734	BLASTX	179	4e-16	81	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM 2 (CDPK 2) gi 1362176 pir S56652 probable calcium-dependent protein kinase (clone OSCPK2) - rice gi 587498 (X81394) calcium-dependent protein kinase [Oryza sativa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13764	GM_196_A2_B11_MR	g99922	BLASTX	209	4e-16	54	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13765	GM_196_A2_C01_MR	g3645899	BLASTX	191	6e-13	57	(U68408) 5' end not determined experimentally [Zea mays]
13766	GM_196_A2_C02_T7	g3540184	BLASTX	259	3e-20	55	(AC004122) Similar to endoxylanases [Arabidopsis thaliana]
13767	GM_196_A2_D02_T7	g2522228	BLASTX	238	2e-26	64	(AB007466) reverse transcriptase-like protein [Vicia faba]
13768	GM_196_A2_D06_MR	g4038056	BLASTX	285	4e-23	43	(AC005897) putative transposon [Arabidopsis thaliana]
13769	GM_196_A2_D07_MR	g507910	BLASTN	451	9e-14	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13770	GM_196_A2_E12_MR	g4063760	BLASTX	209	3e-32	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13771	GM_196_A2_F02_MR	g18559	BLASTN	680	8e-24	76	G.max gene for catalase
13772	GM_196_A2_F07_MR	g3283026	BLASTX	241	1e-18	42	putative transposase [Arabidopsis thaliana]
13773	GM_196_A2_F07_T7	g1769897	BLASTX	136	2e-13	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13774	GM_196_A2_G02_MR	g507910	BLASTN	372	3e-10	76	Glycine max BSR-101 satellite SB92 genomic sequence.
13775	GM_196_A2_G02_T7	g507910	BLASTN	341	8e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13776	GM_196_A2_G04_T7	g3492889	BLASTN	460	1e-13	70	Homo sapiens chromosome 17, clone hRPK.746_E_8, complete sequence [Homo sapiens]
13777	GM_196_A2_G07_MR	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13778	GM_196_A2_G07_T7	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13779	GM_196_A2_G10_T7	g4063760	BLASTX	493	4e-45	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13780	GM_196_A2_H10_MR	g4063760	BLASTX	199	9e-14	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13781	GM_196_B1_A02_MR	g3426334	BLASTN	437	9e-13	64	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
13782	GM_196_B1_B10_MR	g4038056	BLASTX	229	4e-17	45	(AC005897) putative transposon [Arabidopsis thaliana]
13783	GM_196_B1_D08_MR	g2443320	BLASTX	196	2e-13	49	(D85597) polyprotein [Oryza australiensis]
13784	GM_196_B1_F06_MR	g1769898	BLASTX	172	7e-14	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13785	GM_196_B1_H01_MR	g3283026	BLASTX	144	5e-13	36	putative transposase [Arabidopsis thaliana]
13786	GM_196_B1_H06_MR	g2462134	BLASTX	304	7e-26	47	(Y13368) reverse transcriptase [Beta vulgaris]
13787	GM_196_B2_A02_MR	g3777527	BLASTX	516	2e-50	90	(AF053008) gag-pol polyprotein [Glycine max]
13788	GM_196_B2_A08_MR	g3377813	BLASTX	199	3e-15	50	(AF076275) No definition line found [Arabidopsis thaliana]
13789	GM_196_B2_A08_T7	g539602	BLASTX	216	3e-16	61	glycine hydroxymethyltransferase (EC 2.1.2.1) precursor, mitochondrial - human (fragment) gi 703093 (L11932) serine hydroxymethyltransferase [Homo sapiens]
13790	GM_196_B2_B05_T7	g507910	BLASTN	481	4e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
13791	GM_196_B2_B07_MR	g507910	BLASTN	348	4e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13792	GM_196_B2_B10_MR	g2129709	BLASTX	253	2e-19	40	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
13793	GM_196_B2_B12_MR	g82309	BLASTX	187	6e-14	55	myb protein 315 - garden snapdragon

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13794	GM_196_B2_C12_MR	g4150930	BLASTN	428	3e-12	61	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
13795	GM_196_B2_D07_T7	g3097320	BLASTN	381	3e-10	68	Glycine max gene for Bd 30K, complete cds
13796	GM_196_B2_D10_MR	g507910	BLASTN	574	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
13797	GM_196_B2_E01_MR	g4150930	BLASTN	479	1e-14	67	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
13798	GM_196_B2_F01_MR	g18737	BLASTN	349	8e-09	69	Glycine max RPRP3 gene for repetitive proline-rich protein 3
13799	GM_196_B2_F04_MR	g18559	BLASTN	363	2e-09	70	G.max gene for catalase
13800	GM_196_B2_F08_MR	g2190551	BLASTX	205	5e-15	60	(AC001229) Similar to C. elegans hypothetical protein K07C5.6 (gb Z71181). ESTs gb H36844,gb AA394956 come from this gene. [Arabidopsis thaliana]
13801	GM_196_B2_F10_MR	g3142328	BLASTN	1083	4e-42	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13802	GM_196_B2_G02_MR	g3097320	BLASTN	450	2e-13	69	Glycine max gene for Bd 30K, complete cds
13803	GM_196_B2_G08_MR	g3777527	BLASTX	621	1e-58	94	(AF053008) gag-pol polyprotein [Glycine max]
13804	GM_196_B2_H07_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13805	GM_196_B2_H12_T7	g507910	BLASTN	467	2e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13806	GM_197_A1_A02_MR	g3319362	BLASTX	163	4e-10	43	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
13807	GM_197_A1_A08_T7	g3097320	BLASTN	553	5e-18	74	Glycine max gene for Bd 30K, complete cds
13808	GM_197_A1_A09_T7	g2586082	BLASTX	331	1e-27	49	(U72725) retrofit [Oryza longistaminata]
13809	GM_197_A1_A12_T7	g4063760	BLASTX	562	2e-52	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13810	GM_197_A1_B01_MR	g3859610	BLASTN	571	9e-19	64	Arabidopsis thaliana BAC T9E19
13811	GM_197_A1_B02_MR	g4006831	BLASTX	234	2e-17	39	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
13812	GM_197_A1_B03_MR	g4063760	BLASTX	166	3e-10	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13813	GM_197_A1_B06_MR	g507910	BLASTN	423	2e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
13814	GM_197_A1_B06_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13815	GM_197_A1_B12_MR	g2462134	BLASTX	242	5e-19	34	(Y13368) reverse transcriptase [Beta vulgaris]
13816	GM_197_A1_C01_T7	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
13817	GM_197_A1_C02_T7	g4115365	BLASTX	175	4e-11	39	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
13818	GM_197_A1_C04_T7	g507910	BLASTN	406	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13819	GM_197_A1_C05_MR	g3777527	BLASTX	392	4e-34	47	(AF053008) gag-pol polyprotein [Glycine max]
13820	GM_197_A1_C05_T7	g3860247	BLASTX	150	2e-21	90	(AC005824) unknown protein [Arabidopsis thaliana]
13821	GM_197_A1_C06_MR	g1666236	BLASTX	162	9e-11	29	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13822	GM_197_A1_C07_T7	g1171978	BLASTX	503	2e-47	78	POLYADENYLATE-BINDING PROTEIN 2 (POLY(A) BINDING PROTEIN 2) (PABP 2) gi 304109 (L19418) poly(A)-binding protein [Arabidopsis thaliana] gi 2911051 gnl PID e1253339 (AL021961) poly(A)-binding protein [Arabidopsis thaliana]
13823	GM_197_A1_C09_T7	g2522230	BLASTX	223	1e-17	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13824	GM_197_A1_C10_MR	g1769897	BLASTX	371	2e-33	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13825	GM_197_A1_C12_MR	g2522230	BLASTX	205	1e-24	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13826	GM_197_A1_D01_MR	g507910	BLASTN	384	9e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13827	GM_197_A1_D01_T7	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13828	GM_197_A1_D05_MR	g3377848	BLASTX	219	2e-22	56	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
13829	GM_197_A1_D07_MR	g3894211	BLASTN	438	9e-13	62	Homo sapiens PAC clone DJ0888A21 from 7q31, complete sequence [Homo sapiens]
13830	GM_197_A1_D09_MR	g3142328	BLASTN	1789	2e-74	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13831	GM_197_A1_E02_MR	g507910	BLASTN	513	1e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
13832	GM_197_A1_E03_MR	g2801423	BLASTN	670	3e-23	66	Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence [Homo sapiens]
13833	GM_197_A1_E05_MR	g3510340	BLASTN	361	3e-09	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]
13834	GM_197_A1_E11_T7	g3142328	BLASTN	1987	2e-83	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13835	GM_197_A1_F01_MR	g3947735	BLASTX	176	1e-11	37	(AJ009720) NL27 [Solanum tuberosum]
13836	GM_197_A1_F02_MR	g2522230	BLASTX	289	1e-24	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13837	GM_197_A1_F07_MR	g4115365	BLASTX	160	4e-13	32	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
13838	GM_197_A1_F12_T7	g18559	BLASTN	845	3e-31	77	G.max gene for catalase
13839	GM_197_A1_G01_T7	g3005576	BLASTX	210	1e-15	51	(AF047718) putative high affinity nitrate transporter; GmNRT2 [Glycine max]
13840	GM_197_A1_G05_T7	g4092470	BLASTN	409	2e-11	64	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
13841	GM_197_A1_G06_T7	g3142328	BLASTN	1834	2e-76	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13842	GM_197_A1_G08_T7	g3695395	BLASTX	267	2e-21	53	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
13843	GM_197_A1_H02_T7	g507910	BLASTN	415	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13844	GM_197_A1_H03_T7	g507910	BLASTN	366	6e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
13845	GM_197_A1_H04_T7	g2764526	BLASTN	379	4e-10	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
13846	GM_197_A2_A03_T7	g100484	BLASTX	289	9e-24	45	hypothetical protein - garden snapdragon
13847	GM_197_A2_A08_MR	g3845197	BLASTN	446	4e-13	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
13848	GM_197_A2_A10_T7	g13619	BLASTN	385	2e-11	60	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
13849	GM_197_A2_B01_T7	g2342684	BLASTX	392	1e-35	53	(AC000106) F7G19.14 [Arabidopsis thaliana]
13850	GM_197_A2_B02_MR	g1666236	BLASTX	193	3e-14	31	(U76261) unknown [Hordeum vulgare]
13851	GM_197_A2_B04_T7	g3461840	BLASTX	171	3e-14	27	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
13852	GM_197_A2_B05_T7	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13853	GM_197_A2_B06_MR	g3046852	BLASTN	462	8e-14	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQJ16, complete sequence [Arabidopsis thaliana]
13854	GM_197_A2_B06_T7	g3777527	BLASTX	313	9e-26	42	(AF053008) gag-pol polyprotein [Glycine max]
13855	GM_197_A2_B07_MR	g3319362	BLASTX	368	6e-32	47	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
13856	GM_197_A2_B08_MR	g3319345	BLASTX	172	5e-11	34	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
13857	GM_197_A2_B09_T7	g507910	BLASTN	374	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
13858	GM_197_A2_C01_MR	g3777527	BLASTX	209	3e-25	34	(AF053008) gag-pol polyprotein [Glycine max]
13859	GM_197_A2_C03_T7	g170080	BLASTN	407	2e-11	69	Soybean seed lectin gene transposable element tgm1.
13860	GM_197_A2_C04_T7	g4160362	BLASTN	295	1e-12	67	Saccharomyces cerevisiae complete mitochondrial genome
13861	GM_197_A2_C05_T7	g2864621	BLASTX	133	4e-12	30	hypothetical protein [Arabidopsis thaliana]
13862	GM_197_A2_C08_MR	g1769903	BLASTX	150	4e-14	79	(X95738) proline transporter 2 [Arabidopsis thaliana]
13863	GM_197_A2_D01_MR	g3097320	BLASTN	461	8e-14	70	Glycine max gene for Bd 30K, complete cds
13864	GM_197_A2_D02_MR	g905361	BLASTX	883	1e-87	95	(U22103) gag-protease polyprotein [Glycine max]
13865	GM_197_A2_D03_T7	g3097320	BLASTN	772	6e-28	78	Glycine max gene for Bd 30K, complete cds
13866	GM_197_A2_D05_T7	g3845094	BLASTN	398	6e-11	60	Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence
13867	GM_197_A2_D09_T7	g4063760	BLASTX	231	4e-17	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13868	GM_197_A2_D11_MR	g1769897	BLASTX	534	1e-56	80	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13869	GM_197_A2_D11_T7	g905361	BLASTX	838	6e-83	98	(U22103) gag-protease polyprotein [Glycine max]
13870	GM_197_A2_E04_MR	g2462134	BLASTX	291	2e-24	43	(Y13368) reverse transcriptase [Beta vulgaris]
13871	GM_197_A2_E07_MR	g2275215	BLASTX	207	7e-16	64	(AC002337) hypothetical protein [Arabidopsis thaliana]
13872	GM_197_A2_E08_MR	g1769898	BLASTX	288	8e-24	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13873	GM_197_A2_E09_T7	g4063760	BLASTX	264	1e-20	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13874	GM_197_A2_E11_T7	g507910	BLASTN	341	8e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
13875	GM_197_A2_G03_MR	g3947733	BLASTX	182	2e-12	36	(AJ009719) NL25 [Solanum tuberosum]
13876	GM_197_A2_H01_MR	g454847	BLASTN	439	7e-13	63	Glycine max ribosomal protein S11 gene, complete cds
13877	GM_197_A2_H04_MR	g2462058	BLASTX	262	7e-22	60	(Y13389) reverse transcriptase [Antirrhinum majus]
13878	GM_197_A2_H07_MR	g3548816	BLASTX	156	5e-09	42	(AC005313) LEA-like protein [Arabidopsis thaliana]
13879	GM_197_B1_B03_T7	g3645899	BLASTX	153	6e-09	53	(U68408) 5' end not determined experimentally [Zea mays]
13880	GM_197_B1_B06_T7	g4063760	BLASTX	251	3e-19	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13881	GM_197_B1_C03_T7	g507910	BLASTN	351	3e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13882	GM_197_B1_C04_T7	g18559	BLASTN	731	4e-26	86	G.max gene for catalase
13883	GM_197_B1_E04_T7	g3777527	BLASTX	496	2e-66	93	(AF053008) gag-pol polyprotein [Glycine max]
13884	GM_197_B1_G01_T7	g100484	BLASTX	276	2e-22	46	hypothetical protein - garden snapdragon
13885	GM_197_B1_G12_T7	g18559	BLASTN	382	3e-10	72	G.max gene for catalase
13886	GM_197_B1_H07_T7	g1666236	BLASTX	107	3e-10	26	(U76261) unknown [Hordeum vulgare]
13887	GM_198_A2_B04_T7	g3777527	BLASTX	209	1e-14	51	(AF053008) gag-pol polyprotein [Glycine max]
13888	GM_198_A2_B09_MR	g100484	BLASTX	224	9e-17	51	hypothetical protein - garden snapdragon
13889	GM_198_A2_B12_MR	g3250737	BLASTN	367	1e-09	64	Arabidopsis thaliana ASKbeta gene, complete CDS
13890	GM_198_A2_C01_T7	g3777527	BLASTX	181	1e-11	91	(AF053008) gag-pol polyprotein [Glycine max]
13891	GM_198_A2_C04_T7	g4063760	BLASTX	162	5e-24	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13892	GM_198_A2_D01_T7	g4038056	BLASTX	186	2e-12	46	(AC005897) putative transposon [Arabidopsis thaliana]
13893	GM_198_A2_D03_MR	g3250737	BLASTN	370	1e-09	65	Arabidopsis thaliana ASKbeta gene, complete CDS
13894	GM_198_A2_E04_T7	g3142328	BLASTN	668	3e-23	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13895	GM_198_A2_E05_MR	g18559	BLASTN	477	1e-14	71	G.max gene for catalase
13896	GM_198_A2_E11_T7	g2351061	BLASTN	411	2e-11	71	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAF19
13897	GM_198_A2_F07_T7	g3142328	BLASTN	688	4e-24	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13898	GM_198_A2_G11_T7	g3688600	BLASTX	278	2e-22	64	(AB009030) beta-Amyrin Synthase [Panax ginseng]
13899	GM_198_A2_G12_T7	g2264320	BLASTN	352	7e-09	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13900	GM_198_A2_H11_MR	g3142328	BLASTN	509	5e-16	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13901	GM_198_B1_A02_MR	g905361	BLASTX	122	2e-13	28	(U22103) gag-protease polyprotein [Glycine max]
13902	GM_198_B1_A08_MR	g905361	BLASTX	183	2e-12	31	(U22103) gag-protease polyprotein [Glycine max]
13903	GM_198_B1_A09_MR	g2065531	BLASTX	508	6e-48	70	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
13904	GM_198_B1_A10_MR	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
13905	GM_198_B1_B02_MR	g18559	BLASTN	739	2e-26	84	G.max gene for catalase
13906	GM_198_B1_B12_MR	g3645899	BLASTX	268	4e-21	60	(U68408) 5' end not determined experimentally [Zea mays]
13907	GM_198_B1_D03_MR	g2522228	BLASTX	193	8e-22	66	(AB007466) reverse transcriptase-like protein [Vicia faba]
13908	GM_198_B1_D07_MR	g18559	BLASTN	906	5e-34	73	G.max gene for catalase
13909	GM_198_B1_E02_MR	g3777527	BLASTX	535	2e-49	94	(AF053008) gag-pol polyprotein [Glycine max]
13910	GM_198_B1_E11_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13911	GM_198_B1_F03_MR	g3097320	BLASTN	774	5e-28	81	Glycine max gene for Bd 30K, complete cds
13912	GM_198_B1_F06_MR	g18559	BLASTN	512	4e-16	70	G.max gene for catalase
13913	GM_198_B1_F08_MR	g1813978	BLASTN	342	2e-09	65	M.acuminata gene encoding putative partial protein homologous to pol gene
13914	GM_198_B1_G04_MR	g3281868	BLASTX	311	4e-26	54	(AL031004) putative protein [Arabidopsis thaliana]
13915	GM_198_B1_G07_MR	g2760316	BLASTN	507	7e-16	71	The sequence of BAC F1N21 from Arabidopsis thaliana chromosome 1, complete sequence [Arabidopsis thaliana]
13916	GM_198_B1_G12_MR	g3337396	BLASTN	462	8e-14	67	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence [Homo sapiens]
13917	GM_198_B1_H11_MR	g342965	BLASTN	355	2e-09	61	paramecium species 7,227 mt dna dimer: replication init. region.
13918	GM_199_A1_A03_T7	g2997694	BLASTX	183	1e-13	31	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
13919	GM_199_A1_B07_T7	g507910	BLASTN	350	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13920	GM_199_A1_C05_T7	g3282159	BLASTN	495	2e-15	65	Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence [Homo sapiens]
13921	GM_199_A1_C08_MR	g2769655	BLASTN	394	9e-11	62	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
13922	GM_199_A1_D03_T7	g507910	BLASTN	367	6e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
13923	GM_199_A1_D08_MR	g18559	BLASTN	776	4e-28	71	G.max gene for catalase
13924	GM_199_A1_D09_T7	g507910	BLASTN	566	6e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
13925	GM_199_A1_D12_T7	g507910	BLASTN	389	6e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13926	GM_199_A1_G02_T7	g2121303	BLASTN	380	4e-10	60	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
13927	GM_199_A1_G06_MR	g2995405	BLASTX	151	7e-09	55	(Y12432) polyprotein [Ananas comosus]
13928	GM_199_A1_G09_T7	g170606	BLASTN	500	8e-16	67	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
13929	GM_199_A1_H07_T7	g507910	BLASTN	492	1e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
13930	GM_199_A1_H10_MR	g3142328	BLASTN	867	3e-32	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13931	GM_199_A2_A11_MR	g905361	BLASTX	307	8e-26	87	(U22103) gag-protease polyprotein [Glycine max]
13932	GM_199_A2_C01_MR	g3142328	BLASTN	561	2e-18	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13933	GM_199_A2_D02_MR	g507910	BLASTN	485	3e-15	81	Glycine max BSR-101 satellite SB92 genomic sequence.
13934	GM_199_A2_F01_MR	g3786007	BLASTX	176	9e-12	63	(AC005499) hypothetical protein [Arabidopsis thaliana]
13935	GM_199_A2_G08_MR	g2995405	BLASTX	259	2e-20	60	(Y12432) polyprotein [Ananas comosus]
13936	GM_199_B1_A02_MR	g99922	BLASTX	707	5e-69	87	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
13937	GM_199_B1_A09_MR	g3645899	BLASTX	103	1e-09	36	(U68408) 5' end not determined experimentally [Zea mays]
13938	GM_199_B1_A10_MR	g3097320	BLASTN	1175	3e-46	81	Glycine max gene for Bd 30K, complete cds
13939	GM_199_B1_A10_T7	g2129618	BLASTX	184	3e-12	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
13940	GM_199_B1_A11_MR	g1633547	BLASTN	356	5e-09	60	Human chromosome 12p13 sequence, complete sequence [Homo sapiens]
13941	GM_199_B1_A11_T7	g2979597	BLASTN	417	8e-12	65	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
13942	GM_199_B1_A12_MR	g4063756	BLASTN	444	5e-13	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
13943	GM_199_B1_A12_T7	g507910	BLASTN	711	2e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
13944	GM_199_B1_B02_MR	g498931	BLASTX	82	3e-11	36	(Z12825) ORF167; homologous to reverse transcriptases from retroviral-like transposons TNT 1-94 from tobacco and COPIA from Drosophila [Beta vulgaris]
13945	GM_199_B1_B05_T7	g2995405	BLASTX	286	3e-23	40	(Y12432) polyprotein [Ananas comosus]
13946	GM_199_B1_B06_T7	g85105	BLASTX	251	2e-19	41	pol polyprotein - fruit fly (Drosophila melanogaster) transposon 1731 gi 8702 (X07656) pol polypeptide (AA 1-982) [Drosophila melanogaster]
13947	GM_199_B1_B07_T7	g2462134	BLASTX	256	1e-20	38	(Y13368) reverse transcriptase [Beta vulgaris]
13948	GM_199_B1_B09_MR	g507910	BLASTN	622	2e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13949	GM_199_B1_B10_MR	g507910	BLASTN	584	9e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
13950	GM_199_B1_B10_T7	g2522230	BLASTX	150	4e-10	33	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13951	GM_199_B1_B11_T7	g1480927	BLASTN	406	2e-11	86	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
13952	GM_199_B1_C08_MR	g3695019	BLASTX	137	4e-14	72	(AF055848) subtilisin-like protease [Arabidopsis thaliana]
13953	GM_199_B1_C08_T7	g2622367	BLASTX	286	2e-24	48	(AE000892) argininosuccinate synthase [Methanobacterium thermoautotrophicum]
13954	GM_199_B1_C09_T7	g507910	BLASTN	375	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13955	GM_199_B1_D07_MR	g2133392	BLASTX	206	6e-16	37	cyst wall protein 1 - Giardia lamblia gi 606009 (U09330) cyst wall protein 1 [Giardia intestinalis] gi 1097262 prf 2113356A acidic Leu-rich protein [Giardia intestinalis]
13956	GM_199_B1_E02_T7	g4063760	BLASTX	206	2e-14	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13957	GM_199_B1_E03_T7	g3645899	BLASTX	409	3e-36	60	(U68408) 5' end not determined experimentally [Zea mays]
13958	GM_199_B1_E05_T7	g1168518	BLASTX	158	7e-10	68	APURINIC ENDONUCLEASE-REDOX PROTEIN (DNA-(APURINIC OR APYRIMIDINIC SITE) LYASE) gi 472869 (X76912) ARP protein [Arabidopsis thaliana]
13959	GM_199_B1_E09_T7	g2443320	BLASTX	335	3e-28	44	(D85597) polyprotein [Oryza australiensis]
13960	GM_199_B1_E11_MR	g4063760	BLASTX	382	2e-33	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13961	GM_199_B1_F01_MR	g18559	BLASTN	1433	5e-58	91	G.max gene for catalase
13962	GM_199_B1_F02_T7	g3947733	BLASTX	150	5e-09	43	(AJ009719) NL25 [Solanum tuberosum]
13963	GM_199_B1_F06_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
13964	GM_199_B1_F07_T7	g1142701	BLASTN	233	2e-18	75	Glycine max satellite STR120-A.3.
13965	GM_199_B1_F08_MR	g1066856	BLASTN	582	3e-19	74	Glycine max acetyl coenzyme A carboxylase (ACCase-B) gene, 5' end of cds.
13966	GM_199_B1_F11_T7	g2995405	BLASTX	336	1e-28	55	(Y12432) polyprotein [Ananas comosus]
13967	GM_199_B1_G05_MR	g100484	BLASTX	252	9e-20	57	hypothetical protein - garden snapdragon
13968	GM_199_B1_G07_MR	g1785739	BLASTX	159	3e-20	40	(Y08502) orf240b [Arabidopsis thaliana]
13969	GM_199_B1_G11_MR	g3097320	BLASTN	441	6e-13	65	Glycine max gene for Bd 30K, complete cds
13970	GM_199_B1_G11_T7	g3097320	BLASTN	427	3e-12	71	Glycine max gene for Bd 30K, complete cds
13971	GM_199_B1_G12_MR	g2522230	BLASTX	271	7e-23	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
13972	GM_199_B1_H04_MR	g12137	BLASTN	457	1e-13	70	Pea chloroplast DNA (4.7 kb) 5' to ATP-synthase a subunit gene
13973	GM_199_B1_H05_MR	g2829862	BLASTX	311	4e-27	49	(AC002396) Similar to glucosyltransferases [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13974	GM_199_B2_A05_T7	g12144	BLASTN	635	5e-22	80	Pea chloroplast genes for F(O)-ATP synthase subunits a and c (partial)
13975	GM_199_B2_B01_T7	g2829109	BLASTN	409	2e-11	66	Homo sapiens chromosome 21q22.3 PAC 267O10, complete sequence [Homo sapiens]
13976	GM_199_B2_C03_MR	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
13977	GM_199_B2_D04_T7	g421955	BLASTX	169	2e-11	49	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
13978	GM_199_B2_F10_T7	g3097320	BLASTN	858	8e-32	81	Glycine max gene for Bd 30K, complete cds
13979	GM_199_B2_H01_T7	g3645899	BLASTX	205	2e-14	54	(U68408) 5' end not determined experimentally [Zea mays]
13980	GM_200_A1_A04_T7	g4050011	BLASTN	558	3e-18	67	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
13981	GM_200_A1_A07_MR	g2443320	BLASTX	251	3e-19	43	(D85597) polyprotein [Oryza australiensis]
13982	GM_200_A1_A09_T7	g82695	BLASTX	168	8e-21	94	glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12) 3 - maize (fragment) gi 293887 (L13431) glyceraldehyde-3-phosphate dehydrogenase [Zea mays]
13983	GM_200_A1_A10_MR	g4038056	BLASTX	301	7e-25	52	(AC005897) putative transposon [Arabidopsis thaliana]
13984	GM_200_A1_A11_MR	g22490	BLASTX	141	5e-09	45	(X01380) ORF1 [Zea mays]
13985	GM_200_A1_B12_T7	g4063760	BLASTX	209	8e-15	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13986	GM_200_A1_C08_MR	g3023281	BLASTX	178	1e-13	47	HIGH AFFINITY AMMONIUM TRANSPORTER gi 2065194 gnl PID e223603 (X95098) ammonium transporter [Lycopersicon esculentum]
13987	GM_200_A1_D01_MR	g3644031	BLASTN	570	3e-19	80	Glycine max plasma membrane proton-ATPase mRNA, partial cds
13988	GM_200_A1_D02_MR	g4063760	BLASTX	380	4e-35	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
13989	GM_200_A1_D03_T7	g905361	BLASTX	149	8e-09	83	(U22103) gag-protease polyprotein [Glycine max]
13990	GM_200_A1_D07_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
13991	GM_200_A1_E03_MR	g3420054	BLASTX	162	6e-10	35	(AC004680) unknown protein [Arabidopsis thaliana]
13992	GM_200_A1_E08_MR	g3142328	BLASTN	1551	2e-63	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
13993	GM_200_A1_E10_T7	g3688328	BLASTX	122	3e-09	54	(AJ228325) reverse transcriptase [Ginkgo biloba]
13994	GM_200_A1_F01_T7	g507910	BLASTN	382	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
13995	GM_200_A1_F04_MR	g18559	BLASTN	349	9e-09	75	G.max gene for catalase
13996	GM_200_A1_F05_T7	g1769898	BLASTX	196	2e-16	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
13997	GM_200_A1_F06_MR	g3777527	BLASTX	504	4e-46	91	(AF053008) gag-pol polyprotein [Glycine max]
13998	GM_200_A1_F06_T7	g3645899	BLASTX	242	3e-22	54	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
13999	GM_200_A1_F07_MR	g3047066	BLASTX	178	5e-12	31	(AF058825) contains similarity to retrovirus-related POL polyproteins [Arabidopsis thaliana]
14000	GM_200_A1_F08_MR	g18559	BLASTN	742	1e-26	73	G.max gene for catalase
14001	GM_200_A1_G08_MR	g3142328	BLASTN	488	4e-15	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14002	GM_200_A1_H06_MR	g3142328	BLASTN	569	9e-19	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14003	GM_200_A1_H07_MR	g4056431	BLASTX	159	4e-10	86	(AC005990) Similar to gb AJ002532 endo-polygalacturonase from Arabidopsis thaliana and is a member of the polygalacturonase family PF 00295. [Arabidopsis thaliana]
14004	GM_200_A1_H08_MR	g3319362	BLASTX	256	5e-20	85	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
14005	GM_200_A1_H11_MR	g3097320	BLASTN	656	1e-22	79	Glycine max gene for Bd 30K, complete cds
14006	GM_200_A2_A05_MR	g4063760	BLASTX	176	3e-11	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14007	GM_200_A2_A10_MR	g905361	BLASTX	295	1e-24	67	(U22103) gag-protease polyprotein [Glycine max]
14008	GM_200_A2_C03_T7	g99922	BLASTX	160	2e-19	84	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
14009	GM_200_A2_C09_MR	g507910	BLASTN	341	8e-09	68	Glycine max BSR-101 satellite SB92 genomic sequence.
14010	GM_200_A2_C12_MR	g2443320	BLASTX	164	6e-10	53	(D85597) polyprotein [Oryza australiensis]
14011	GM_200_A2_D10_MR	g3645899	BLASTX	151	1e-08	41	(U68408) 5' end not determined experimentally [Zea mays]
14012	GM_200_A2_F10_MR	g3176806	BLASTN	365	2e-10	66	Homo sapiens allele 17 fragile site locus (FRA10B) minisatellite, 5' sequence
14013	GM_200_A2_G04_MR	g2462058	BLASTX	177	7e-13	46	(Y13389) reverse transcriptase [Antirrhinum majus]
14014	GM_200_A2_G09_T7	g2264320	BLASTN	467	5e-14	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
14015	GM_200_A2_H06_MR	g507910	BLASTN	500	6e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
14016	GM_200_A2_H06_T7	g3142328	BLASTN	495	2e-15	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14017	GM_200_A2_H08_MR	g2565273	BLASTX	145	8e-09	43	(AF023481) o-methytransferase [Medicago sativa]
14018	GM_200_A2_H10_MR	g3510340	BLASTN	551	7e-18	76	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDN11, complete sequence [Arabidopsis thaliana]
14019	GM_200_B1_A02_MR	g99922	BLASTX	428	1e-44	63	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
14020	GM_200_B1_A04_T7	g629693	BLASTX	206	1e-31	62	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14021	GM_200_B1_A05_T7	g3319362	BLASTX	231	3e-17	42	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
14022	GM_200_B1_A08_MR	g1040717	BLASTN	347	1e-09	60	D.polychroa microsatellite sequence (clone Dp ch1 F3)
14023	GM_200_B1_A10_MR	g3047068	BLASTX	166	4e-12	41	(AF058825) similar to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
14024	GM_200_B1_A10_T7	g3142328	BLASTN	1164	8e-46	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14025	GM_200_B1_A12_MR	g4063760	BLASTX	402	2e-35	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14026	GM_200_B1_B03_T7	g4092470	BLASTN	427	3e-12	64	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
14027	GM_200_B1_B04_MR	g507910	BLASTN	618	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
14028	GM_200_B1_B05_MR	g3142328	BLASTN	671	2e-23	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14029	GM_200_B1_B07_MR	g4063760	BLASTX	285	2e-33	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14030	GM_200_B1_B07_T7	g2522228	BLASTX	158	4e-10	50	(AB007466) reverse transcriptase-like protein [Vicia faba]
14031	GM_200_B1_B09_MR	g4063770	BLASTX	215	1e-15	40	(AB004906) transposase [Ipomoea purpurea]
14032	GM_200_B1_B11_MR	g1167523	BLASTX	350	8e-30	48	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14033	GM_200_B1_C05_MR	g1171583	BLASTN	357	4e-09	64	P.falciparum complete gene map of plastid-like DNA (IR-A)
14034	GM_200_B1_C05_T7	g2853071	BLASTN	350	9e-09	65	Arabidopsis thaliana DNA chromosome 4, BAC clone F24J7 (ESSAII project)
14035	GM_200_B1_C08_T7	g507910	BLASTN	367	6e-10	79	Glycine max BSR-101 satellite SB92 genomic sequence.
14036	GM_200_B1_C12_T7	g2218024	BLASTN	355	6e-10	64	Apis mellifera mitochondrial tRNA-Leu gene
14037	GM_200_B1_D01_T7	g1167523	BLASTX	136	2e-09	46	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14038	GM_200_B1_D03_T7	g170602	BLASTN	575	5e-20	64	Broad bean (V.faba) BamHI repetitive element, 900 bp family.
14039	GM_200_B1_D05_MR	g507910	BLASTN	398	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14040	GM_200_B1_D08_T7	g4038056	BLASTX	170	8e-11	46	(AC005897) putative transposon [Arabidopsis thaliana]
14041	GM_200_B1_D09_MR	g2995405	BLASTX	123	4e-19	57	(Y12432) polyprotein [Ananas comosus]
14042	GM_200_B1_D09_T7	g2522228	BLASTX	505	1e-47	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
14043	GM_200_B1_E01_MR	g507910	BLASTN	527	3e-17	82	Glycine max BSR-101 satellite SB92 genomic sequence.
14044	GM_200_B1_E10_T7	g507910	BLASTN	362	9e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14045	GM_200_B1_E12_MR	g531389	BLASTX	270	3e-33	63	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
14046	GM_200_B1_F04_MR	g3142328	BLASTN	1178	2e-46	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14047	GM_200_B1_F06_MR	g4063760	BLASTX	239	4e-18	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14048	GM_200_B1_F07_MR	g507910	BLASTN	499	6e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
14049	GM_200_B1_F11_MR	g629693	BLASTX	363	1e-32	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
14050	GM_200_B1_F12_MR	g18559	BLASTN	789	9e-29	74	G.max gene for catalase
14051	GM_200_B1_G02_T7	g3510344	BLASTN	455	2e-13	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJG14, complete sequence [Arabidopsis thaliana]
14052	GM_200_B1_G05_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14053	GM_200_B1_G08_MR	g3845197	BLASTN	407	2e-11	63	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
14054	GM_200_B1_G10_MR	g2583123	BLASTX	180	2e-17	68	(AC002387) putative nucleotide sugar epimerase [Arabidopsis thaliana]
14055	GM_200_B1_H01_T7	g3426334	BLASTN	484	7e-15	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
14056	GM_200_B1_H03_MR	g507910	BLASTN	395	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14057	GM_200_B1_H06_T7	g3930515	BLASTX	105	2e-10	45	(AF059674) putative gag protein [Nicotiana tabacum]
14058	GM_200_B1_H07_MR	g905361	BLASTX	179	5e-12	29	(U22103) gag-protease polyprotein [Glycine max]
14059	GM_200_B1_H09_T7	g1732513	BLASTX	191	2e-14	76	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]
14060	GM_200_B1_H10_T7	g4092470	BLASTN	497	2e-15	68	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
14061	GM_200_B2_C11_T7	g3142379	BLASTX	189	1e-17	86	(AF053008) envelope-like [Glycine max]
14062	GM_200_B2_E12_T7	g507910	BLASTN	460	4e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14063	GM_200_B2_G04_T7	g507910	BLASTN	683	3e-24	87	Glycine max BSR-101 satellite SB92 genomic sequence.
14064	GM_201_A2_A02_MR	g18559	BLASTN	510	4e-16	66	G.max gene for catalase
14065	GM_201_A2_A06_MR	g3786021	BLASTX	239	9e-19	50	(AC005499) hypothetical protein [Arabidopsis thaliana]
14066	GM_201_A2_A12_MR	g2642333	BLASTN	845	3e-32	73	Sorghum bicolor tandemly repetitive Sau3A10 DNA element
14067	GM_201_A2_B03_MR	g4063760	BLASTX	182	6e-12	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14068	GM_201_A2_B04_MR	g2462134	BLASTX	224	4e-17	31	(Y13368) reverse transcriptase [Beta vulgaris]
14069	GM_201_A2_B07_MR	g3337395	BLASTN	482	1e-14	64	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
14070	GM_201_A2_B10_MR	g13988	BLASTN	388	2e-10	67	C. elegans complete mitochondrial genome
14071	GM_201_A2_B11_MR	g18559	BLASTN	822	3e-30	75	G.max gene for catalase
14072	GM_201_A2_C01_MR	g3777527	BLASTX	667	2e-63	90	(AF053008) gag-pol polyprotein [Glycine max]
14073	GM_201_A2_C03_MR	g507910	BLASTN	364	8e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
14074	GM_201_A2_C06_MR	g3738325	BLASTX	212	5e-18	46	(AC005170) putative CaMB-channel protein [Arabidopsis thaliana]
14075	GM_201_A2_C10_MR	g3097320	BLASTN	1009	1e-38	79	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14076	GM_201_A2_D03_MR	g4063760	BLASTX	343	4e-34	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14077	GM_201_A2_D09_MR	g3142328	BLASTN	2035	1e-85	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14078	GM_201_A2_D11_MR	g3097320	BLASTN	380	4e-10	62	Glycine max gene for Bd 30K, complete cds
14079	GM_201_A2_E02_MR	g2129618	BLASTX	123	1e-12	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
14080	GM_201_A2_E10_MR	g3319362	BLASTX	413	8e-37	77	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
14081	GM_201_A2_F10_MR	g3777527	BLASTX	228	8e-17	42	(AF053008) gag-pol polyprotein [Glycine max]
14082	GM_201_A2_G02_MR	g507910	BLASTN	398	2e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
14083	GM_201_A2_G04_MR	g3608480	BLASTN	401	4e-12	76	Petunia x hybrida ribosomal protein L27a mRNA, complete cds
14084	GM_201_A2_G06_MR	g905361	BLASTX	199	4e-14	33	(U22103) gag-protease polyprotein [Glycine max]
14085	GM_201_A2_H07_MR	g507910	BLASTN	396	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14086	GM_201_A2_H08_MR	g3777527	BLASTX	662	6e-63	93	(AF053008) gag-pol polyprotein [Glycine max]
14087	GM_201_A2_H09_MR	g507910	BLASTN	344	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
14088	GM_201_B2_A05_MR	g507910	BLASTN	394	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14089	GM_201_B2_A11_MR	g3097320	BLASTN	534	4e-17	78	Glycine max gene for Bd 30K, complete cds
14090	GM_201_B2_D01_MR	g2522227	BLASTX	186	1e-13	48	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14091	GM_201_B2_D06_MR	g2352492	BLASTX	228	2e-17	64	(AF005047) transport inhibitor response 1 [Arabidopsis thaliana] gi 2352494 (AF005048) transport inhibitor response 1 [Arabidopsis thaliana]
14092	GM_201_B2_D09_MR	g1769899	BLASTX	122	8e-10	70	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14093	GM_201_B2_E11_MR	g2522228	BLASTX	238	6e-19	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
14094	GM_201_B2_F05_MR	g3176803	BLASTN	471	3e-15	67	Homo sapiens allele 15 fragile site locus (FRA10B) minisatellite sequence
14095	GM_201_B2_G09_MR	g226407	BLASTX	172	9e-11	52	retrotransposon del1-46 [Lilium henryi]
14096	GM_202_A1_A01_MR	g2995405	BLASTX	376	6e-33	58	(Y12432) polyprotein [Ananas comosus]
14097	GM_202_A1_A08_MR	g3176664	BLASTX	338	6e-30	76	(AC004393) Contains similarity to beta scruin gb Z47541 from Limulus polyphemus. ESTs gb T04493 and gb AA585955 come from this gene. [Arabidopsis thaliana]
14098	GM_202_A1_A08_T7	g3510346	BLASTN	449	3e-13	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNL12, complete sequence [Arabidopsis thaliana]
14099	GM_202_A1_A11_MR	g3097320	BLASTN	352	7e-09	68	Glycine max gene for Bd 30K, complete cds
14100	GM_202_A1_B04_MR	g4107343	BLASTX	123	8e-09	47	(AJ224922) ATP citrate lyase [Sordaria macrospora]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14101	GM_202_A1_B09_MR	g3395435	BLASTX	312	1e-26	47	(AC004683) myosin heavy chain-like protein [Arabidopsis thaliana]
14102	GM_202_A1_B10_MR	g3930515	BLASTX	125	2e-12	43	(AF059674) putative gag protein [Nicotiana tabacum]
14103	GM_202_A1_C07_MR	g2522227	BLASTX	158	2e-10	51	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14104	GM_202_A1_C11_MR	g1167523	BLASTX	234	2e-17	44	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14105	GM_202_A1_D01_MR	g905361	BLASTX	190	4e-13	29	(U22103) gag-protease polyprotein [Glycine max]
14106	GM_202_A1_D03_MR	g2224927	BLASTX	275	8e-24	55	(AF004213) ethylene-insensitive3-like1 [Arabidopsis thaliana]
14107	GM_202_A1_D08_MR	g1769897	BLASTX	174	1e-11	36	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14108	GM_202_A1_D10_MR	g1769897	BLASTX	302	2e-25	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14109	GM_202_A1_F02_MR	g3858933	BLASTN	372	9e-10	75	Arabidopsis thaliana DNA chromosome 4, BAC clone F10N7 (ESSAII project)
14110	GM_202_A1_F04_MR	g2454214	BLASTN	1906	2e-80	96	Glycine max nodule-specific phosphoribosylpyrophosphate amidotransferase (PRAT) gene, 5' upstream sequence and partial cds
14111	GM_202_A1_F05_MR	g507910	BLASTN	521	6e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
14112	GM_202_A1_H10_MR	g4038056	BLASTX	169	1e-10	32	(AC005897) putative transposon [Arabidopsis thaliana]
14113	GM_202_A2_A03_T7	g507910	BLASTN	484	3e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14114	GM_202_A2_A04_T7	g18559	BLASTN	1080	6e-42	77	G.max gene for catalase
14115	GM_202_A2_B02_T7	g507910	BLASTN	587	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
14116	GM_202_A2_C05_T7	g507910	BLASTN	341	8e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
14117	GM_202_A2_C10_T7	g4038056	BLASTX	341	4e-29	44	(AC005897) putative transposon [Arabidopsis thaliana]
14118	GM_202_A2_D07_T7	g507910	BLASTN	702	4e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
14119	GM_202_A2_D12_T7	g3142330	BLASTX	182	2e-39	78	(U96295) envelope-like [Glycine max]
14120	GM_202_A2_E08_T7	g2264311	BLASTN	426	3e-12	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MLN1, complete sequence [Arabidopsis thaliana]
14121	GM_202_A2_E10_T7	g2462134	BLASTX	241	3e-25	49	(Y13368) reverse transcriptase [Beta vulgaris]
14122	GM_202_A2_F02_T7	g3402684	BLASTX	487	1e-45	67	(AC004697) hypothetical protein [Arabidopsis thaliana]
14123	GM_202_B1_A02_MR	g1840106	BLASTN	411	3e-12	65	Human fragile site locus (FRA16B) minisatellite repeat
14124	GM_202_B1_A07_MR	g3645899	BLASTX	213	6e-17	59	(U68408) 5' end not determined experimentally [Zea mays]
14125	GM_202_B1_A07_T7	g629693	BLASTX	205	4e-29	57	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
14126	GM_202_B1_A12_MR	g20861	BLASTN	357	4e-09	71	P.sativum retrotransposon
14127	GM_202_B1_A12_T7	g387902	BLASTX	143	3e-09	30	(L23524) ORF [Hordeum vulgare]
14128	GM_202_B1_B03_MR	g467491	BLASTN	605	5e-21	73	Chlorella vulgaris genomic DNA, telomeric repeat
14129	GM_202_B1_B03_T7	g1167523	BLASTX	239	6e-18	48	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14130	GM_202_B1_B07_MR	g3142328	BLASTN	1103	5e-43	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14131	GM_202_B1_B10_MR	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14132	GM_202_B1_C02_MR	g3513747	BLASTX	179	4e-17	46	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
14133	GM_202_B1_C06_MR	g4063760	BLASTX	326	3e-27	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14134	GM_202_B1_C10_T7	g905360	BLASTN	363	2e-09	79	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
14135	GM_202_B1_D02_T7	g3758836	BLASTN	333	6e-10	71	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
14136	GM_202_B1_D08_MR	g2264320	BLASTN	609	2e-20	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
14137	GM_202_B1_E01_T7	g1769898	BLASTX	150	4e-17	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14138	GM_202_B1_E09_MR	g3777527	BLASTX	526	2e-48	92	(AF053008) gag-pol polyprotein [Glycine max]
14139	GM_202_B1_F01_MR	g18559	BLASTN	669	3e-25	72	G.max gene for catalase
14140	GM_202_B1_F02_T7	g1906825	BLASTN	581	2e-19	76	A.thaliana hsp81.2 gene
14141	GM_202_B1_F05_MR	g2959734	BLASTX	170	3e-17	72	(Y13650) homologous to GATA-binding transcription factors [Arabidopsis thaliana]
14142	GM_202_B1_F05_T7	g2264318	BLASTN	472	3e-14	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUP24, complete sequence [Arabidopsis thaliana]
14143	GM_202_B1_F06_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14144	GM_202_B1_F09_MR	g218269	BLASTX	365	8e-33	86	(D12839) reverse transcriptase [Glycine max]
14145	GM_202_B1_F12_MR	g3283026	BLASTX	163	3e-10	30	putative transposase [Arabidopsis thaliana]
14146	GM_202_B1_G01_MR	g340796	BLASTN	411	2e-12	62	Figure 6. DNA sequence of three 3' apoB VNTR alleles.
14147	GM_202_B1_G07_MR	g4063760	BLASTX	282	1e-22	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14148	GM_202_B1_G09_MR	g507910	BLASTN	368	5e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14149	GM_203_A1_A05_T7	g3777527	BLASTX	225	2e-16	81	(AF053008) gag-pol polyprotein [Glycine max]
14150	GM_203_A1_A06_MR	g840618	BLASTN	369	7e-10	59	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
14151	GM_203_A1_A07_MR	g4063756	BLASTN	597	6e-20	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14152	GM_203_A1_A08_MR	g4063760	BLASTX	336	2e-28	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14153	GM_203_A1_A10_MR	g2443329	BLASTX	156	2e-09	35	(D86122) Mei2-like protein [Arabidopsis thaliana]
14154	GM_203_A1_B02_MR	g4063760	BLASTX	175	3e-11	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14155	GM_203_A1_B06_MR	g3283026	BLASTX	284	3e-23	40	putative transposase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14156	GM_203_A1_B12_MR	g99729	BLASTX	238	2e-19	45	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
14157	GM_203_A1_C08_MR	g507910	BLASTN	582	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
14158	GM_203_A1_C12_MR	g505129	BLASTN	385	2e-10	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
14159	GM_203_A1_D01_T7	g2842490	BLASTX	163	8e-11	40	(AL021749) heat-shock protein [Arabidopsis thaliana]
14160	GM_203_A1_D04_MR	g507910	BLASTN	634	5e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
14161	GM_203_A1_D08_MR	g4006833	BLASTX	259	4e-20	39	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
14162	GM_203_A1_E03_MR	g2522230	BLASTX	170	4e-12	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14163	GM_203_A1_E06_MR	g4063756	BLASTN	506	8e-16	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14164	GM_203_A1_E07_MR	g4063760	BLASTX	454	5e-41	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14165	GM_203_A1_F03_MR	g3319372	BLASTX	239	5e-18	42	(AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]
14166	GM_203_A1_F06_MR	g1418331	BLASTX	219	2e-16	32	(X95909) receptor like protein kinase [Arabidopsis thaliana]
14167	GM_203_A1_F11_T7	g2443320	BLASTX	180	1e-11	52	(D85597) polyprotein [Oryza australiensis]
14168	GM_203_A1_G09_MR	g1142703	BLASTN	273	8e-15	75	Glycine max satellite STR120-B.1.
14169	GM_203_A1_G10_MR	g3142328	BLASTN	1242	2e-49	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14170	GM_203_A1_G12_MR	g507910	BLASTN	414	4e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14171	GM_203_A1_H11_T7	g178823	BLASTN	336	5e-09	62	Human apolipoprotein B gene hypervariable region, 3' flank.
14172	GM_203_A2_A09_T7	g4038056	BLASTX	319	9e-27	50	(AC005897) putative transposon [Arabidopsis thaliana]
14173	GM_203_A2_B04_T7	g2244803	BLASTX	241	5e-24	44	(Z97336) reverse transcriptase-like protein [Arabidopsis thaliana]
14174	GM_203_A2_B07_T7	g3283026	BLASTX	197	7e-14	36	putative transposase [Arabidopsis thaliana]
14175	GM_203_A2_B09_T7	g1850550	BLASTX	103	5e-09	45	(U88030) reverse transcriptase [Secale cereale]
14176	GM_203_A2_C07_T7	g4063760	BLASTX	124	2e-12	36	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14177	GM_203_A2_C10_T7	g2522228	BLASTX	187	3e-13	78	(AB007466) reverse transcriptase-like protein [Vicia faba]
14178	GM_203_A2_C12_T7	g3513747	BLASTX	175	5e-11	47	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
14179	GM_203_A2_D03_T7	g3668073	BLASTN	388	2e-10	65	Arabidopsis thaliana chromosome II BAC T4C15 genomic sequence, complete sequence [Arabidopsis thaliana]
14180	GM_203_A2_D04_T7	g3097320	BLASTN	845	3e-31	82	Glycine max gene for Bd 30K, complete cds
14181	GM_203_A2_E02_T7	g4063760	BLASTX	296	4e-24	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14182	GM_203_A2_E03_T7	g905361	BLASTX	321	2e-47	82	(U22103) gag-protease polyprotein [Glycine max]
14183	GM_203_A2_E07_T7	g2764526	BLASTN	467	4e-14	64	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
14184	GM_203_A2_F03_T7	g2129618	BLASTX	152	7e-09	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
14185	GM_203_A2_F04_T7	g2586082	BLASTX	184	4e-16	48	(U72725) retrofit [Oryza longistaminata]
14186	GM_203_B1_A09_MR	g3142328	BLASTN	951	4e-36	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14187	GM_203_B1_B06_T7	g1167523	BLASTX	169	1e-10	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14188	GM_203_B1_B08_T7	g3645899	BLASTX	192	4e-13	50	(U68408) 5' end not determined experimentally [Zea mays]
14189	GM_203_B1_C03_T7	g416692	BLASTX	151	1e-12	70	AUXIN-INDUCED PROTEIN 6B gi 81764 pir JQ1098 auxin-induced protein 6B - soybean gi 255577 bbs 113700 (S44175) orf 6B [Glycine max=soybeans, cv. Wayne, Peptide, 90 aa] [Glycine max]
14190	GM_203_B1_D05_T7	g3599418	BLASTN	785	1e-28	84	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
14191	GM_203_B1_D08_MR	g3142328	BLASTN	582	2e-19	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14192	GM_203_B1_F03_MR	g3142328	BLASTN	437	9e-13	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14193	GM_203_B1_G03_T7	g3928750	BLASTN	354	4e-09	75	Broad bean necrosis virus genes for triple-gene-block proteins and glycine-rich protein, partial and complete cds
14194	GM_203_B2_A01_MR	g507910	BLASTN	387	7e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14195	GM_203_B2_B04_MR	g507910	BLASTN	429	9e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
14196	GM_203_B2_B05_MR	g2160694	BLASTX	534	1e-50	88	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
14197	GM_203_B2_B05_T7	g1002593	BLASTN	444	3e-13	69	Lycopersicon peruvianum self incompatibility (s11) gene, complete cds.
14198	GM_203_B2_B07_MR	g4156188	BLASTN	389	9e-13	68	Homo sapiens clone DJ0784G16, complete sequence [Homo sapiens]
14199	GM_203_B2_B08_MR	g13767	BLASTN	396	9e-12	61	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
14200	GM_203_B2_B09_MR	g4038056	BLASTX	330	6e-28	52	(AC005897) putative transposon [Arabidopsis thaliana]
14201	GM_203_B2_C01_MR	g3645899	BLASTX	232	5e-28	50	(U68408) 5' end not determined experimentally [Zea mays]
14202	GM_203_B2_C02_MR	g4038056	BLASTX	236	7e-18	49	(AC005897) putative transposon [Arabidopsis thaliana]
14203	GM_203_B2_D03_MR	g18559	BLASTN	916	2e-34	75	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14204	GM_203_B2_D08_MR	g3645899	BLASTX	175	3e-11	58	(U68408) 5' end not determined experimentally [Zea mays]
14205	GM_203_B2_F08_MR	g2098708	BLASTN	558	3e-18	69	Citrus sinensis pectinesterase (PECS-2.1) gene, complete cds.
14206	GM_203_B2_F10_MR	g1142702	BLASTN	342	6e-09	75	Glycine max satellite STR120-A.4.
14207	GM_203_B2_G04_MR	g2129618	BLASTX	268	3e-21	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
14208	GM_203_B2_G06_MR	g3176768	BLASTN	396	7e-12	63	Homo sapiens allele 1 fragile site locus (FRA10B) minisatellite, 3' sequence
14209	GM_203_B2_G10_MR	g3810596	BLASTX	181	6e-12	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
14210	GM_203_B2_H07_MR	g1769898	BLASTX	439	1e-40	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14211	GM_204_A1_A01_T7	g3142328	BLASTN	855	9e-32	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14212	GM_204_A1_B02_T7	g3142328	BLASTN	469	3e-14	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14213	GM_204_A1_D03_T7	g100484	BLASTX	225	2e-19	63	hypothetical protein - garden snapdragon
14214	GM_204_A1_E04_T7	g3599418	BLASTN	1816	2e-75	91	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
14215	GM_204_A1_F07_T7	g3176784	BLASTN	445	7e-14	64	Homo sapiens allele 7 fragile site locus (FRA10B) minisatellite sequence
14216	GM_204_A1_G09_T7	g507910	BLASTN	407	9e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14217	GM_204_A1_G12_T7	g507910	BLASTN	346	5e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
14218	GM_204_A1_H10_T7	g13581	BLASTN	351	1e-09	66	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTCG10 Saccharomyces cerevisiae mitochondrion DNA segment.
14219	GM_204_A2_A05_T7	g553114	BLASTX	101	3e-09	82	(M80491) plasma membrane H+ ATPase [Nicotiana plumbaginifolia]
14220	GM_204_A2_B03_T7	g3645899	BLASTX	142	3e-16	36	(U68408) 5' end not determined experimentally [Zea mays]
14221	GM_204_A2_B06_T7	g3695395	BLASTX	163	3e-10	37	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
14222	GM_204_A2_B11_T7	g507910	BLASTN	382	1e-10	77	Glycine max BSR-101 satellite SB92 genomic sequence.
14223	GM_204_A2_D09_T7	g3264544	BLASTN	360	3e-09	65	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
14224	GM_204_A2_F01_T7	g99730	BLASTX	122	7e-16	51	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
14225	GM_204_A2_F12_T7	g905361	BLASTX	495	2e-46	93	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14226	GM_204_A2_G01_T7	g2225930	BLASTN	363	2e-09	64	Human DNA sequence from PAC 522O2 on chromosome 6q21 contains ESTs, STSs and polymorphic CA repeat
14227	GM_204_A2_G08_T7	g3687222	BLASTX	137	2e-16	36	(AC005169) hypothetical protein [Arabidopsis thaliana]
14228	GM_204_A2_H03_T7	g3142328	BLASTN	1347	4e-54	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14229	GM_204_A2_H04_T7	g3142328	BLASTN	1366	5e-55	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14230	GM_204_A2_H09_T7	g3845111	BLASTN	357	4e-09	61	Plasmodium falciparum chromosome 2, section 14 of 73 of the complete sequence
14231	GM_204_B1_A01_T7	g2894606	BLASTX	172	2e-11	67	(AL021889) putative protein [Arabidopsis thaliana]
14232	GM_204_B1_A03_MR	g4006838	BLASTN	477	2e-14	63	Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence [Homo sapiens]
14233	GM_204_B1_A03_T7	g3142328	BLASTN	1745	3e-72	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14234	GM_204_B1_A09_MR	g18559	BLASTN	467	4e-14	78	G.max gene for catalase
14235	GM_204_B1_B09_T7	g4038056	BLASTX	242	1e-18	48	(AC005897) putative transposon [Arabidopsis thaliana]
14236	GM_204_B1_B11_MR	g1769898	BLASTX	454	3e-42	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14237	GM_204_B1_B12_MR	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14238	GM_204_B1_B12_T7	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14239	GM_204_B1_C02_T7	g3283026	BLASTX	194	1e-13	35	putative transposase [Arabidopsis thaliana]
14240	GM_204_B1_C12_MR	g100484	BLASTX	400	9e-36	50	hypothetical protein - garden snapdragon
14241	GM_204_B1_D03_MR	g2522228	BLASTX	470	6e-44	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
14242	GM_204_B1_D04_MR	g3777527	BLASTX	493	2e-59	90	(AF053008) gag-pol polyprotein [Glycine max]
14243	GM_204_B1_D10_MR	g2961349	BLASTX	350	6e-30	52	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
14244	GM_204_B1_D10_T7	g1881562	BLASTN	364	2e-09	62	Human cosmid g1346a045, complete sequence [Homo sapiens]
14245	GM_204_B1_D12_T7	g226407	BLASTX	188	2e-12	41	retrotransposon del1-46 [Lilium henryi]
14246	GM_204_B1_E06_MR	g3777527	BLASTX	175	5e-11	36	(AF053008) gag-pol polyprotein [Glycine max]
14247	GM_204_B1_E11_MR	g2865424	BLASTX	238	3e-23	48	(AF039371) polyprotein [Arabidopsis thaliana]
14248	GM_204_B1_F05_T7	g1769898	BLASTX	140	3e-15	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14249	GM_204_B1_F07_MR	g3930515	BLASTX	120	2e-12	35	(AF059674) putative gag protein [Nicotiana tabacum]
14250	GM_204_B1_F08_T7	g4038029	BLASTN	450	3e-13	62	Arabidopsis thaliana chromosome II BAC F5O4 genomic sequence, complete sequence [Arabidopsis thaliana]
14251	GM_204_B1_F09_MR	g3688328	BLASTX	140	3e-18	65	(AJ228325) reverse transcriptase [Ginkgo biloba]
14252	GM_204_B1_F10_MR	g3142328	BLASTN	714	2e-25	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14253	GM_204_B1_G08_MR	g1171583	BLASTN	353	6e-09	63	P.falciparum complete gene map of plastid-like DNA (IR-A)
14254	GM_204_B1_H03_MR	g4063760	BLASTX	316	3e-26	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14255	GM_204_B1_H08_T7	g2522227	BLASTX	147	3e-09	41	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14256	GM_204_B1_H11_MR	g3097320	BLASTN	894	2e-33	83	Glycine max gene for Bd 30K, complete cds
14257	GM_204_B2_A04_MR	g2995405	BLASTX	261	1e-20	58	(Y12432) polyprotein [Ananas comosus]
14258	GM_204_B2_A08_MR	g507910	BLASTN	382	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14259	GM_204_B2_C12_MR	g507910	BLASTN	374	3e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14260	GM_204_B2_D11_T7	g2586082	BLASTX	254	2e-19	53	(U72725) retrofit [Oryza longistaminata]
14261	GM_204_B2_E02_T7	g507910	BLASTN	368	5e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14262	GM_204_B2_E08_MR	g507910	BLASTN	354	2e-09	81	Glycine max BSR-101 satellite SB92 genomic sequence.
14263	GM_204_B2_F01_MR	g3777527	BLASTX	253	2e-19	94	(AF053008) gag-pol polyprotein [Glycine max]
14264	GM_204_B2_F11_MR	g100484	BLASTX	159	9e-10	48	hypothetical protein - garden snapdragon
14265	GM_205_A1_A03_MR	g1769898	BLASTX	383	1e-37	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14266	GM_205_A1_A04_MR	g1167523	BLASTX	204	3e-14	38	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14267	GM_205_A1_A09_MR	g4140712	BLASTX	177	7e-13	40	(AF110183) putative integrase [Oryza sativa]
14268	GM_205_A1_B07_MR	g1066856	BLASTN	441	7e-13	68	Glycine max acetyl coenzyme A carboxylase (ACCase-B) gene, 5' end of cds.
14269	GM_205_A1_B08_MR	g507910	BLASTN	383	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14270	GM_205_A1_B12_MR	g2522230	BLASTX	297	1e-25	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14271	GM_205_A1_C10_T7	g507910	BLASTN	506	3e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
14272	GM_205_A1_C11_T7	g3548810	BLASTX	78	3e-11	77	(AC005313) putative chloroplast nucleoid DNA binding protein [Arabidopsis thaliana]
14273	GM_205_A1_D01_MR	g1351780	BLASTX	228	2e-23	78	HYPOTHETICAL 23.2 KD PROTEIN (ORF 203) gi 984311 (U26948) unknown [Glycine max]
14274	GM_205_A1_D01_T7	g984307	BLASTN	1537	1e-62	96	Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precurso...
14275	GM_205_A1_D04_T7	g3845197	BLASTN	436	1e-12	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
14276	GM_205_A1_D05_MR	g3142328	BLASTN	1156	2e-45	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14277	GM_205_A1_D12_MR	g1167523	BLASTX	278	6e-25	48	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14278	GM_205_A1_E02_MR	g3142328	BLASTN	651	1e-38	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14279	GM_205_A1_E04_T7	g1621465	BLASTX	217	3e-29	82	(U73105) laccase [Liriodendron tulipifera]
14280	GM_205_A1_E05_MR	g3097320	BLASTN	978	3e-37	79	Glycine max gene for Bd 30K, complete cds
14281	GM_205_A1_E10_T7	g2854105	BLASTN	378	1e-10	67	Citrus limon copia-like retrotransposon Ccr15 reverse transcriptase pseudogene, partial sequence
14282	GM_205_A1_E11_MR	g4063760	BLASTX	232	3e-17	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14283	GM_205_A1_F02_T7	g2462134	BLASTX	196	5e-14	35	(Y13368) reverse transcriptase [Beta vulgaris]
14284	GM_205_A1_F03_MR	g130582	BLASTX	155	5e-09	30	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
14285	GM_205_A1_F05_MR	g170029	BLASTN	396	7e-11	81	Glycine max cv. Dare nodulin 26 gene fragment.
14286	GM_205_A1_F11_MR	g4056489	BLASTX	266	3e-21	72	(AC005896) putative white protein [Arabidopsis thaliana]
14287	GM_205_A1_F12_MR	g18559	BLASTN	396	6e-11	72	G.max gene for catalase
14288	GM_205_A1_G03_MR	g3142328	BLASTN	645	3e-22	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14289	GM_205_A1_G03_T7	g18559	BLASTN	382	3e-10	74	G.max gene for catalase
14290	GM_205_A1_G09_MR	g507910	BLASTN	529	3e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
14291	GM_205_A1_G10_MR	g507910	BLASTN	348	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
14292	GM_205_A1_G10_T7	g507910	BLASTN	388	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14293	GM_205_A1_G12_MR	g100484	BLASTX	354	9e-31	56	hypothetical protein - garden snapdragon
14294	GM_205_A1_H01_T7	g4050011	BLASTN	378	4e-10	61	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
14295	GM_205_A1_H06_T7	g3777527	BLASTX	200	2e-31	72	(AF053008) gag-pol polyprotein [Glycine max]
14296	GM_205_A1_H11_MR	g3777527	BLASTX	500	1e-45	84	(AF053008) gag-pol polyprotein [Glycine max]
14297	GM_205_A1_H12_T7	g3645899	BLASTX	169	1e-10	58	(U68408) 5' end not determined experimentally [Zea mays]
14298	GM_205_A2_A01_MR	g4038056	BLASTX	280	1e-22	50	(AC005897) putative transposon [Arabidopsis thaliana]
14299	GM_205_A2_A03_T7	g2443320	BLASTX	305	5e-25	45	(D85597) polyprotein [Oryza australiensis]
14300	GM_205_A2_A06_MR	g3142328	BLASTN	830	1e-30	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14301	GM_205_A2_A07_MR	g2995405	BLASTX	222	2e-16	37	(Y12432) polyprotein [Ananas comosus]
14302	GM_205_A2_A07_T7	g4063760	BLASTX	233	2e-28	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14303	GM_205_A2_A11_MR	g421953	BLASTX	163	7e-11	33	hypothetical protein 2 - potato transposon Tst1 gi 21432 (X52387) ORF2 [Solanum tuberosum]
14304	GM_205_A2_A12_T7	g2739003	BLASTN	575	3e-19	81	Glycine max cytochrome P450 monooxygenase CYP82C1p (CYP82C1) mRNA, complete cds
14305	GM_205_A2_B03_T7	g3337395	BLASTN	447	4e-13	62	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
14306	GM_205_A2_B05_MR	g3097320	BLASTN	480	1e-14	71	Glycine max gene for Bd 30K, complete cds
14307	GM_205_A2_C01_T7	g3142328	BLASTN	1880	2e-78	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14308	GM_205_A2_C05_MR	g342954	BLASTN	375	1e-10	63	paramecium species 4.51b mt dna dimer: replication init. region, clone-1.
14309	GM_205_A2_C08_MR	g2980793	BLASTX	341	3e-30	71	(AL022197) putative protein [Arabidopsis thaliana]
14310	GM_205_A2_C11_MR	g2995405	BLASTX	244	9e-19	40	(Y12432) polyprotein [Ananas comosus]
14311	GM_205_A2_D01_T7	g3645899	BLASTX	178	1e-11	33	(U68408) 5' end not determined experimentally [Zea mays]
14312	GM_205_A2_D07_MR	g2827662	BLASTX	368	3e-32	64	(AL021637) Phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14313	GM_205_A2_D08_MR	g507910	BLASTN	378	2e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14314	GM_205_A2_D12_MR	g99755	BLASTX	285	6e-32	52	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
14315	GM_205_A2_E04_MR	g731058	BLASTX	167	8e-12	62	URACIL-DNA GLYCOSYLASE (UDG) >gi 2118057 pir S39712 probable uracil-DNA glycosylase - Bacillus subtilis >gi 580875 (X73124) ipa-57d gene product [Bacillus subtilis] >gi 2636332 gnl PID e1186296 (Z99123) uracil-DNA glycosylase [Bacillus subtilis]
14316	GM_205_A2_E11_MR	g18559	BLASTN	1120	9e-44	75	G.max gene for catalase
14317	GM_205_A2_E11_T7	g3319363	BLASTX	307	2e-25	42	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score: 33.26) [Arabidopsis thaliana]
14318	GM_205_A2_F01_T7	g3549652	BLASTX	214	2e-15	49	(AJ224982) MAP3K epsilon protein kinase [Arabidopsis thaliana]
14319	GM_205_B1_E09_T7	g507910	BLASTN	439	3e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14320	GM_205_B1_E11_T7	g3176694	BLASTN	366	8e-11	74	Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence [Arabidopsis thaliana]
14321	GM_205_B1_F10_T7	g2980777	BLASTX	173	1e-17	70	(AL022198) putative protein [Arabidopsis thaliana]
14322	GM_206_A1_A01_T7	g905360	BLASTN	949	3e-36	83	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
14323	GM_206_A1_C12_T7	g2262105	BLASTX	199	4e-14	80	(AC002343) unknown protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14324	GM_206_A1_D02_T7	g3142328	BLASTN	384	2e-10	83	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14325	GM_206_A1_D12_T7	g1666236	BLASTX	212	2e-16	30	(U76261) unknown [Hordeum vulgare]
14326	GM_206_A1_E08_T7	g507910	BLASTN	390	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14327	GM_206_A1_F02_T7	g507910	BLASTN	427	1e-12	81	Glycine max BSR-101 satellite SB92 genomic sequence.
14328	GM_206_A1_F07_T7	g507910	BLASTN	560	1e-18	82	Glycine max BSR-101 satellite SB92 genomic sequence.
14329	GM_206_A1_G08_T7	g170080	BLASTN	469	3e-14	93	Soybean seed lectin gene transposable element tgm1.
14330	GM_206_A1_G10_T7	g1770127	BLASTN	345	2e-09	61	C.difficile pathogenicity locus, strain 2022 (566bp)
14331	GM_206_A1_H10_T7	g2921625	BLASTN	357	4e-09	62	Lupinus luteus leghemoglobin (LbI) gene, complete cds
14332	GM_206_A1_H12_T7	g4103987	BLASTX	174	2e-16	89	(AF030516) 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum]
14333	GM_206_B1_A11_T7	g905361	BLASTX	580	1e-55	92	(U22103) gag-protease polyprotein [Glycine max]
14334	GM_206_B1_B07_T7	g3142328	BLASTN	650	2e-22	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14335	GM_206_B1_C04_T7	g2494415	BLASTX	380	2e-34	88	FRUCTOSE-1,6-BISPHOSPHATASE, CHLOROPLAST PRECURSOR (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) gi 515747 (L34841) fructose-1,6-bisphosphatase [Glycine max]
14336	GM_206_B1_E07_T7	g13764	BLASTN	382	4e-11	65	Torulopsis glabrata mitochondrial DNA for ATPase 8 downstream of cytochrome oxidase 1 gene >gi 343953 gb M11874 YSLMTIG03 Yeast (T.glabrata) mitochondrial DNA between cytochrome oxidase subunit I and ATPase subunit 8 genes.
14337	GM_206_B1_F03_T7	g507910	BLASTN	519	8e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
14338	GM_206_B1_H05_T7	g294042	BLASTN	300	7e-10	66	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
14339	GM_206_B1_H10_T7	g3097320	BLASTN	1120	1e-43	80	Glycine max gene for Bd 30K, complete cds
14340	GM_206_B1_H11_T7	g507910	BLASTN	498	7e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
14341	GM_206_B1_H12_T7	g3097320	BLASTN	722	1e-25	73	Glycine max gene for Bd 30K, complete cds
14342	GM_208_A1_A01_T7	g2997694	BLASTX	187	6e-14	40	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
14343	GM_208_A1_A03_T7	g421955	BLASTX	143	3e-14	40	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
14344	GM_208_A1_A06_T7	g170067	BLASTN	372	7e-10	66	Soybean (G.max) proline-rich cell wall protein (SbPRP3) gene, complete cds.
14345	GM_208_A1_B09_T7	g4038056	BLASTX	169	2e-17	41	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14346	GM_208_A1_C03_T7	g2995405	BLASTX	146	9e-17	37	(Y12432) polyprotein [Ananas comosus]
14347	GM_208_A1_C09_T7	g4160362	BLASTN	318	9e-11	62	Saccharomyces cerevisiae complete mitochondrial genome
14348	GM_208_A1_C11_T7	g507910	BLASTN	523	5e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
14349	GM_208_A1_D10_T7	g99729	BLASTX	141	6e-09	30	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
14350	GM_208_A1_D11_T7	g3777527	BLASTX	499	1e-45	88	(AF053008) gag-pol polyprotein [Glycine max]
14351	GM_208_A1_E02_T7	g3845316	BLASTN	379	4e-10	62	Plasmodium falciparum chromosome 2, section 65 of 73 of the complete sequence
14352	GM_208_A1_E04_T7	g130582	BLASTX	436	5e-39	66	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
14353	GM_208_A1_E08_T7	g226407	BLASTX	261	3e-20	61	retrotransposon del1-46 [Lilium henryi]
14354	GM_208_A1_F11_T7	g1167523	BLASTX	201	6e-14	48	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14355	GM_208_A1_G06_T7	g2323254	BLASTN	354	6e-09	63	Human Chromosome X, complete sequence [Homo sapiens]
14356	GM_208_A1_G08_T7	g4063760	BLASTX	136	5e-10	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14357	GM_208_A1_H08_T7	g3810596	BLASTX	289	2e-23	52	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
14358	GM_208_B1_A10_MR	g3097320	BLASTN	661	7e-23	77	Glycine max gene for Bd 30K, complete cds
14359	GM_208_B1_A12_MR	g2522230	BLASTX	235	5e-19	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14360	GM_208_B1_B03_MR	g2522230	BLASTX	163	2e-11	36	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14361	GM_208_B1_B08_MR	g3142328	BLASTN	841	4e-31	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14362	GM_208_B1_B10_MR	g3176791	BLASTN	349	1e-09	62	Homo sapiens allele 11 fragile site locus (FRA10B) minisatellite, 5' sequence
14363	GM_208_B1_C01_MR	g4063760	BLASTX	189	2e-16	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14364	GM_208_B1_C02_MR	g3142328	BLASTN	717	2e-25	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14365	GM_208_B1_C03_T7	g1142702	BLASTN	419	2e-12	72	Glycine max satellite STR120-A.4.
14366	GM_208_B1_C05_MR	g2129618	BLASTX	225	1e-16	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14367	GM_208_B1_C05_T7	g3650039	BLASTX	176	1e-11	38	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
14368	GM_208_B1_D04_MR	g507910	BLASTN	356	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14369	GM_208_B1_D04_T7	g3377855	BLASTX	251	1e-20	81	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
14370	GM_208_B1_E06_T7	g3287696	BLASTX	453	2e-41	66	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]
14371	GM_208_B1_E08_T7	g3650035	BLASTX	216	1e-15	39	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
14372	GM_208_B1_E10_T7	g294042	BLASTN	356	5e-09	64	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
14373	GM_208_B1_E11_T7	g3702735	BLASTN	349	1e-08	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MQL5, complete sequence [Arabidopsis thaliana]
14374	GM_208_B1_E12_T7	g294042	BLASTN	375	6e-10	65	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
14375	GM_208_B1_F03_T7	g2288979	BLASTN	402	4e-11	63	Arabidopsis thaliana chromosome II BAC T01O24 genomic sequence, complete sequence [Arabidopsis thaliana]
14376	GM_208_B1_F09_T7	g13619	BLASTN	371	1e-10	61	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
14377	GM_208_B1_F12_T7	g3702323	BLASTX	569	2e-54	82	(AC005397) unknown protein [Arabidopsis thaliana]
14378	GM_208_B1_G03_T7	g507910	BLASTN	549	3e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
14379	GM_208_B1_G04_T7	g905361	BLASTX	231	1e-17	41	(U22103) gag-protease polyprotein [Glycine max]
14380	GM_208_B1_G08_MR	g342964	BLASTN	354	7e-10	68	paramecium species 5,311 mt dna dimer: replication init. region.
14381	GM_208_B1_H10_MR	g1666236	BLASTX	164	6e-11	26	(U76261) unknown [Hordeum vulgare]
14382	GM_209_A1_A04_T7	g976178	BLASTX	278	1e-23	44	(L47183) reverse transcriptase [Arabidopsis thaliana]
14383	GM_209_A1_A05_T7	g3985931	BLASTN	351	1e-17	67	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K21H1, complete sequence [Arabidopsis thaliana]
14384	GM_209_A1_A07_MR	g507910	BLASTN	507	3e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14385	GM_209_A1_A08_T7	g18559	BLASTN	740	2e-26	77	G.max gene for catalase
14386	GM_209_A1_A10_MR	g3142328	BLASTN	1462	2e-59	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14387	GM_209_A1_B02_MR	g1666236	BLASTX	144	9e-09	32	(U76261) unknown [Hordeum vulgare]
14388	GM_209_A1_B02_T7	g3810596	BLASTX	243	3e-21	46	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14389	GM_209_A1_B05_MR	g3142328	BLASTN	808	1e-29	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14390	GM_209_A1_B06_MR	g905361	BLASTX	359	2e-31	92	(U22103) gag-protease polyprotein [Glycine max]
14391	GM_209_A1_B07_T7	g3810596	BLASTX	290	5e-30	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
14392	GM_209_A1_B10_MR	g2522227	BLASTX	115	6e-10	57	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14393	GM_209_A1_B12_T7	g2160165	BLASTX	213	2e-15	39	(AC000132) F21M12.11 gene product [Arabidopsis thaliana]
14394	GM_209_A1_C02_T7	g18559	BLASTN	384	2e-10	69	G.max gene for catalase
14395	GM_209_A1_C05_MR	g905361	BLASTX	401	3e-36	94	(U22103) gag-protease polyprotein [Glycine max]
14396	GM_209_A1_C05_T7	g1666236	BLASTX	188	1e-13	30	(U76261) unknown [Hordeum vulgare]
14397	GM_209_A1_C06_T7	g18559	BLASTN	647	3e-22	73	G.max gene for catalase
14398	GM_209_A1_C08_T7	g3142328	BLASTN	686	4e-24	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14399	GM_209_A1_C10_T7	g976178	BLASTX	266	3e-22	46	(L47183) reverse transcriptase [Arabidopsis thaliana]
14400	GM_209_A1_D02_MR	g1840106	BLASTN	488	4e-16	65	Human fragile site locus (FRA16B) minisatellite repeat
14401	GM_209_A1_D02_T7	g2961349	BLASTX	287	3e-23	57	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
14402	GM_209_A1_D04_T7	g3810596	BLASTX	398	3e-35	48	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
14403	GM_209_A1_D08_T7	g4063760	BLASTX	398	1e-45	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14404	GM_209_A1_E03_T7	g14222	BLASTN	403	3e-12	61	Saccharomyces cerevisiae mitochondrial gene aap1 for mitochondrial ATPase subunit 8
14405	GM_209_A1_E06_MR	g3785984	BLASTX	183	5e-12	37	(AC005560) putative reverse transcriptase [Arabidopsis thaliana]
14406	GM_209_A1_E07_MR	g2398523	BLASTX	151	1e-09	58	(Y13721) Transcription factor [Arabidopsis thaliana]
14407	GM_209_A1_E08_T7	g2335067	BLASTN	351	8e-09	60	Human BAC clone GS200K05 from 7q21-q22, complete sequence [Homo sapiens]
14408	GM_209_A1_E10_MR	g2995405	BLASTX	172	5e-11	38	(Y12432) polyprotein [Ananas comosus]
14409	GM_209_A1_E11_MR	g3461834	BLASTN	434	1e-12	64	Arabidopsis thaliana chromosome II BAC T9I4 genomic sequence, complete sequence [Arabidopsis thaliana]
14410	GM_209_A1_F04_T7	g507910	BLASTN	402	1e-11	77	Glycine max BSR-101 satellite SB92 genomic sequence.
14411	GM_209_A1_F08_T7	g2522228	BLASTX	258	3e-21	45	(AB007466) reverse transcriptase-like protein [Vicia faba]
14412	GM_209_A1_F10_T7	g99922	BLASTX	240	1e-19	65	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
14413	GM_209_A1_G01_T7	g507910	BLASTN	597	2e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
14414	GM_209_A1_G08_T7	g3097320	BLASTN	560	3e-18	80	Glycine max gene for Bd 30K, complete cds
14415	GM_209_A1_G09_MR	g531389	BLASTX	246	1e-18	48	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14416	GM_209_A1_G11_MR	g2245068	BLASTX	253	6e-21	76	(Z97342) serine protease homolog [Arabidopsis thaliana]
14417	GM_209_A1_H01_MR	g1658457	BLASTX	193	1e-23	75	(U75248) reverse transcriptase [Gossypium barbadense]
14418	GM_209_A1_H01_T7	g905361	BLASTX	743	7e-73	91	(U22103) gag-protease polyprotein [Glycine max]
14419	GM_209_A1_H08_T7	g3777527	BLASTX	113	9e-18	54	(AF053008) gag-pol polyprotein [Glycine max]
14420	GM_209_A1_H10_T7	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14421	GM_209_A1_H11_T7	g4156185	BLASTN	418	8e-12	62	Homo sapiens PAC clone DJ0803F10 from 7q33-q36, complete sequence [Homo sapiens]
14422	GM_209_B1_A07_MR	g3695395	BLASTX	229	2e-17	37	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
14423	GM_209_B1_A12_MR	g3777527	BLASTX	556	1e-51	86	(AF053008) gag-pol polyprotein [Glycine max]
14424	GM_209_B1_B08_MR	g507910	BLASTN	351	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
14425	GM_209_B1_B12_MR	g4063770	BLASTX	156	2e-09	35	(AB004906) transposase [Ipomoea purpurea]
14426	GM_209_B1_C01_MR	g2501493	BLASTX	92	1e-10	54	FLAVONOL 3-O-GLUCOSYLTRANSFERASE 4 (UDP-GLUCOSE FLAVONOID 3-O-GLUCOSYLTRANSFERASE 4) gi 458547 (X77460) UTP-glucose glucosyltransferase [Manihot esculenta]
14427	GM_209_B1_C08_MR	g3142328	BLASTN	595	1e-41	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14428	GM_209_B1_D05_MR	g3600044	BLASTX	163	8e-10	50	(AF080119) contains similarity to proteases [Arabidopsis thaliana]
14429	GM_209_B1_D09_MR	g507910	BLASTN	386	8e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14430	GM_209_B1_D10_MR	g2522228	BLASTX	203	5e-15	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
14431	GM_209_B1_D12_MR	g3941524	BLASTX	384	8e-35	75	(AF062916) putative transcription factor [Arabidopsis thaliana]
14432	GM_209_B1_E02_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14433	GM_209_B1_E04_MR	g976284	BLASTX	207	4e-16	37	reverse transcriptase [Arabidopsis thaliana]
14434	GM_209_B1_E05_MR	g3941524	BLASTX	341	3e-30	71	(AF062916) putative transcription factor [Arabidopsis thaliana]
14435	GM_209_B1_E06_MR	g2992164	BLASTX	210	2e-15	56	(AB012580) eIF3 p66 [Mus musculus]
14436	GM_209_B1_E11_MR	g100484	BLASTX	346	7e-30	62	hypothetical protein - garden snapdragon
14437	GM_209_B1_F06_MR	g507910	BLASTN	503	4e-16	81	Glycine max BSR-101 satellite SB92 genomic sequence.
14438	GM_209_B1_F11_MR	g2522230	BLASTX	158	7e-11	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14439	GM_209_B1_G12_MR	g3319362	BLASTX	158	2e-09	36	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
14440	GM_209_B1_H02_MR	g3777527	BLASTX	206	2e-14	40	(AF053008) gag-pol polyprotein [Glycine max]
14441	GM_209_B1_H09_MR	g507910	BLASTN	373	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14442	GM_209_B1_H11_MR	g3097320	BLASTN	646	3e-22	74	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14443	GM_210_A1_A03_MR	g170029	BLASTN	380	4e-10	79	Glycine max cv. Dare nodulin 26 gene fragment.
14444	GM_210_A1_B10_MR	g4063760	BLASTX	359	7e-31	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14445	GM_210_A1_C08_MR	g3777527	BLASTX	158	3e-09	45	(AF053008) gag-pol polyprotein [Glycine max]
14446	GM_210_A1_E05_MR	g1666236	BLASTX	171	9e-12	37	(U76261) unknown [Hordeum vulgare]
14447	GM_210_A1_G04_MR	g507910	BLASTN	531	2e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
14448	GM_210_A1_G07_MR	g3930515	BLASTX	100	5e-11	38	(AF059674) putative gag protein [Nicotiana tabacum]
14449	GM_210_A1_G08_MR	g1769898	BLASTX	353	1e-32	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14450	GM_210_A2_B01_MR	g3645899	BLASTX	227	9e-17	54	(U68408) 5' end not determined experimentally [Zea mays]
14451	GM_210_A2_C08_MR	g4115365	BLASTX	214	3e-15	42	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
14452	GM_210_A2_D05_MR	g3142379	BLASTX	216	2e-16	73	(AF053008) envelope-like [Glycine max]
14453	GM_210_A2_D11_MR	g3510336	BLASTN	494	3e-15	68	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]
14454	GM_210_A2_E03_MR	g18575	BLASTN	511	3e-16	89	Soybean ENOD2A gene for Ngm-75
14455	GM_210_A2_F01_MR	g3645899	BLASTX	328	1e-27	56	(U68408) 5' end not determined experimentally [Zea mays]
14456	GM_210_A2_F03_MR	g4115365	BLASTX	228	9e-17	43	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
14457	GM_210_A2_F07_MR	g3142330	BLASTX	324	1e-27	86	(U96295) envelope-like [Glycine max]
14458	GM_210_A2_F10_MR	g3777527	BLASTX	642	8e-61	96	(AF053008) gag-pol polyprotein [Glycine max]
14459	GM_210_A2_F12_MR	g629693	BLASTX	219	7e-17	40	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
14460	GM_210_A2_H02_MR	g1402883	BLASTX	176	6e-16	47	(X98130) unknown [Arabidopsis thaliana] gi 1495263 gnl PID e242837 (X97487) orf09 [Arabidopsis thaliana]
14461	GM_210_A2_H06_MR	g2995405	BLASTX	472	3e-43	62	(Y12432) polyprotein [Ananas comosus]
14462	GM_210_B1_A01_MR	g3063708	BLASTX	221	6e-16	42	(AL022537) putative protein [Arabidopsis thaliana]
14463	GM_210_B1_A03_T7	g2129618	BLASTX	192	4e-13	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
14464	GM_210_B1_A04_MR	g3097320	BLASTN	833	1e-30	82	Glycine max gene for Bd 30K, complete cds
14465	GM_210_B1_B01_MR	g4063760	BLASTX	202	4e-14	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14466	GM_210_B1_B04_T7	g3319362	BLASTX	179	2e-25	53	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
14467	GM_210_B1_B06_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14468	GM_210_B1_B06_T7	g507910	BLASTN	394	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14469	GM_210_B1_B10_T7	g4063756	BLASTN	458	1e-13	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14470	GM_210_B1_C09_T7	g4140712	BLASTX	307	1e-26	40	(AF110183) putative integrase [Oryza sativa]
14471	GM_210_B1_D03_T7	g226407	BLASTX	132	1e-11	54	retrotransposon del1-46 [Lilium henryi]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14472	GM_210_B1_D04_T7	g166884	BLASTN	1047	5e-41	78	A.thaliana telomeric DNA. >gi 589934 gb I07744 Sequence 1 from Patent EP 0338266
14473	GM_210_B1_D08_T7	g2764525	BLASTN	946	4e-36	69	Pisum sativum genomic DNA encoding truncated Ty3/Gypsy-like retroelement Cyclops-1
14474	GM_210_B1_D11_MR	g170080	BLASTN	460	7e-14	73	Soybean seed lectin gene transposable element tgm1.
14475	GM_210_B1_E02_T7	g18559	BLASTN	654	1e-22	75	G.max gene for catalase
14476	GM_210_B1_E04_MR	g1666236	BLASTX	166	3e-11	30	(U76261) unknown [Hordeum vulgare]
14477	GM_210_B1_E05_T7	g507910	BLASTN	873	8e-33	97	Glycine max BSR-101 satellite SB92 genomic sequence.
14478	GM_210_B1_E06_MR	g4063756	BLASTN	407	2e-11	71	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14479	GM_210_B1_F02_MR	g2129618	BLASTX	156	2e-09	32	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
14480	GM_210_B1_F03_T7	g3142328	BLASTN	634	1e-21	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14481	GM_210_B1_F05_T7	g3097320	BLASTN	601	4e-20	79	Glycine max gene for Bd 30K, complete cds
14482	GM_210_B1_F11_MR	g416692	BLASTX	335	1e-29	74	AUXIN-INDUCED PROTEIN 6B gi 81764 pir JQ1098 auxin-induced protein 6B - soybean gi 255577 bbs 113700 (S44175) orf 6B [Glycine max=soybeans, cv. Wayne, Peptide, 90 aa] [Glycine max]
14483	GM_210_B1_F12_MR	g1769898	BLASTX	385	2e-34	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14484	GM_210_B2_A01_MR	g4038056	BLASTX	399	2e-35	52	(AC005897) putative transposon [Arabidopsis thaliana]
14485	GM_210_B2_A06_T7	g905361	BLASTX	171	4e-11	28	(U22103) gag-protease polyprotein [Glycine max]
14486	GM_210_B2_A10_MR	g2522227	BLASTX	217	4e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14487	GM_210_B2_B05_MR	g992916	BLASTN	473	2e-14	70	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
14488	GM_210_B2_B12_T7	g1769898	BLASTX	261	7e-21	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14489	GM_210_B2_C02_T7	g3913420	BLASTX	225	4e-30	77	S-ADENOSYLMETHIONINE DECARBOXYLASE PROENZYME (ADOMETDC) (SAMDC) >gi 1421752 (U60592) S-adenosylmethionine decarboxylase [Pisum sativum]
14490	GM_210_B2_C05_MR	g2244950	BLASTN	350	9e-09	67	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 5
14491	GM_210_B2_C07_MR	g507910	BLASTN	606	9e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
14492	GM_210_B2_D01_MR	g18559	BLASTN	752	5e-27	70	G.max gene for catalase
14493	GM_210_B2_D10_MR	g3645899	BLASTX	227	4e-29	45	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14494	GM_210_B2_D10_T7	g1402877	BLASTX	171	1e-11	73	(X98130) unknown [Arabidopsis thaliana] gi 1495257 gnl PID e242925 (X97485) orf03 [Arabidopsis thaliana]
14495	GM_210_B2_E06_T7	g3935157	BLASTX	182	4e-12	80	(AC005106) T25N20.21 [Arabidopsis thaliana]
14496	GM_210_B2_E08_T7	g3873182	BLASTN	444	5e-13	63	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
14497	GM_210_B2_E12_T7	g2351066	BLASTN	632	2e-21	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP9
14498	GM_210_B2_F01_MR	g507910	BLASTN	702	4e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
14499	GM_210_B2_F01_T7	g4092470	BLASTN	349	1e-08	67	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
14500	GM_210_B2_F07_MR	g2464905	BLASTX	194	1e-14	67	(Z99708) minor allergen [Arabidopsis thaliana]
14501	GM_210_B2_F09_MR	g170080	BLASTN	430	2e-12	64	Soybean seed lectin gene transposable element tgm1.
14502	GM_210_B2_F10_MR	g507910	BLASTN	451	9e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14503	GM_210_B2_G02_MR	g3283026	BLASTX	318	7e-27	43	putative transposase [Arabidopsis thaliana]
14504	GM_210_B2_G04_MR	g2979567	BLASTN	350	9e-09	62	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence [Homo sapiens]
14505	GM_210_B2_G06_MR	g507910	BLASTN	413	5e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14506	GM_210_B2_G06_T7	g507910	BLASTN	401	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14507	GM_210_B2_G10_MR	g2462935	BLASTX	154	4e-13	40	(Y12321) open reading frame 1 [Brassica oleracea]
14508	GM_210_B2_H02_MR	g2522230	BLASTX	230	2e-18	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14509	GM_210_B2_H02_T7	g3142328	BLASTN	1084	4e-42	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14510	GM_210_B2_H04_MR	g3319372	BLASTX	217	1e-15	38	(AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]
14511	GM_210_B2_H07_T7	g3930515	BLASTX	103	6e-10	45	(AF059674) putative gag protein [Nicotiana tabacum]
14512	GM_211_A1_A07_T7	g2323254	BLASTN	465	6e-14	62	Human Chromosome X, complete sequence [Homo sapiens]
14513	GM_211_A1_A09_MR	g4038056	BLASTX	311	6e-26	50	(AC005897) putative transposon [Arabidopsis thaliana]
14514	GM_211_A1_B12_T7	g3645899	BLASTX	192	2e-14	49	(U68408) 5' end not determined experimentally [Zea mays]
14515	GM_211_A1_C01_T7	g3142328	BLASTN	562	2e-18	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14516	GM_211_A1_C12_T7	g3142328	BLASTN	872	2e-32	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14517	GM_211_A1_D10_T7	g4063760	BLASTX	195	2e-13	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14518	GM_211_A1_E05_MR	g1142699	BLASTN	251	3e-12	69	Glycine max satellite STR120-A.1.
14519	GM_211_A1_E05_T7	g3550435	BLASTN	387	2e-10	62	Hordeum vulgare Hotr1 gene

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14520	GM_211_A1_E06_T7	g507910	BLASTN	562	9e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
14521	GM_211_A1_E10_MR	g2462134	BLASTX	337	1e-29	40	(Y13368) reverse transcriptase [Beta vulgaris]
14522	GM_211_A1_F02_T7	g4063760	BLASTX	293	8e-24	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14523	GM_211_A1_F05_T7	g1184075	BLASTX	162	7e-10	44	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
14524	GM_211_A1_F10_MR	g100484	BLASTX	353	1e-30	59	hypothetical protein - garden snapdragon
14525	GM_211_A1_F10_T7	g3426334	BLASTN	538	2e-17	64	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
14526	GM_211_A1_G10_T7	g507910	BLASTN	341	8e-09	68	Glycine max BSR-101 satellite SB92 genomic sequence.
14527	GM_211_A2_A04_MR	g3097320	BLASTN	431	2e-12	67	Glycine max gene for Bd 30K, complete cds
14528	GM_211_A2_A04_T7	g4063760	BLASTX	613	5e-58	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14529	GM_211_A2_A07_MR	g4063760	BLASTX	352	5e-33	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14530	GM_211_A2_A10_T7	g2773249	BLASTX	112	9e-13	79	(AF039707) glutamate carboxypeptidase II [Rattus norvegicus]
14531	GM_211_A2_A11_MR	g507910	BLASTN	357	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14532	GM_211_A2_B02_MR	g3845197	BLASTN	378	5e-10	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
14533	GM_211_A2_B03_MR	g3097320	BLASTN	370	1e-09	66	Glycine max gene for Bd 30K, complete cds
14534	GM_211_A2_B03_T7	g507910	BLASTN	479	5e-15	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14535	GM_211_A2_B04_MR	g4063760	BLASTX	472	7e-43	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14536	GM_211_A2_B05_MR	g3645899	BLASTX	392	2e-34	42	(U68408) 5' end not determined experimentally [Zea mays]
14537	GM_211_A2_B08_MR	g3645899	BLASTX	313	4e-30	54	(U68408) 5' end not determined experimentally [Zea mays]
14538	GM_211_A2_B10_MR	g3645899	BLASTX	291	1e-23	40	(U68408) 5' end not determined experimentally [Zea mays]
14539	GM_211_A2_B11_MR	g3319362	BLASTX	190	6e-13	32	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
14540	GM_211_A2_B11_T7	g2522228	BLASTX	270	1e-22	75	(AB007466) reverse transcriptase-like protein [Vicia faba]
14541	GM_211_A2_C01_T7	g2522227	BLASTX	156	3e-10	42	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14542	GM_211_A2_C02_T7	g1769898	BLASTX	437	2e-40	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14543	GM_211_A2_C03_MR	g1669680	BLASTN	370	1e-09	64	Human DNA sequence from PAC 293E14 contains ESTs, STS
14544	GM_211_A2_C05_MR	g2914758	BLASTN	496	2e-15	64	Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds
14545	GM_211_A2_C09_MR	g3142328	BLASTN	2339	4e-100	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14546	GM_211_A2_C09_T7	g170002	BLASTN	357	3e-09	67	soybean leghemoglobin pseudogene, segment 2.
14547	GM_211_A2_C11_MR	g2995405	BLASTX	359	1e-40	57	(Y12432) polyprotein [Ananas comosus]
14548	GM_211_A2_D03_MR	g1769897	BLASTX	203	1e-14	34	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14549	GM_211_A2_D05_T7	g4063760	BLASTX	545	1e-50	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14550	GM_211_A2_D06_T7	g2961349	BLASTX	287	4e-23	56	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
14551	GM_211_A2_D07_T7	g3779030	BLASTX	143	5e-09	29	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
14552	GM_211_A2_E03_T7	g18559	BLASTN	585	2e-19	81	G.max gene for catalase
14553	GM_211_A2_E07_T7	g3142328	BLASTN	1866	7e-78	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14554	GM_211_A2_E09_MR	g3097320	BLASTN	1504	4e-61	80	Glycine max gene for Bd 30K, complete cds
14555	GM_211_A2_E09_T7	g3142328	BLASTN	2020	6e-85	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14556	GM_211_A2_F04_MR	g836954	BLASTX	178	9e-12	41	(U20948) receptor protein kinase [Ipomoea trifida]
14557	GM_211_A2_F07_MR	g992916	BLASTN	947	9e-36	92	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
14558	GM_211_A2_F08_MR	g342964	BLASTN	386	2e-11	61	paramecium species 5,311 mt dna dimer: replication init. region.
14559	GM_211_A2_F09_MR	g905361	BLASTX	617	2e-59	90	(U22103) gag-protease polyprotein [Glycine max]
14560	GM_211_A2_G09_MR	g3777527	BLASTX	741	2e-71	93	(AF053008) gag-pol polyprotein [Glycine max]
14561	GM_211_A2_H01_MR	g1769897	BLASTX	195	2e-26	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14562	GM_211_B1_A04_MR	g1658457	BLASTX	297	1e-25	65	(U75248) reverse transcriptase [Gossypium barbadense]
14563	GM_211_B1_A08_MR	g2522227	BLASTX	236	4e-19	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14564	GM_211_B1_A10_T7	g1142701	BLASTN	1008	3e-39	82	Glycine max satellite STR120-A.3.
14565	GM_211_B1_A12_MR	g18559	BLASTN	832	1e-30	78	G.max gene for catalase
14566	GM_211_B1_B01_MR	g18559	BLASTN	519	2e-16	69	G.max gene for catalase
14567	GM_211_B1_B07_MR	g4063760	BLASTX	310	1e-25	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14568	GM_211_B1_B08_MR	g2995405	BLASTX	342	3e-41	58	(Y12432) polyprotein [Ananas comosus]
14569	GM_211_B1_C01_T7	g629693	BLASTX	162	1e-10	39	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
14570	GM_211_B1_C05_MR	g507910	BLASTN	405	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14571	GM_211_B1_C05_T7	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14572	GM_211_B1_D02_T7	g4063770	BLASTX	199	5e-14	41	(AB004906) transposase [Ipomoea purpurea]
14573	GM_211_B1_D07_MR	g2522230	BLASTX	170	4e-12	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14574	GM_211_B1_D08_T7	g2656030	BLASTN	720	2e-25	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL8
14575	GM_211_B1_D11_MR	g1707017	BLASTX	495	3e-46	76	(U78721) RNA helicase isolog [Arabidopsis thaliana]
14576	GM_211_B1_D12_MR	g2995405	BLASTX	257	4e-20	45	(Y12432) polyprotein [Ananas comosus]
14577	GM_211_B1_E01_T7	g3080426	BLASTX	151	8e-09	41	(AL022604) putative protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14578	GM_211_B1_E02_T7	g3142328	BLASTN	1022	2e-39	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14579	GM_211_B1_E05_T7	g3426334	BLASTN	388	1e-10	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
14580	GM_211_B1_E12_MR	g4063760	BLASTX	429	3e-38	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14581	GM_211_B1_F01_MR	g2129618	BLASTX	154	4e-09	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
14582	GM_211_B1_F06_T7	g4038056	BLASTX	195	2e-13	39	(AC005897) putative transposon [Arabidopsis thaliana]
14583	GM_211_B1_G09_T7	g507910	BLASTN	372	3e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14584	GM_211_B1_H05_T7	g3777527	BLASTX	181	1e-11	89	(AF053008) gag-pol polyprotein [Glycine max]
14585	GM_211_B1_H10_T7	g507910	BLASTN	686	2e-24	87	Glycine max BSR-101 satellite SB92 genomic sequence.
14586	GM_211_B1_H12_T7	g3746069	BLASTX	183	5e-12	37	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
14587	GM_211_B2_A01_MR	g4102692	BLASTX	345	9e-31	81	(AF004810) late-embryogenesis abundant protein [Glycine max]
14588	GM_211_B2_A06_MR	g1168972	BLASTX	242	1e-18	77	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA PRECURSOR gi 480969 pir S37557 clpA protein - rape (fragment) gi 406311 (X75328) clpA gene product [Brassica napus]
14589	GM_211_B2_A07_MR	g507910	BLASTN	426	1e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14590	GM_211_B2_A09_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
14591	GM_211_B2_A10_MR	g1421730	BLASTX	178	5e-12	39	(U43082) RF2 [Zea mays]
14592	GM_211_B2_B01_MR	g3941725	BLASTN	486	6e-15	62	Homo sapiens clone BAC 72m22 chromosome 8 map 8p21, complete sequence [Homo sapiens]
14593	GM_211_B2_B04_T7	g3777527	BLASTX	241	3e-29	90	(AF053008) gag-pol polyprotein [Glycine max]
14594	GM_211_B2_B12_T7	g4063760	BLASTX	247	7e-19	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14595	GM_211_B2_C01_MR	g3319362	BLASTX	168	5e-21	56	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
14596	GM_211_B2_C04_MR	g18559	BLASTN	997	3e-38	77	G.max gene for catalase
14597	GM_211_B2_D03_MR	g13619	BLASTN	405	3e-12	61	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
14598	GM_211_B2_D05_MR	g507910	BLASTN	610	6e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
14599	GM_211_B2_D05_T7	g507910	BLASTN	362	9e-10	80	Glycine max BSR-101 satellite SB92 genomic sequence.
14600	GM_211_B2_D12_MR	g3845197	BLASTN	466	5e-14	63	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
14601	GM_211_B2_E04_MR	g507910	BLASTN	387	7e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14602	GM_211_B2_E09_T7	g507910	BLASTN	481	4e-15	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14603	GM_211_B2_F04_T7	g2129618	BLASTX	171	6e-11	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14604	GM_211_B2_F05_MR	g226407	BLASTX	498	2e-45	62	retrotransposon del1-46 [Lilium henryi]
14605	GM_211_B2_F08_MR	g1840106	BLASTN	367	4e-10	62	Human fragile site locus (FRA16B) minisatellite repeat
14606	GM_211_B2_F10_MR	g4063756	BLASTN	402	4e-11	69	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14607	GM_211_B2_G01_MR	g3695395	BLASTX	166	1e-10	34	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
14608	GM_211_B2_G04_T7	g3779021	BLASTX	142	3e-10	44	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]
14609	GM_211_B2_G05_MR	g3645899	BLASTX	246	7e-19	44	(U68408) 5' end not determined experimentally [Zea mays]
14610	GM_211_B2_G07_T7	g3821288	BLASTN	389	5e-11	62	Pisum sativum repeated element highly similar to the BamHI repeated sequence families of Vicia faba
14611	GM_211_B2_G10_MR	g4063760	BLASTX	445	5e-40	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14612	GM_211_B2_G12_MR	g3128143	BLASTN	369	1e-09	71	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTI20, complete sequence [Arabidopsis thaliana]
14613	GM_211_B2_H05_MR	g4038056	BLASTX	268	3e-21	43	(AC005897) putative transposon [Arabidopsis thaliana]
14614	GM_211_B2_H09_MR	g1142699	BLASTN	325	8e-19	71	Glycine max satellite STR120-A.1.
14615	GM_211_B2_H11_MR	g507910	BLASTN	404	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14616	GM_212_A1_A12_MR	g2865437	BLASTX	184	4e-12	41	(AF039376) polyprotein [Arabidopsis arenosa]
14617	GM_212_A1_B05_MR	g4063760	BLASTX	382	3e-33	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14618	GM_212_A1_C11_MR	g507910	BLASTN	588	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
14619	GM_212_A1_D06_MR	g4063760	BLASTX	207	1e-14	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14620	GM_212_A1_D09_MR	g3142328	BLASTN	1142	8e-45	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14621	GM_212_A1_D12_MR	g507910	BLASTN	646	1e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
14622	GM_212_A1_E10_MR	g3097320	BLASTN	889	3e-33	80	Glycine max gene for Bd 30K, complete cds
14623	GM_212_A1_G01_MR	g2104945	BLASTN	293	2e-10	74	Glycine max copia-like retrotransposon Tgmr, complete sequence
14624	GM_212_A1_G04_MR	g2209031	BLASTX	167	7e-11	40	(AB001569) ORF of 1.56 kb [Daucus carota]
14625	GM_212_A1_G09_MR	g2522230	BLASTX	245	4e-20	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14626	GM_212_A1_G11_MR	g2522227	BLASTX	219	2e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14627	GM_212_A1_H09_MR	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14628	GM_212_A1_H11_MR	g100484	BLASTX	409	9e-37	54	hypothetical protein - garden snapdragon
14629	GM_212_A2_A01_T7	g3176795	BLASTN	462	9e-15	68	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
14630	GM_212_A2_A02_T7	g2809251	BLASTX	315	2e-27	48	(AC002560) F21B7.20 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14631	GM_212_A2_A03_T7	g4063756	BLASTN	421	6e-12	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14632	GM_212_A2_A12_MR	g1881585	BLASTX	155	1e-10	45	(U72489) remorin [Solanum tuberosum]
14633	GM_212_A2_B01_MR	g4063760	BLASTX	357	3e-32	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14634	GM_212_A2_B03_T7	g170029	BLASTN	460	8e-14	86	Glycine max cv. Dare nodulin 26 gene fragment.
14635	GM_212_A2_B06_MR	g3142328	BLASTN	909	3e-34	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14636	GM_212_A2_B11_MR	g905361	BLASTX	495	5e-50	96	(U22103) gag-protease polyprotein [Glycine max]
14637	GM_212_A2_C01_MR	g4115363	BLASTX	209	6e-15	46	(AC005957) putative disease resistance protein [Arabidopsis thaliana]
14638	GM_212_A2_C03_T7	g1769898	BLASTX	385	2e-34	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14639	GM_212_A2_C04_MR	g3953470	BLASTX	150	6e-09	61	(AC002328) F20N2.15 [Arabidopsis thaliana]
14640	GM_212_A2_C05_MR	g1666236	BLASTX	209	4e-16	33	(U76261) unknown [Hordeum vulgare]
14641	GM_212_A2_C12_T7	g1928960	BLASTX	184	9e-16	63	(U92286) pyrroline-5-carboxylate synthetase [Actinidia deliciosa]
14642	GM_212_A2_D01_MR	g4063760	BLASTX	176	2e-11	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14643	GM_212_A2_D02_T7	g3142328	BLASTN	1573	2e-64	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14644	GM_212_A2_D06_MR	g4063756	BLASTN	421	6e-12	69	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14645	GM_212_A2_D08_T7	g4063760	BLASTX	203	3e-14	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14646	GM_212_A2_E02_T7	g2735745	BLASTN	361	1e-09	64	Oncorhynchus kisutch growth hormone 1 gene, intron C, complete sequence
14647	GM_212_A2_E04_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14648	GM_212_A2_E05_MR	g2656024	BLASTN	465	6e-14	66	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6
14649	GM_212_A2_E09_T7	g2129618	BLASTX	200	5e-14	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
14650	GM_212_A2_E10_T7	g2618605	BLASTN	483	9e-15	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUK11, complete sequence [Arabidopsis thaliana]
14651	GM_212_A2_F01_MR	g3513747	BLASTX	275	1e-21	50	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
14652	GM_212_A2_F05_T7	g3777527	BLASTX	637	3e-60	83	(AF053008) gag-pol polyprotein [Glycine max]
14653	GM_212_B1_A06_MR	g507910	BLASTN	615	4e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
14654	GM_212_B1_A08_MR	g507910	BLASTN	386	8e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14655	GM_212_B1_A11_MR	g18559	BLASTN	826	2e-30	75	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14656	GM_212_B1_C01_MR	g507910	BLASTN	644	2e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
14657	GM_212_B1_C02_MR	g3273387	BLASTN	422	5e-12	66	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
14658	GM_212_B1_C04_MR	g1666236	BLASTX	179	3e-15	32	(U76261) unknown [Hordeum vulgare]
14659	GM_212_B1_C07_MR	g2351060	BLASTX	436	2e-40	82	(AB006660) sucrose-phosphate synthase [Citrus unshiu]
14660	GM_212_B1_D03_MR	g1480927	BLASTN	500	9e-16	91	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
14661	GM_212_B1_E12_MR	g3283026	BLASTX	139	2e-17	38	putative transposase [Arabidopsis thaliana]
14662	GM_212_B1_F01_MR	g703220	BLASTN	656	3e-23	76	Pisum sativum (clone HW16-26) gene fragment.
14663	GM_212_B1_F07_MR	g400636	BLASTX	166	6e-13	67	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 1, CHLOROPLAST gi 320098 pir JQ1671 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - maize chloroplast gi 12420 (X62370) NADH Dehydrogenase subunit A [Zea mays] gi 902289 (X86563) NADH dehydrogenase ND1 [Zea mays]
14664	GM_212_B1_F09_MR	g2522230	BLASTX	257	2e-21	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14665	GM_212_B1_G12_MR	g1658455	BLASTX	342	2e-30	66	(U75247) reverse transcriptase [Gossypium barbadense]
14666	GM_213_A1_A01_T7	g3777527	BLASTX	142	2e-11	38	(AF053008) gag-pol polyprotein [Glycine max]
14667	GM_213_A1_A02_T7	g4063760	BLASTX	152	1e-08	36	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14668	GM_213_A1_A05_MR	g2443320	BLASTX	253	3e-20	46	(D85597) polyprotein [Oryza australiensis]
14669	GM_213_A1_A08_MR	g531389	BLASTX	274	1e-21	50	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
14670	GM_213_A1_A09_T7	g507910	BLASTN	534	2e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
14671	GM_213_A1_A10_T7	g2828293	BLASTX	244	1e-18	56	(AL021687) putative protein [Arabidopsis thaliana]
14672	GM_213_A1_A12_MR	g2462134	BLASTX	229	1e-17	51	(Y13368) reverse transcriptase [Beta vulgaris]
14673	GM_213_A1_B01_T7	g18559	BLASTN	355	5e-09	65	G.max gene for catalase
14674	GM_213_A1_B03_T7	g3097320	BLASTN	941	1e-35	73	Glycine max gene for Bd 30K, complete cds
14675	GM_213_A1_B08_MR	g18559	BLASTN	552	5e-18	74	G.max gene for catalase
14676	GM_213_A1_B08_T7	g100484	BLASTX	377	3e-33	52	hypothetical protein - garden snapdragon
14677	GM_213_A1_B11_T7	g1142699	BLASTN	1429	3e-58	88	Glycine max satellite STR120-A.1.
14678	GM_213_A1_C05_T7	g1934969	BLASTN	262	1e-09	64	P.falciparum mRNA for AARP1 protein, partial
14679	GM_213_A1_C06_MR	g1167523	BLASTX	222	4e-16	54	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14680	GM_213_A1_D02_T7	g18559	BLASTN	1047	2e-40	76	G.max gene for catalase
14681	GM_213_A1_D03_MR	g3777527	BLASTX	310	2e-25	89	(AF053008) gag-pol polyprotein [Glycine max]
14682	GM_213_A1_E03_T7	g507910	BLASTN	353	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14683	GM_213_A1_E05_MR	g1769898	BLASTX	179	5e-12	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14684	GM_213_A1_E09_T7	g2120736	BLASTX	168	1e-10	32	X-Pro dipeptidyl-peptidase (EC 3.4.14.11) - Xanthomonas maltophilia gi 1753197 gnl PID d1012539 (D83263) dipeptidyl peptidase IV [Stenotrophomonas maltophilia]
14685	GM_213_A1_F03_T7	g169360	BLASTN	270	2e-14	92	P.vulgaris PVPK-1 protein, complete cds.
14686	GM_213_A1_F06_T7	g173088	BLASTX	182	6e-12	36	has homology to retroviral pol genes; ORF2 TYB3-2 (5' end of coding region not precisely determined)
14687	GM_213_A1_G01_T7	g507910	BLASTN	370	4e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14688	GM_213_A1_G05_T7	g2801423	BLASTN	416	9e-12	61	Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence [Homo sapiens]
14689	GM_213_A1_G06_T7	g2315153	BLASTX	229	4e-18	76	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
14690	GM_213_A1_G07_T7	g4063760	BLASTX	405	7e-38	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14691	GM_213_A1_G08_T7	g2642431	BLASTX	433	1e-38	58	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
14692	GM_213_A1_G09_T7	g100484	BLASTX	438	6e-40	54	hypothetical protein - garden snapdragon
14693	GM_213_A1_H07_T7	g1633547	BLASTN	448	3e-13	63	Human chromosome 12p13 sequence, complete sequence [Homo sapiens]
14694	GM_213_A1_H12_T7	g4049647	BLASTN	405	3e-11	63	Melanoplus sanguinipes entomopoxvirus, complete genome
14695	GM_213_B1_A06_MR	g2160150	BLASTX	265	3e-22	69	(AC000375) EST gb T43829 comes from this gene. [Arabidopsis thaliana]
14696	GM_213_B1_A07_MR	g1589778	BLASTX	189	7e-13	77	(U62135) SPINDLY [Arabidopsis thaliana]
14697	GM_213_B1_A08_MR	g531389	BLASTX	223	3e-16	57	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
14698	GM_213_B1_A09_MR	g170029	BLASTN	352	7e-09	81	Glycine max cv. Dare nodulin 26 gene fragment.
14699	GM_213_B1_A10_T7	g2522228	BLASTX	290	8e-25	80	(AB007466) reverse transcriptase-like protein [Vicia faba]
14700	GM_213_B1_A12_MR	g3885339	BLASTX	222	2e-16	46	(AC005623) putative bzip protein [Arabidopsis thaliana]
14701	GM_213_B1_A12_T7	g3142328	BLASTN	1043	3e-40	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14702	GM_213_B1_B01_MR	g1041702	BLASTX	122	3e-11	64	(U30476) expansin At-EXP1 [Arabidopsis thaliana]
14703	GM_213_B1_B05_MR	g2244915	BLASTX	169	1e-10	41	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
14704	GM_213_B1_B09_T7	g421894	BLASTX	200	4e-29	78	1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) 5 - mung bean (fragment) gi 297850 (Z12134) ACC synthase [Vigna radiata] gi 553115 (M94863) 1-aminocyclopropane-1-carboxylate synthase [Vigna radiata]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14705	GM_213_B1_B12_MR	g2281100	BLASTX	204	1e-26	49	(AC002333) LecRK1 protein kinase isolog [Arabidopsis thaliana]
14706	GM_213_B1_C03_MR	g507910	BLASTN	356	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
14707	GM_213_B1_C03_T7	g507910	BLASTN	386	8e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14708	GM_213_B1_C08_T7	g4150930	BLASTN	435	1e-12	63	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
14709	GM_213_B1_C10_MR	g3777527	BLASTX	258	2e-38	89	(AF053008) gag-pol polyprotein [Glycine max]
14710	GM_213_B1_C11_T7	g3024126	BLASTX	199	1e-14	94	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) gi 1655576 gnl PID e236742 (Z71271) S-adenosyl-L-methionine synthetase 1 [Catharanthus roseus]
14711	GM_213_B1_D04_MR	g3097320	BLASTN	813	9e-30	77	Glycine max gene for Bd 30K, complete cds
14712	GM_213_B1_D06_T7	g4063756	BLASTN	450	3e-13	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14713	GM_213_B1_D12_T7	g170029	BLASTN	399	5e-11	81	Glycine max cv. Dare nodulin 26 gene fragment.
14714	GM_213_B1_E02_MR	g3097320	BLASTN	468	4e-14	71	Glycine max gene for Bd 30K, complete cds
14715	GM_213_B1_E04_MR	g2522228	BLASTX	195	4e-14	65	(AB007466) reverse transcriptase-like protein [Vicia faba]
14716	GM_213_B1_E10_T7	g3142328	BLASTN	2032	2e-85	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14717	GM_213_B1_E11_T7	g4063760	BLASTX	189	9e-13	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14718	GM_213_B1_E12_T7	g2522230	BLASTX	313	3e-27	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14719	GM_213_B1_F02_T7	g3142328	BLASTN	1024	2e-39	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14720	GM_213_B1_G01_T7	g3097320	BLASTN	483	8e-15	74	Glycine max gene for Bd 30K, complete cds
14721	GM_214_A2_A02_MR	g2961384	BLASTX	147	1e-18	51	(AL022141) aldehyde dehydrogenase like protein [Arabidopsis thaliana]
14722	GM_214_A2_A03_T7	g3097320	BLASTN	586	2e-19	80	Glycine max gene for Bd 30K, complete cds
14723	GM_214_A2_A06_T7	g4063760	BLASTX	403	2e-35	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14724	GM_214_A2_A07_T7	g3142328	BLASTN	651	2e-22	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14725	GM_214_A2_A09_MR	g3551960	BLASTX	200	2e-23	49	(AF082033) senescence-associated protein 15 [Hemerocallis hybrid cultivar]
14726	GM_214_A2_A12_MR	g507910	BLASTN	413	5e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14727	GM_214_A2_B01_T7	g18559	BLASTN	723	9e-26	84	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14728	GM_214_A2_C01_MR	g2129709	BLASTX	248	6e-19	37	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
14729	GM_214_A2_C04_T7	g2842542	BLASTN	456	1e-13	60	Ipomoea purpurea DNA, LTR retrotransposon RTip1
14730	GM_214_A2_C07_T7	g3599418	BLASTN	509	5e-16	74	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
14731	GM_214_A2_C08_MR	g4063760	BLASTX	165	4e-10	31	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14732	GM_214_A2_C11_MR	g3142328	BLASTN	660	7e-23	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14733	GM_214_A2_D10_MR	g507910	BLASTN	377	2e-10	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14734	GM_214_A2_D11_MR	g1171591	BLASTN	313	2e-11	67	P.falciparum complete gene map of plastid-like DNA (IR-B)
14735	GM_214_A2_E03_MR	g3645899	BLASTX	449	1e-40	60	(U68408) 5' end not determined experimentally [Zea mays]
14736	GM_214_A2_E04_MR	g3367520	BLASTX	167	5e-11	48	(AC004392) Similar to protein kinase APK1A, tyrosine-serine-threonine kinase gb D12522 from A. thaliana. [Arabidopsis thaliana]
14737	GM_214_A2_E10_MR	g2995405	BLASTX	182	2e-13	38	(Y12432) polyprotein [Ananas comosus]
14738	GM_214_A2_G10_T7	g3283026	BLASTX	238	3e-18	34	putative transposase [Arabidopsis thaliana]
14739	GM_214_A2_H09_T7	g4063760	BLASTX	156	3e-09	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14740	GM_214_B1_A10_MR	g3193306	BLASTX	101	5e-09	39	(AF069300) contains similarity to Arabidopsis membrane-associated salt-inducible-like protein (GB:AL021637) [Arabidopsis thaliana]
14741	GM_214_B1_E03_MR	g3928116	BLASTN	364	2e-09	61	, complete sequence [Homo sapiens]
14742	GM_214_B1_E10_MR	g2522230	BLASTX	100	4e-10	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14743	GM_215_A1_A03_MR	g18559	BLASTN	1574	2e-64	89	G.max gene for catalase
14744	GM_215_A1_A07_MR	g3645899	BLASTX	442	8e-40	67	(U68408) 5' end not determined experimentally [Zea mays]
14745	GM_215_A1_B07_MR	g2623307	BLASTX	159	1e-09	69	(AC002409) putative ubiquitin protease [Arabidopsis thaliana]
14746	GM_215_A1_C02_MR	g2341016	BLASTN	353	7e-09	66	Human PAC clone RG212D03, complete sequence [Homo sapiens]
14747	GM_215_A1_C04_MR	g4063760	BLASTX	436	5e-39	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14748	GM_215_A1_C05_MR	g507910	BLASTN	406	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14749	GM_215_A1_C06_MR	g1663537	BLASTX	321	4e-28	61	(U55803) disease resistance protein homolog [Glycine max]
14750	GM_215_A1_C10_MR	g3892061	BLASTX	209	2e-15	43	(AC002330) putative reverse transcriptase [Arabidopsis thaliana]
14751	GM_215_A1_D01_MR	g1769898	BLASTX	225	5e-17	33	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14752	GM_215_A1_D09_MR	g3096949	BLASTX	183	2e-12	35	(Y16328) putative cyclic nucleotide-regulated ion channel [Arabidopsis thaliana]
14753	GM_215_A1_D11_MR	g3695395	BLASTX	176	1e-11	34	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
14754	GM_215_A1_F01_MR	g4063760	BLASTX	126	3e-16	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14755	GM_215_A1_F06_MR	g4038471	BLASTX	204	4e-19	90	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]
14756	GM_215_A1_F12_MR	g2522230	BLASTX	180	3e-13	34	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14757	GM_215_A1_G03_MR	g1769898	BLASTX	321	2e-27	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14758	GM_215_A1_G04_MR	g1840106	BLASTN	385	5e-11	65	Human fragile site locus (FRA16B) minisatellite repeat
14759	GM_215_A1_H08_MR	g507910	BLASTN	370	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
14760	GM_215_B1_A07_T7	g2245081	BLASTX	132	1e-09	82	(Z97343) myosin II heavy chain homolog [Arabidopsis thaliana]
14761	GM_215_B1_B08_T7	g4115363	BLASTX	160	1e-09	47	(AC005957) putative disease resistance protein [Arabidopsis thaliana]
14762	GM_215_B1_C05_T7	g100484	BLASTX	261	1e-20	60	hypothetical protein - garden snapdragon
14763	GM_215_B1_E02_T7	g4063760	BLASTX	202	5e-14	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14764	GM_215_B1_F12_T7	g166884	BLASTN	688	7e-25	76	A.thaliana telomeric DNA. >gi 589934 gb I07744 Sequence 1 from Patent EP 0338266
14765	GM_215_B1_G06_T7	g3777527	BLASTX	180	3e-12	58	(AF053008) gag-pol polyprotein [Glycine max]
14766	GM_216_A1_A01_MR	g18559	BLASTN	703	8e-25	75	G.max gene for catalase
14767	GM_216_A1_A04_T7	g1091678	BLASTX	237	4e-18	39	activator-like transposable element [Pennisetum glaucum]
14768	GM_216_A1_B05_MR	g2769655	BLASTN	466	5e-14	64	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
14769	GM_216_A1_B07_MR	g4063756	BLASTN	387	2e-10	73	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
14770	GM_216_A1_B07_T7	g3810596	BLASTX	117	2e-10	28	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
14771	GM_216_A1_B08_MR	g18695	BLASTN	395	5e-11	69	Soybean nodulin 22 gene
14772	GM_216_A1_B09_MR	g1785729	BLASTN	513	4e-16	63	A.thaliana mitochondrial genome, part B
14773	GM_216_A1_B11_T7	g4092470	BLASTN	432	2e-12	66	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
14774	GM_216_A1_C03_T7	g2258315	BLASTX	220	5e-16	48	(AF004878) resistance complex protein I2C-1 [Lycopersicon esculentum]
14775	GM_216_A1_D06_T7	g1173642	BLASTX	207	5e-17	93	(U36191) lipoxygenase [Glycine max] gi 1588566 prf 2208476A lipoxygenase [Glycine max]
14776	GM_216_A1_E01_MR	g3777527	BLASTX	804	3e-78	98	(AF053008) gag-pol polyprotein [Glycine max]
14777	GM_216_A1_E01_T7	g4063760	BLASTX	170	1e-10	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14778	GM_216_A1_E10_MR	g3319351	BLASTX	219	7e-16	55	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14779	GM_216_A2_B02_T7	g3097320	BLASTN	885	5e-33	85	Glycine max gene for Bd 30K, complete cds
14780	GM_216_A2_D05_T7	g4063760	BLASTX	159	4e-10	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14781	GM_216_A2_E06_T7	g3947735	BLASTX	124	4e-09	40	(AJ009720) NL27 [Solanum tuberosum]
14782	GM_216_A2_F06_T7	g4115341	BLASTX	189	1e-12	49	(U51100) chromaffin granule ATPase II [Bos taurus]
14783	GM_216_B2_A05_MR	g2655308	BLASTN	353	3e-09	60	Bactrocera xanthodes strain Samoa mitochondrial D-loop region, complete sequence
14784	GM_216_B2_B01_MR	g629693	BLASTX	257	2e-21	51	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
14785	GM_216_B2_B05_MR	g507910	BLASTN	472	1e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.
14786	GM_216_B2_C04_MR	g3097320	BLASTN	488	5e-15	71	Glycine max gene for Bd 30K, complete cds
14787	GM_216_B2_C07_MR	g3142328	BLASTN	1118	1e-43	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14788	GM_216_B2_C08_MR	g18559	BLASTN	585	5e-28	74	G.max gene for catalase
14789	GM_216_B2_D02_MR	g3695395	BLASTX	127	1e-13	46	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
14790	GM_216_B2_D03_MR	g507910	BLASTN	347	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14791	GM_216_B2_D08_MR	g3777527	BLASTX	362	5e-31	85	(AF053008) gag-pol polyprotein [Glycine max]
14792	GM_216_B2_D12_MR	g3695387	BLASTX	249	4e-20	55	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
14793	GM_216_B2_E04_MR	g3777527	BLASTX	464	8e-42	83	(AF053008) gag-pol polyprotein [Glycine max]
14794	GM_216_B2_G04_MR	g3097320	BLASTN	457	1e-13	70	Glycine max gene for Bd 30K, complete cds
14795	GM_216_B2_G05_MR	g505129	BLASTN	349	8e-09	69	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
14796	GM_216_B2_G06_MR	g507910	BLASTN	657	4e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
14797	GM_216_B2_G07_MR	g507910	BLASTN	565	6e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
14798	GM_216_B2_G09_MR	g505129	BLASTN	369	1e-09	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
14799	GM_216_B2_H03_MR	g3928074	BLASTN	350	9e-09	68	Arabidopsis thaliana chromosome II BAC T7F6 genomic sequence, complete sequence [Arabidopsis thaliana]
14800	GM_216_B2_H07_MR	g2462134	BLASTX	209	2e-15	33	(Y13368) reverse transcriptase [Beta vulgaris]
14801	GM_216_B2_H08_MR	g2564750	BLASTN	447	4e-13	62	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
14802	GM_217_A1_A03_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14803	GM_217_A1_A05_MR	g2997694	BLASTX	168	6e-12	47	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14804	GM_217_A1_C02_MR	g99922	BLASTX	292	5e-43	64	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
14805	GM_217_A1_C06_MR	g100484	BLASTX	183	4e-15	54	hypothetical protein - garden snapdragon
14806	GM_217_A1_C09_MR	g2522227	BLASTX	214	8e-17	57	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
14807	GM_217_A1_D03_MR	g4038056	BLASTX	164	7e-17	48	(AC005897) putative transposon [Arabidopsis thaliana]
14808	GM_217_A1_D05_MR	g3776029	BLASTX	165	1e-11	64	(AJ010476) RNA helicase [Arabidopsis thaliana]
14809	GM_217_A1_E01_MR	g3645899	BLASTX	297	3e-24	51	(U68408) 5' end not determined experimentally [Zea mays]
14810	GM_217_A1_E02_MR	g4063760	BLASTX	101	4e-09	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14811	GM_217_A1_E07_MR	g905361	BLASTX	521	2e-57	92	(U22103) gag-protease polyprotein [Glycine max]
14812	GM_217_A1_E08_MR	g3142328	BLASTN	786	1e-28	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14813	GM_217_A2_B04_MR	g3687234	BLASTX	246	7e-23	55	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
14814	GM_217_A2_B06_MR	g3641865	BLASTX	150	7e-09	58	(AJ011010) beta-galactosidase [Cicer arietinum]
14815	GM_217_A2_B11_MR	g130582	BLASTX	159	2e-09	36	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
14816	GM_217_A2_C01_MR	g507910	BLASTN	615	4e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
14817	GM_217_A2_D03_MR	g4063760	BLASTX	160	1e-09	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14818	GM_217_A2_E01_MR	g2995405	BLASTX	388	3e-34	57	(Y12432) polyprotein [Ananas comosus]
14819	GM_217_A2_F04_MR	g479178	BLASTX	201	7e-14	45	pol polyprotein - Volvox carteri f. nagariensis retrotransposon Osser gi 288597 (X69552) gag,protease,endonuclease, reverse transcriptase,RNaseH [Volvox carteri]
14820	GM_217_A2_F08_MR	g18559	BLASTN	1423	2e-57	88	G.max gene for catalase
14821	GM_217_A2_G01_MR	g3777527	BLASTX	171	1e-10	44	(AF053008) gag-pol polyprotein [Glycine max]
14822	GM_217_A2_G04_MR	g1666236	BLASTX	178	2e-12	31	(U76261) unknown [Hordeum vulgare]
14823	GM_217_A2_H01_MR	g3777527	BLASTX	171	1e-10	39	(AF053008) gag-pol polyprotein [Glycine max]
14824	GM_218_A1_A03_MR	g3777527	BLASTX	248	7e-19	40	(AF053008) gag-pol polyprotein [Glycine max]
14825	GM_218_A1_A05_T7	g3097320	BLASTN	423	4e-12	72	Glycine max gene for Bd 30K, complete cds
14826	GM_218_A1_B07_T7	g3201680	BLASTX	285	4e-23	47	(AF060941) extra-large G-protein [Arabidopsis thaliana]
14827	GM_218_A1_B09_T7	g3377834	BLASTX	154	3e-09	28	(AF075598) No definition line found [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14828	GM_218_A1_B11_T7	g114268	BLASTX	469	8e-44	62	L-ASCORBATE OXIDASE HOMOLOG PRECURSOR (ASCORBASE) gi 541907 pir S23763 gene Bp10 protein - rape gi 17789 (X64257) protein homologous to ascorbate oxidase [Brassica napus]
14829	GM_218_A1_C03_MR	g3142328	BLASTN	1349	3e-54	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14830	GM_218_A1_C03_T7	g2911075	BLASTX	182	3e-19	80	(AL021960) putative protein [Arabidopsis thaliana]
14831	GM_218_A1_C04_MR	g4063760	BLASTX	419	3e-37	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14832	GM_218_A1_C04_T7	g507910	BLASTN	405	1e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14833	GM_218_A1_C11_T7	g905361	BLASTX	153	3e-09	83	(U22103) gag-protease polyprotein [Glycine max]
14834	GM_218_A1_C12_T7	g100484	BLASTX	361	2e-31	54	hypothetical protein - garden snapdragon
14835	GM_218_A1_D04_MR	g2462936	BLASTX	107	4e-10	44	(Y12321) open reading frame 2 [Brassica oleracea]
14836	GM_218_A1_E03_MR	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14837	GM_218_A1_E06_MR	g3930515	BLASTX	107	6e-11	47	(AF059674) putative gag protein [Nicotiana tabacum]
14838	GM_218_A1_E11_T7	g4115365	BLASTX	111	3e-11	48	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
14839	GM_218_A1_E12_T7	g3287696	BLASTX	196	3e-18	57	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]
14840	GM_218_A1_F10_T7	g18695	BLASTN	395	5e-11	70	Soybean nodulin 22 gene
14841	GM_218_A1_G06_MR	g3097320	BLASTN	733	4e-26	74	Glycine max gene for Bd 30K, complete cds
14842	GM_218_A1_G06_T7	g3645899	BLASTX	358	8e-31	50	(U68408) 5' end not determined experimentally [Zea mays]
14843	GM_218_A1_G11_T7	g4063770	BLASTX	215	1e-15	35	(AB004906) transposase [Ipomoea purpurea]
14844	GM_218_A1_H04_MR	g3142328	BLASTN	1135	2e-44	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14845	GM_218_A2_A02_MR	g4038056	BLASTX	262	1e-20	50	(AC005897) putative transposon [Arabidopsis thaliana]
14846	GM_218_A2_A07_MR	g3097320	BLASTN	376	5e-10	62	Glycine max gene for Bd 30K, complete cds
14847	GM_218_A2_A08_MR	g3097320	BLASTN	541	2e-17	72	Glycine max gene for Bd 30K, complete cds
14848	GM_218_A2_A11_MR	g3142328	BLASTN	460	8e-14	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14849	GM_218_A2_B08_MR	g507910	BLASTN	538	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
14850	GM_218_A2_C01_MR	g1480927	BLASTN	1410	3e-58	91	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
14851	GM_218_A2_D07_MR	g3097320	BLASTN	406	2e-11	70	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14852	GM_218_A2_D09_MR	g3687234	BLASTX	164	4e-10	36	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
14853	GM_218_A2_F03_MR	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
14854	GM_218_A2_F06_MR	g3097320	BLASTN	439	8e-13	68	Glycine max gene for Bd 30K, complete cds
14855	GM_218_A2_G03_MR	g3176795	BLASTN	344	6e-09	62	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
14856	GM_218_A2_G08_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14857	GM_218_B1_A04_MR	g2522230	BLASTX	250	1e-20	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
14858	GM_218_B1_B01_MR	g18768	BLASTN	437	2e-13	71	Soybean Tgm6 transposable element 3' end
14859	GM_218_B1_B02_MR	g3645899	BLASTX	242	2e-18	43	(U68408) 5' end not determined experimentally [Zea mays]
14860	GM_218_B1_B05_MR	g1167523	BLASTX	435	7e-39	60	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14861	GM_218_B1_B07_MR	g507910	BLASTN	634	5e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
14862	GM_218_B1_B11_MR	g18559	BLASTN	873	2e-32	72	G.max gene for catalase
14863	GM_218_B1_C01_MR	g3914535	BLASTX	208	3e-16	87	60S RIBOSOMAL PROTEIN L13A >gi 2791948 gnl PID e1237871 (AJ223363) ribosomal protein L13a [Lupinus luteus]
14864	GM_218_B1_C12_MR	g18559	BLASTN	843	3e-31	76	G.max gene for catalase
14865	GM_218_B1_D02_MR	g4160362	BLASTN	323	3e-09	62	Saccharomyces cerevisiae complete mitochondrial genome
14866	GM_218_B1_D09_MR	g2642443	BLASTX	341	5e-30	43	(AC002391) putative cytochrome P450 [Arabidopsis thaliana]
14867	GM_218_B1_E01_MR	g4063760	BLASTX	377	1e-32	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14868	GM_218_B1_E11_MR	g4156185	BLASTN	586	2e-19	65	Homo sapiens PAC clone DJ0803F10 from 7q33-q36, complete sequence [Homo sapiens]
14869	GM_218_B1_F04_MR	g2995405	BLASTX	338	7e-29	67	(Y12432) polyprotein [Ananas comosus]
14870	GM_218_B1_G04_MR	g3097320	BLASTN	446	4e-13	69	Glycine max gene for Bd 30K, complete cds
14871	GM_218_B1_H04_MR	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
14872	GM_218_B2_A08_T7	g507910	BLASTN	580	1e-19	85	Glycine max BSR-101 satellite SB92 genomic sequence.
14873	GM_218_B2_A11_T7	g2827715	BLASTX	224	1e-16	42	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
14874	GM_218_B2_B01_T7	g3687234	BLASTX	177	2e-24	53	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
14875	GM_218_B2_B05_MR	g3599418	BLASTN	359	3e-09	88	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
14876	GM_218_B2_B07_MR	g3777527	BLASTX	307	4e-25	40	(AF053008) gag-pol polyprotein [Glycine max]
14877	GM_218_B2_B08_MR	g1732513	BLASTX	142	4e-09	68	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14878	GM_218_B2_B09_MR	g2995405	BLASTX	241	2e-34	65	(Y12432) polyprotein [Ananas comosus]
14879	GM_218_B2_C10_MR	g2315153	BLASTX	209	7e-16	74	(Y14316) MAP3K gamma protein kinase [Arabidopsis thaliana]
14880	GM_218_B2_D04_MR	g3426334	BLASTN	417	7e-12	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
14881	GM_218_B2_D05_T7	g3779030	BLASTX	154	2e-10	30	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
14882	GM_218_B2_D11_MR	g2121303	BLASTN	359	3e-09	60	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
14883	GM_218_B2_D11_T7	g2959767	BLASTX	312	1e-25	52	(AJ002584) AtMRP4 [Arabidopsis thaliana]
14884	GM_218_B2_E01_MR	g3097320	BLASTN	438	9e-13	71	Glycine max gene for Bd 30K, complete cds
14885	GM_218_B2_E02_MR	g3097320	BLASTN	472	2e-14	72	Glycine max gene for Bd 30K, complete cds
14886	GM_218_B2_E06_MR	g3097320	BLASTN	449	3e-13	70	Glycine max gene for Bd 30K, complete cds
14887	GM_218_B2_F05_MR	g3599418	BLASTN	895	1e-33	73	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
14888	GM_218_B2_F07_MR	g3386611	BLASTX	279	5e-23	52	(AC004665) unknown protein [Arabidopsis thaliana]
14889	GM_219_B2_B01_T7	g507910	BLASTN	369	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14890	GM_219_B2_B03_T7	g133917	BLASTX	185	9e-14	79	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 gi 70856 pir R3NT2 ribosomal protein S2 - common tobacco chloroplast gi 11814 (Z00044) ribosomal protein S2 [Nicotiana tabacum] gi 225274 prf 1211235J ribosomal protein S2 [Nicotiana tabacum]
14891	GM_219_B2_C10_T7	g950319	BLASTX	153	6e-09	50	(M11240) unknown protein [Drosophila melanogaster]
14892	GM_219_B2_D04_T7	g2160130	BLASTN	359	3e-09	62	Genomic sequence from Human 17, complete sequence [Homo sapiens]
14893	GM_219_B2_D06_T7	g905361	BLASTX	155	2e-09	32	(U22103) gag-protease polyprotein [Glycine max]
14894	GM_219_B2_D09_T7	g3142328	BLASTN	424	3e-12	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14895	GM_219_B2_D11_T7	g1666236	BLASTX	161	1e-10	28	(U76261) unknown [Hordeum vulgare]
14896	GM_219_B2_E09_T7	g18559	BLASTN	300	1e-10	74	G.max gene for catalase
14897	GM_219_B2_F01_T7	g1785729	BLASTN	364	2e-09	59	A.thaliana mitochondrial genome, part B
14898	GM_219_B2_F02_T7	g170065	BLASTN	361	2e-09	78	Soybean (G.max) proline-rich cell wall protein (SbPRP2) gene, complete cds.
14899	GM_219_B2_G01_T7	g507910	BLASTN	455	6e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14900	GM_219_B2_H09_T7	g2995405	BLASTX	159	2e-11	60	(Y12432) polyprotein [Ananas comosus]
14901	GM_220_B1_A01_MR	g507910	BLASTN	361	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
14902	GM_220_B1_B05_MR	g3193287	BLASTX	603	5e-58	80	(AF069298) Arabidopsis predicted protein of unknown function T10P11.19 (GB:AC002330) [Arabidopsis thaliana]
14903	GM_220_B1_E01_MR	g18559	BLASTN	782	2e-28	72	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14904	GM_220_B1_E04_MR	g2995405	BLASTX	341	3e-29	67	(Y12432) polyprotein [Ananas comosus]
14905	GM_220_B2_B06_T7	g4159704	BLASTN	596	7e-20	65	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCB17, complete sequence [Arabidopsis thaliana]
14906	GM_220_B2_B10_T7	g2129618	BLASTX	166	3e-16	46	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
14907	GM_220_B2_B11_T7	g99922	BLASTX	206	1e-15	50	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
14908	GM_220_B2_D08_T7	g22490	BLASTX	271	8e-23	36	(X01380) ORF1 [Zea mays]
14909	GM_220_B2_E01_T7	g13774	BLASTN	474	8e-15	66	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
14910	GM_220_B2_E12_T7	g3738114	BLASTN	560	3e-18	64	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
14911	GM_220_B2_H04_T7	g535454	BLASTX	162	2e-16	61	(U13940) cysteine proteinase [Alnus glutinosa]
14912	GM_220_B2_H10_T7	g507910	BLASTN	339	1e-08	69	Glycine max BSR-101 satellite SB92 genomic sequence.
14913	GM_221_A1_A03_T7	g2801677	BLASTN	555	6e-19	67	Glycine max telomere-associated sequence STAS6
14914	GM_221_A1_B01_T7	g1743354	BLASTX	117	6e-12	67	(Y09876) aldehyde dehydrogenase (NAD+) [Nicotiana tabacum]
14915	GM_221_A1_C03_T7	g2827662	BLASTX	283	4e-23	49	(AL021637) Phosphoribosylanthranilate transferase [Arabidopsis thaliana]
14916	GM_221_A1_C05_T7	g3319366	BLASTX	192	2e-14	39	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
14917	GM_221_A1_C12_T7	g2687856	BLASTN	394	9e-11	63	Human genomic DNA sequence from cosmid B44H3 on chromosome 22, complete sequence [Homo sapiens]
14918	GM_221_A1_D05_T7	g507910	BLASTN	600	2e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
14919	GM_221_A1_E04_T7	g507910	BLASTN	393	4e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
14920	GM_221_A1_E11_T7	g507910	BLASTN	531	2e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
14921	GM_221_A1_F10_T7	g1688049	BLASTX	254	5e-21	59	(D50034) 4-coumarate:CoA ligase [Nicotiana tabacum]
14922	GM_221_B1_B03_MR	g2443320	BLASTX	249	5e-19	63	(D85597) polyprotein [Oryza australiensis]
14923	GM_221_B1_C09_MR	g1769898	BLASTX	163	2e-10	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14924	GM_221_B1_E02_MR	g3777527	BLASTX	235	2e-17	44	(AF053008) gag-pol polyprotein [Glycine max]
14925	GM_221_B1_H12_T7	g18559	BLASTN	954	3e-36	84	G.max gene for catalase
14926	GM_222_B1_A02_MR	g1167523	BLASTX	177	2e-11	44	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
14927	GM_222_B1_B02_MR	g3777527	BLASTX	173	7e-11	31	(AF053008) gag-pol polyprotein [Glycine max]
14928	GM_222_B1_D08_MR	g3319351	BLASTX	175	4e-11	62	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
14929	GM_222_B1_F11_MR	g2865437	BLASTX	153	9e-09	61	(AF039376) polyprotein [Arabidopsis arenosa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14930	GM_223_A1_A04_MR	g2351073	BLASTN	785	2e-28	74	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24
14931	GM_223_A1_A04_T7	g3810595	BLASTX	239	6e-18	42	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
14932	GM_223_A1_A05_MR	g1685114	BLASTN	369	1e-09	64	Dictyostelium discoideum putative transcription factor (stkA) mRNA, complete cds
14933	GM_223_A1_A09_MR	g1143381	BLASTX	164	5e-11	34	(Z49063) polygalacturonase inhibitor [Actinidia deliciosa]
14934	GM_223_A1_B02_T7	g3319366	BLASTX	191	2e-14	33	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
14935	GM_223_A1_B03_T7	g531389	BLASTX	90	3e-10	61	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
14936	GM_223_A1_B07_MR	g507910	BLASTN	410	6e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14937	GM_223_A1_B09_T7	g1480927	BLASTN	458	8e-14	81	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
14938	GM_223_A1_B12_MR	g2262107	BLASTX	152	3e-09	93	(AC002343) Ser/Thr protein kinase isolog [Arabidopsis thaliana]
14939	GM_223_A1_B12_T7	g629693	BLASTX	138	1e-15	38	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
14940	GM_223_A1_C07_MR	g507910	BLASTN	400	2e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
14941	GM_223_A1_D01_MR	g3695387	BLASTX	256	6e-20	47	(AF096371) contains similarity to replication protein A1 [Arabidopsis thaliana]
14942	GM_223_A1_D03_MR	g3599418	BLASTN	361	2e-09	82	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
14943	GM_223_A1_D03_T7	g905361	BLASTX	474	4e-49	88	(U22103) gag-protease polyprotein [Glycine max]
14944	GM_223_A1_D06_T7	g1658062	BLASTX	496	1e-46	78	ACC synthase [Malus domestica]
14945	GM_223_A1_D07_T7	g2995405	BLASTX	388	3e-34	56	(Y12432) polyprotein [Ananas comosus]
14946	GM_223_A1_D11_MR	g3142328	BLASTN	1670	7e-69	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14947	GM_223_A1_D12_MR	g3599418	BLASTN	351	7e-09	80	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
14948	GM_223_A1_D12_T7	g905361	BLASTX	625	2e-60	87	(U22103) gag-protease polyprotein [Glycine max]
14949	GM_223_A1_E01_T7	g3150396	BLASTN	415	1e-11	64	Arabidopsis thaliana chromosome II BAC T27E13 genomic sequence, complete sequence.
14950	GM_223_A1_E02_MR	g2316016	BLASTX	395	2e-34	60	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
14951	GM_223_A1_E03_T7	g507910	BLASTN	513	1e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
14952	GM_223_A1_E04_MR	g3097320	BLASTN	421	5e-12	72	Glycine max gene for Bd 30K, complete cds
14953	GM_223_A1_E04_T7	g3779026	BLASTX	198	1e-13	39	(AC005171) putative retrotransposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14954	GM_223_A1_E05_MR	g1087068	BLASTN	365	5e-10	70	GH2/4=glutathione S-transferase {promoter} [Glycine max=soybeans, seedlings, Genomic, 858 nt]
14955	GM_223_A1_E10_MR	g2462936	BLASTX	110	1e-10	39	(Y12321) open reading frame 2 [Brassica oleracea]
14956	GM_223_A1_F03_MR	g4063760	BLASTX	242	4e-31	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14957	GM_223_A1_F04_T7	g3695395	BLASTX	218	3e-16	41	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
14958	GM_223_A1_F07_MR	g3777527	BLASTX	574	1e-53	95	(AF053008) gag-pol polyprotein [Glycine max]
14959	GM_223_A1_F07_T7	g3142328	BLASTN	1611	3e-66	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14960	GM_223_A1_F09_T7	g3142328	BLASTN	1368	4e-55	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14961	GM_223_A1_F11_MR	g3930515	BLASTX	105	8e-10	35	(AF059674) putative gag protein [Nicotiana tabacum]
14962	GM_223_A1_G10_MR	g22491	BLASTX	102	2e-11	44	(X01380) ORF2 [Zea mays]
14963	GM_223_A1_G12_MR	g507910	BLASTN	388	6e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14964	GM_223_A1_H08_MR	g1771160	BLASTX	135	3e-15	48	(X98929) SBT1 [Lycopersicon esculentum] gi 3687305 gnl PID e1299610 (AJ006378) subtilisin-like protease [Lycopersicon esculentum]
14965	GM_223_A1_H10_MR	g4063760	BLASTX	323	6e-27	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14966	GM_223_B1_A03_T7	g507910	BLASTN	503	4e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
14967	GM_223_B1_B07_T7	g3763850	BLASTN	745	1e-26	78	Glycine max GmENOD93 gene for early nodulin, complete cds
14968	GM_223_B1_C08_T7	g18559	BLASTN	455	1e-13	67	G.max gene for catalase
14969	GM_223_B1_D07_T7	g4050011	BLASTN	477	1e-14	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
14970	GM_223_B1_D08_T7	g2995405	BLASTX	265	5e-21	49	(Y12432) polyprotein [Ananas comosus]
14971	GM_223_B1_E02_T7	g1769899	BLASTX	169	4e-12	38	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
14972	GM_224_A1_A03_T7	g130582	BLASTX	158	2e-09	33	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
14973	GM_224_A1_A07_T7	g3645899	BLASTX	135	7e-16	43	(U68408) 5' end not determined experimentally [Zea mays]
14974	GM_224_A1_B03_T7	g3033375	BLASTX	406	4e-37	63	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]
14975	GM_224_A1_B07_T7	g905361	BLASTX	308	6e-26	91	(U22103) gag-protease polyprotein [Glycine max]
14976	GM_224_A1_B11_T7	g3142328	BLASTN	1894	4e-79	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
14977	GM_224_A1_B12_T7	g18768	BLASTN	400	1e-11	69	Soybean Tgm6 transposable element 3' end
14978	GM_224_A1_C02_T7	g1666236	BLASTX	188	1e-13	32	(U76261) unknown [Hordeum vulgare]
14979	GM_224_A1_C03_T7	g507910	BLASTN	368	5e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14980	GM_224_A1_D03_T7	g507910	BLASTN	404	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
14981	GM_224_A1_D11_T7	g507910	BLASTN	440	3e-13	73	Glycine max BSR-101 satellite SB92 genomic sequence.
14982	GM_224_A1_E05_T7	g2995405	BLASTX	468	7e-43	59	(Y12432) polyprotein [Ananas comosus]
14983	GM_224_A1_F11_T7	g3560029	BLASTN	462	5e-14	64	Schistosoma intercalatum ribosomal intergenic spacer DNA (2169 bp)
14984	GM_224_A1_G02_T7	g3142328	BLASTN	1418	2e-57	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
14985	GM_224_A1_G03_T7	g3777527	BLASTX	752	1e-72	92	(AF053008) gag-pol polyprotein [Glycine max]
14986	GM_224_A1_H04_T7	g2801681	BLASTN	609	3e-21	69	Glycine max telomere-associated sequence STAS10
14987	GM_224_A1_H09_T7	g4063760	BLASTX	264	1e-20	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14988	GM_225_B2_A01_T7	g3319351	BLASTX	380	5e-33	63	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
14989	GM_225_B2_A03_MR	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
14990	GM_225_B2_A03_T7	g507910	BLASTN	386	8e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
14991	GM_225_B2_A04_T7	g3337395	BLASTN	367	1e-09	61	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
14992	GM_225_B2_A08_T7	g905361	BLASTX	159	7e-10	100	(U22103) gag-protease polyprotein [Glycine max]
14993	GM_225_B2_A09_MR	g3777527	BLASTX	226	2e-16	35	(AF053008) gag-pol polyprotein [Glycine max]
14994	GM_225_B2_B01_T7	g1666236	BLASTX	111	4e-13	28	(U76261) unknown [Hordeum vulgare]
14995	GM_225_B2_B02_T7	g3319362	BLASTX	183	3e-12	40	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
14996	GM_225_B2_B06_T7	g2864614	BLASTX	199	1e-14	40	(AL021811) putative protein [Arabidopsis thaliana]
14997	GM_225_B2_B07_MR	g4063760	BLASTX	419	3e-37	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
14998	GM_225_B2_B08_T7	g100484	BLASTX	277	2e-22	53	hypothetical protein - garden snapdragon
14999	GM_225_B2_B11_MR	g1839022	BLASTX	142	1e-08	57	(Y11121) amino acid carrier [Ricinus communis]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15000	GM_225_B2_C01_T7	g3142328	BLASTN	1520	5e-62	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15001	GM_225_B2_C05_MR	g3097320	BLASTN	904	7e-34	75	Glycine max gene for Bd 30K, complete cds
15002	GM_225_B2_C05_T7	g3777527	BLASTX	154	7e-10	36	(AF053008) gag-pol polyprotein [Glycine max]
15003	GM_225_B2_C12_MR	g505129	BLASTN	397	5e-11	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
15004	GM_225_B2_D01_T7	g22490	BLASTX	215	6e-17	46	(X01380) ORF1 [Zea mays]
15005	GM_225_B2_D04_MR	g507910	BLASTN	539	1e-17	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15006	GM_225_B2_D07_MR	g2129618	BLASTX	249	3e-19	46	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15007	GM_225_B2_D09_T7	g3319362	BLASTX	157	2e-09	50	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
15008	GM_225_B2_D10_MR	g421955	BLASTX	428	2e-39	61	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
15009	GM_225_B2_E07_MR	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15010	GM_225_B2_E07_T7	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15011	GM_225_B2_E11_T7	g2828184	BLASTN	536	4e-17	76	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSN9, complete sequence [Arabidopsis thaliana]
15012	GM_225_B2_F01_MR	g4063743	BLASTX	239	1e-23	63	(AC005851) hypothetical protein [Arabidopsis thaliana]
15013	GM_225_B2_F07_T7	g3600044	BLASTX	145	1e-09	39	(AF080119) contains similarity to proteases [Arabidopsis thaliana]
15014	GM_226_A1_A12_MR	g3097320	BLASTN	407	2e-11	71	Glycine max gene for Bd 30K, complete cds
15015	GM_226_A1_B03_MR	g507910	BLASTN	491	1e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15016	GM_226_A1_B04_MR	g18559	BLASTN	449	2e-13	74	G.max gene for catalase
15017	GM_226_A1_B05_MR	g1142701	BLASTN	822	8e-31	86	Glycine max satellite STR120-A.3.
15018	GM_226_A1_C08_MR	g507910	BLASTN	351	3e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15019	GM_226_A1_C11_MR	g1172584	BLASTX	215	2e-18	42	POLYPHENOL OXIDASE PRECURSOR (PPO) (CATECHOL OXIDASE) gi 1076478 pir S52984 catechol oxidase (EC 1.10.3.1) precursor - apple tree gi 507280 (L29450) polyphenol oxidase [Malus domestica]
15020	GM_226_A1_D11_MR	g2052034	BLASTN	407	2e-11	68	Human DNA sequence from PAC 450C20 on chromosome X
15021	GM_226_B1_B03_MR	g2129618	BLASTX	235	9e-18	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15022	GM_226_B1_B09_MR	g4104931	BLASTX	160	7e-10	75	(AF042196) auxin response factor 8 [Arabidopsis thaliana]
15023	GM_226_B1_F04_MR	g1707020	BLASTX	189	4e-13	30	(U78721) hypothetical protein [Arabidopsis thaliana]
15024	GM_226_B1_F06_MR	g2462058	BLASTX	252	8e-21	52	(Y13389) reverse transcriptase [Antirrhinum majus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15025	GM_227_B1_H12_MR	g3777527	BLASTX	175	3e-13	37	(AF053008) gag-pol polyprotein [Glycine max]
15026	GM_227_B2_A01_MR	g342953	BLASTN	494	3e-16	62	paramecium species 4.51a mt dna dimer: replication init. region.
15027	GM_227_B2_A03_MR	g3377855	BLASTX	373	2e-40	73	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
15028	GM_227_B2_A09_MR	g587603	BLASTN	347	1e-08	61	P.falciparum gene for beta subunit RNA polymerase
15029	GM_227_B2_B04_MR	g2462927	BLASTX	208	2e-15	65	(Y10342) putative amidase [Arabidopsis thaliana]
15030	GM_227_B2_B08_MR	g905361	BLASTX	428	3e-39	96	(U22103) gag-protease polyprotein [Glycine max]
15031	GM_227_B2_C04_MR	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15032	GM_227_B2_D08_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15033	GM_227_B2_E02_MR	g905361	BLASTX	192	2e-13	29	(U22103) gag-protease polyprotein [Glycine max]
15034	GM_227_B2_E03_MR	g507910	BLASTN	615	4e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15035	GM_227_B2_F03_MR	g4063760	BLASTX	295	5e-24	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15036	GM_228_A2_A05_T7	g507910	BLASTN	568	5e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15037	GM_228_A2_B05_T7	g3097320	BLASTN	939	2e-35	81	Glycine max gene for Bd 30K, complete cds
15038	GM_228_A2_D03_T7	g3294511	BLASTN	357	4e-09	66	Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
15039	GM_228_A2_D05_T7	g255572	BLASTN	419	7e-13	75	small auxin up RNA gene cluster: orf 15A [Glycine max=soybeans, cv. Wayne, Genomic, 637 nt]
15040	GM_228_A2_G04_T7	g2706515	BLASTX	103	5e-13	56	(Y12689) isoflavone reductase-like protein [Citrus X paradisi]
15041	GM_229_A2_A11_T7	g507910	BLASTN	419	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15042	GM_229_A2_B04_T7	g118514	BLASTX	199	5e-17	93	TURGOR-RESPONSIVE PROTEIN 26G gi 100051 pir S11863 aldehyde dehydrogenase homolog - garden pea gi 20681 (X54359) 508 aa peptide [Pisum sativum]
15043	GM_229_A2_B06_MR	g4063760	BLASTX	173	9e-22	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15044	GM_229_A2_C07_MR	g3142328	BLASTN	480	1e-14	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15045	GM_229_A2_D01_T7	g2522228	BLASTX	270	1e-22	71	(AB007466) reverse transcriptase-like protein [Vicia faba]
15046	GM_229_A2_D05_T7	g507910	BLASTN	354	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15047	GM_229_A2_D06_T7	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15048	GM_229_A2_E08_MR	g3915082	BLASTX	149	1e-17	63	TUBULIN ALPHA CHAIN >gi 1220545 (M97956) alpha tubulin [Trypanosoma cruzi] >gi 1220548 (M96849) alpha tubulin [Trypanosoma cruzi]
15049	GM_229_A2_E11_T7	g2462936	BLASTX	369	3e-33	55	(Y12321) open reading frame 2 [Brassica oleracea]
15050	GM_229_A2_F01_T7	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15051	GM_229_A2_F02_T7	g4092471	BLASTN	506	8e-16	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
15052	GM_229_A2_F09_T7	g99922	BLASTX	310	2e-47	76	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
15053	GM_229_B2_A07_MR	g2642163	BLASTX	298	1e-24	55	(AC003000) hypothetical protein [Arabidopsis thaliana]
15054	GM_229_B2_B08_MR	g2760165	BLASTN	350	9e-09	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]
15055	GM_229_B2_C08_MR	g2244771	BLASTX	196	3e-13	80	(Z97335) kinesin homolog [Arabidopsis thaliana]
15056	GM_229_B2_C10_MR	g18559	BLASTN	1635	3e-67	85	G.max gene for catalase
15057	GM_229_B2_C12_MR	g3142328	BLASTN	723	9e-26	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15058	GM_229_B2_D08_MR	g1934969	BLASTN	359	3e-09	61	P.falciparum mRNA for AARP1 protein, partial
15059	GM_229_B2_E07_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15060	GM_229_B2_E08_MR	g4063756	BLASTN	365	2e-09	61	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15061	GM_240_B1_H12_MR	g507910	BLASTN	398	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15062	GM_375_B2_B10_MR	g18559	BLASTN	777	3e-28	75	G.max gene for catalase
15063	GM_M01_A1_B09_MR	g1785739	BLASTX	163	1e-17	43	(Y08502) orf240b [Arabidopsis thaliana]
15064	GM_M01_A1_D05_MR	g3426334	BLASTN	354	5e-09	65	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
15065	GM_M01_A1_G02_MR	g3645899	BLASTX	197	4e-16	48	(U68408) 5' end not determined experimentally [Zea mays]
15066	GM_M01_A1_H11_MR	g1813979	BLASTX	135	2e-12	64	(Y10860) hypothetical protein [Musa acuminata]
15067	GM_M01_A2_A07_MR	g2292907	BLASTX	242	2e-18	44	(Y10099) P-glycoprotein homologue [Hordeum vulgare]
15068	GM_M01_A2_A09_MF	g1531758	BLASTX	145	5e-11	90	(X98772) AUX1 [Arabidopsis thaliana] gi 3335360 (AC003028) unknown protein [Arabidopsis thaliana]
15069	GM_M01_A2_B01_MR	g2765244	BLASTX	220	2e-17	48	(Y12807) invertase inhibitor homolog [Arabidopsis thaliana]
15070	GM_M01_A2_B02_MR	g507910	BLASTN	365	7e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15071	GM_M01_A2_B03_MF	g1850554	BLASTX	149	7e-10	57	(U88032) reverse transcriptase [Secale cereale]
15072	GM_M01_A2_B04_MR	g1814403	BLASTX	437	1e-39	80	(U84889) methionine synthase [Mesembryanthemum crystallinum]
15073	GM_M01_A2_B06_MF	g507910	BLASTN	401	2e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15074	GM_M01_A2_B09_MF	g4063760	BLASTX	279	3e-22	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15075	GM_M01_A2_B12_MF	g3777527	BLASTX	169	2e-10	33	(AF053008) gag-pol polyprotein [Glycine max]
15076	GM_M01_A2_C01_MF	g507910	BLASTN	383	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15077	GM_M01_A2_C01_MR	g507910	BLASTN	370	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
15078	GM_M01_A2_C09_MF	g4063760	BLASTX	220	5e-16	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15079	GM_M01_A2_D01_MR	g3097320	BLASTN	457	1e-13	69	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15080	GM_M01_A2_D04_MF	g3176791	BLASTN	429	4e-13	61	Homo sapiens allele 11 fragile site locus (FRA10B) minisatellite, 5' sequence
15081	GM_M01_A2_D05_MR	g2465773	BLASTX	146	1e-09	37	(AF022186) homologous to orf238 in Porphyra purpurea [Cyanidium caldarium]
15082	GM_M01_A2_D07_MF	g4063760	BLASTX	195	2e-13	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15083	GM_M01_A2_D08_MF	g3283026	BLASTX	178	7e-12	36	putative transposase [Arabidopsis thaliana]
15084	GM_M01_A2_D11_MF	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15085	GM_M01_A2_D11_MR	g402616	BLASTN	352	5e-09	86	G.max satellite DNA
15086	GM_M01_A2_E01_MF	g3097320	BLASTN	449	3e-13	70	Glycine max gene for Bd 30K, complete cds
15087	GM_M01_A2_E08_MR	g3777527	BLASTX	386	2e-33	51	(AF053008) gag-pol polyprotein [Glycine max]
15088	GM_M01_A2_E09_MR	g3097320	BLASTN	1082	6e-42	78	Glycine max gene for Bd 30K, complete cds
15089	GM_M01_A2_E11_MF	g3777527	BLASTX	384	2e-33	77	(AF053008) gag-pol polyprotein [Glycine max]
15090	GM_M01_A2_F01_MR	g4063756	BLASTN	699	1e-24	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15091	GM_M01_A2_F09_MF	g226407	BLASTX	302	1e-24	58	retrotransposon del1-46 [Lilium henryi]
15092	GM_M01_A2_G01_MR	g3097320	BLASTN	515	3e-16	70	Glycine max gene for Bd 30K, complete cds
15093	GM_M01_A2_G02_MR	g507910	BLASTN	345	6e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15094	GM_M01_A2_G03_MR	g18561	BLASTN	631	9e-22	85	G.max Gmachs1 gene for chalcone synthase
15095	GM_M01_A2_G11_MF	g4063760	BLASTX	253	1e-19	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15096	GM_M01_A2_G12_MR	g1402883	BLASTX	171	2e-17	45	(X98130) unknown [Arabidopsis thaliana] gi 1495263 gnl PID e242837 (X97487) orf09 [Arabidopsis thaliana]
15097	GM_M01_A2_H03_MR	g507910	BLASTN	369	4e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15098	GM_M01_A2_H05_MF	g3142328	BLASTN	453	2e-13	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15099	GM_M01_A2_H11_MF	g3790154	BLASTN	358	4e-09	61	Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVEP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs ...
15100	GM_M01_A2_H12_MF	g3582000	BLASTX	157	9e-10	72	(AJ010942) hexose transporter protein [Lycopersicon esculentum]
15101	GM_M01_B1_A04_MF	g4050011	BLASTN	518	2e-16	64	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
15102	GM_M01_B1_A04_MR	g4063760	BLASTX	186	2e-12	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15103	GM_M01_B1_B06_MF	g2232254	BLASTX	195	6e-21	87	(AF005237) old-yellow-enzyme homolog [Catharanthus roseus]
15104	GM_M01_B1_B07_MF	g2129618	BLASTX	209	6e-15	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15105	GM_M01_B1_C06_MF	g3777527	BLASTX	600	2e-56	92	(AF053008) gag-pol polyprotein [Glycine max]
15106	GM_M01_B1_C07_MF	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
15107	GM_M01_B1_C08_MF	g3142328	BLASTN	1091	2e-42	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15108	GM_M01_B1_C08_MR	g507910	BLASTN	399	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15109	GM_M01_B1_D06_MR	g1142701	BLASTN	231	2e-17	72	Glycine max satellite STR120-A.3.
15110	GM_M01_B1_E02_MR	g4063760	BLASTX	210	5e-15	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15111	GM_M01_B1_E08_MR	g507910	BLASTN	388	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15112	GM_M01_B1_F04_MF	g2656031	BLASTN	591	1e-19	73	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC20
15113	GM_M01_B1_F05_MR	g1575536	BLASTX	156	3e-09	65	(U65533) regulator of nonsense transcript stability [Homo sapiens]
15114	GM_M01_B1_F06_MF	g507910	BLASTN	629	8e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
15115	GM_M01_B1_F06_MR	g507910	BLASTN	368	5e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15116	GM_M01_B1_F09_MF	g2522226	BLASTN	564	1e-18	69	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
15117	GM_M01_B1_G02_MF	g729092	BLASTX	214	2e-19	88	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK) gi 477484 pir A49082 calcium-dependent protein kinase isoform AK1 - Arabidopsis thaliana gi 304105 (L14771) calcium-dependent protein kinase [Arabidopsis thaliana]
15118	GM_M01_B1_H06_MF	g4063760	BLASTX	253	1e-19	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15119	GM_M01_B1_H06_MR	g3777527	BLASTX	431	2e-38	87	(AF053008) gag-pol polyprotein [Glycine max]
15120	GM_M01_B1_H10_MR	g2522228	BLASTX	202	6e-15	69	(AB007466) reverse transcriptase-like protein [Vicia faba]
15121	GM_M01_B1_H11_MF	g2852690	BLASTX	82	2e-09	48	(AF017754) resistance protein candidate [Lactuca sativa]
15122	GM_M01_B2_A02_MF	g3645899	BLASTX	287	3e-27	60	(U68408) 5' end not determined experimentally [Zea mays]
15123	GM_M01_B2_A04_MF	g2708743	BLASTX	233	2e-17	36	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
15124	GM_M01_B2_A05_MF	g3513745	BLASTX	228	1e-16	36	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
15125	GM_M01_B2_B01_MF	g2443320	BLASTX	241	3e-18	50	(D85597) polyprotein [Oryza australiensis]
15126	GM_M01_B2_B07_MF	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15127	GM_M01_B2_B08_MF	g99922	BLASTX	548	3e-52	87	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
15128	GM_M01_B2_C03_MF	g3452231	BLASTN	237	1e-08	63	Plasmodium falciparum merozoite surface protein 4, merozoite surface protein 5, merozoite surface protein 2, and adenylosuccinate lyase genes, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15129	GM_M01_B2_C06_MF	g476213	BLASTN	663	2e-23	77	Glycine max Century 84 p24 oleosin isoform A gene, complete cds.
15130	GM_M01_B2_C11_MR	g3142328	BLASTN	892	2e-33	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15131	GM_M01_B2_D03_MF	g421955	BLASTX	306	2e-26	54	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
15132	GM_M01_B2_D05_MF	g3608150	BLASTX	263	6e-22	52	(AC005314) putative peroxidase [Arabidopsis thaliana]
15133	GM_M01_B2_D11_MF	g4063760	BLASTX	312	8e-26	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15134	GM_M01_B2_E11_MF	g1071913	BLASTX	186	2e-13	72	cysteine synthase (EC 4.2.99.8) C precursor, mitochondrial - spinach gi 1066153 gnl PID d1007754 (D37963) cysteine synthase [Spinacia oleracea]
15135	GM_M01_B2_F01_MF	g905361	BLASTX	421	8e-54	86	(U22103) gag-protease polyprotein [Glycine max]
15136	GM_M01_B2_G03_MF	g3810596	BLASTX	176	9e-17	52	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
15137	GM_M01_B2_G06_MF	g4063760	BLASTX	192	5e-13	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15138	GM_M01_B2_G09_MR	g2522227	BLASTX	182	3e-13	54	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
15139	GM_M01_B2_G11_MF	g3142328	BLASTN	1514	9e-62	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15140	GM_M01_B2_G12_MF	g3645899	BLASTX	147	5e-14	38	(U68408) 5' end not determined experimentally [Zea mays]
15141	GM_M01_B2_G12_MR	g3152618	BLASTX	200	2e-14	56	(AC004482) putative pectinesterase [Arabidopsis thaliana] gi 3242724 (AC003040) putative pectinesterase [Arabidopsis thaliana]
15142	GM_M01_B2_H02_MF	g2462134	BLASTX	203	6e-19	40	(Y13368) reverse transcriptase [Beta vulgaris]
15143	GM_M01_B2_H05_MF	g4063760	BLASTX	484	4e-44	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15144	GM_M02_A1_A12_MR	g3599418	BLASTN	557	3e-18	71	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
15145	GM_M02_A1_B07_MR	g992916	BLASTN	866	4e-32	84	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
15146	GM_M02_A1_B08_MR	g226407	BLASTX	254	1e-21	44	retrotransposon del1-46 [Lilium henryi]
15147	GM_M02_A1_B09_MR	g3142328	BLASTN	1050	1e-40	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15148	GM_M02_A1_B10_MF	g4063760	BLASTX	328	2e-27	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15149	GM_M02_A1_C10_MR	g2827663	BLASTX	412	3e-37	65	(AL021637) membrane-associated salt-inducible-like protein [Arabidopsis thaliana]
15150	GM_M02_A1_D03_MR	g2995405	BLASTX	462	3e-42	57	(Y12432) polyprotein [Ananas comosus]
15151	GM_M02_A1_D04_MR	g507910	BLASTN	348	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15152	GM_M02_A1_D10_MR	g3449329	BLASTN	425	4e-12	67	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDH9, complete sequence [Arabidopsis thaliana]
15153	GM_M02_A1_D11_MR	g3367567	BLASTN	395	8e-11	72	Arabidopsis thaliana DNA chromosome 4, BAC clone F8D20 (ESSAII project)
15154	GM_M02_A1_E11_MF	g3777526	BLASTN	758	3e-27	97	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
15155	GM_M02_A1_F04_MR	g3702323	BLASTX	500	2e-49	77	(AC005397) unknown protein [Arabidopsis thaliana]
15156	GM_M02_A1_F08_MR	g3777527	BLASTX	535	3e-50	86	(AF053008) gag-pol polyprotein [Glycine max]
15157	GM_M02_A1_F09_MF	g1769899	BLASTX	91	3e-09	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15158	GM_M02_A1_F09_MR	g2443320	BLASTX	286	6e-23	49	(D85597) polyprotein [Oryza australiensis]
15159	GM_M02_A1_F10_MR	g1040717	BLASTN	364	2e-10	61	D.polychroa microsatellite sequence (clone Dp ch1 F3)
15160	GM_M02_A1_G08_MF	g2244994	BLASTX	261	9e-21	78	(Z97341) similarity to isp4 protein - fission yeast [Arabidopsis thaliana]
15161	GM_M02_A1_H03_MR	g3097320	BLASTN	530	6e-17	72	Glycine max gene for Bd 30K, complete cds
15162	GM_M02_A1_H05_MR	g3661610	BLASTX	345	6e-29	81	(AF092565) splicing factor Prp8 [Homo sapiens]
15163	GM_M02_A1_H06_MR	g507910	BLASTN	420	2e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15164	GM_M02_A1_H07_MF	g507910	BLASTN	342	7e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15165	GM_M02_A1_H07_MR	g507910	BLASTN	403	1e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
15166	GM_M02_A2_A02_MF	g1854442	BLASTN	458	6e-14	75	Vigna unguiculata mRNA for CPRD8 protein, complete cds
15167	GM_M02_A2_B08_MF	g13767	BLASTN	423	6e-13	64	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
15168	GM_M02_A2_B10_MR	g3641780	BLASTN	360	3e-09	62	Homo sapiens PAC clone DJ1159C10 from 7q34-q36, complete sequence [Homo sapiens]
15169	GM_M02_A2_C04_MF	g3142328	BLASTN	1631	4e-67	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15170	GM_M02_A2_C05_MF	g507910	BLASTN	431	7e-13	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15171	GM_M02_A2_C12_MF	g3810595	BLASTX	160	1e-09	43	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
15172	GM_M02_A2_D08_MF	g3142328	BLASTN	735	3e-26	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15173	GM_M02_A2_D11_MF	g2995405	BLASTX	237	5e-18	47	(Y12432) polyprotein [Ananas comosus]
15174	GM_M02_A2_E05_MF	g2522227	BLASTX	228	3e-18	41	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15175	GM_M02_A2_E07_MF	g2982431	BLASTX	262	2e-20	42	(AL022224) leucine rich repeat-like protein [Arabidopsis thaliana]
15176	GM_M02_A2_E08_MF	g1854442	BLASTN	497	1e-18	73	Vigna unguiculata mRNA for CPRD8 protein, complete cds
15177	GM_M02_A2_E12_MR	g4063760	BLASTX	219	7e-16	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15178	GM_M02_A2_F02_MF	g3249094	BLASTN	391	1e-10	67	Arabidopsis thaliana chromosome 1 BAC T12M4 sequence, complete sequence [Arabidopsis thaliana]
15179	GM_M02_A2_F07_MF	g507910	BLASTN	555	2e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
15180	GM_M02_A2_F11_MF	g507910	BLASTN	401	2e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15181	GM_M02_A2_G01_MF	g4063760	BLASTX	353	6e-31	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15182	GM_M02_A2_G09_MF	g1142701	BLASTN	1322	2e-53	84	Glycine max satellite STR120-A.3.
15183	GM_M02_A2_G12_MF	g2522228	BLASTX	199	1e-14	63	(AB007466) reverse transcriptase-like protein [Vicia faba]
15184	GM_M02_A2_H05_MF	g3097320	BLASTN	465	5e-14	70	Glycine max gene for Bd 30K, complete cds
15185	GM_M02_A2_H05_MR	g118964	BLASTX	154	1e-09	31	DYNEIN HEAVY CHAIN (DYHC) gi 103902 pir S09598 dynein heavy chain - rainbow trout (fragment) gi 64319 (X15476) dynein (515 AA) [Oncorhynchus mykiss]
15186	GM_M02_B1_A04_MF	g2708743	BLASTX	182	2e-13	36	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
15187	GM_M02_B1_A07_MR	g2335065	BLASTN	365	2e-09	62	Human BAC clone RG180F08 from 7q31, complete sequence [Homo sapiens]
15188	GM_M02_B1_B03_MR	g3097320	BLASTN	901	9e-34	76	Glycine max gene for Bd 30K, complete cds
15189	GM_M02_B1_B12_MF	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15190	GM_M02_B1_B12_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15191	GM_M02_B1_C06_MF	g507910	BLASTN	546	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
15192	GM_M02_B1_C08_MF	g2522230	BLASTX	159	6e-11	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
15193	GM_M02_B1_C12_MR	g4063760	BLASTX	245	1e-18	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15194	GM_M02_B1_D03_MR	g3142328	BLASTN	829	1e-30	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15195	GM_M02_B1_D05_MR	g3176077	BLASTN	500	7e-16	67	Medicago sativa mRNA for protein phosphatase 1, epsilon subunit
15196	GM_M02_B1_D10_MR	g3695388	BLASTX	187	6e-14	71	(AF096371) No definition line found [Arabidopsis thaliana]
15197	GM_M02_B1_D12_MF	g3097320	BLASTN	520	2e-16	69	Glycine max gene for Bd 30K, complete cds
15198	GM_M02_B1_E11_MR	g1769898	BLASTX	372	5e-33	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15199	GM_M02_B1_F02_MF	g100484	BLASTX	261	1e-20	68	hypothetical protein - garden snapdragon
15200	GM_M02_B1_F06_MF	g2924730	BLASTN	443	6e-13	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MPI7, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15201	GM_M02_B1_F06_MR	g2564046	BLASTN	372	9e-10	71	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MGI19, complete sequence [Arabidopsis thaliana]
15202	GM_M02_B1_F07_MF	g1514643	BLASTX	292	1e-23	61	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
15203	GM_M02_B1_F11_MF	g507910	BLASTN	695	8e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
15204	GM_M02_B1_F12_MF	g507910	BLASTN	344	6e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15205	GM_M02_B1_F12_MR	g3777527	BLASTX	477	3e-43	86	(AF053008) gag-pol polyprotein [Glycine max]
15206	GM_M02_B1_G03_MR	g3097320	BLASTN	364	2e-09	76	Glycine max gene for Bd 30K, complete cds
15207	GM_M02_B1_G06_MF	g3097320	BLASTN	483	8e-15	71	Glycine max gene for Bd 30K, complete cds
15208	GM_M02_B1_G10_MR	g3695388	BLASTX	145	2e-09	61	(AF096371) No definition line found [Arabidopsis thaliana]
15209	GM_M02_B2_A03_MF	g2245070	BLASTX	185	4e-12	55	(Z97342) hypothetical protein [Arabidopsis thaliana]
15210	GM_M02_B2_A07_MF	g3810596	BLASTX	152	6e-09	35	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
15211	GM_M02_B2_A12_MF	g99729	BLASTX	316	1e-27	46	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
15212	GM_M02_B2_B07_MF	g3645899	BLASTX	307	2e-25	53	(U68408) 5' end not determined experimentally [Zea mays]
15213	GM_M02_B2_B07_MR	g2443320	BLASTX	331	9e-28	53	(D85597) polyprotein [Oryza australiensis]
15214	GM_M02_B2_C07_MF	g4106979	BLASTN	366	2e-09	64	Homo sapiens chromosome 19, cosmid F15658, complete sequence [Homo sapiens]
15215	GM_M02_B2_C09_MF	g1769899	BLASTX	160	4e-11	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15216	GM_M02_B2_C11_MF	g507910	BLASTN	416	3e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
15217	GM_M02_B2_D02_MF	g3367528	BLASTX	185	5e-13	39	(AC004392) Strong similarity to gi 2160138 F19K23.6 gene product from A. thaliana BAC gb AC000375. [Arabidopsis thaliana]
15218	GM_M02_B2_D06_MR	g3150402	BLASTX	181	5e-17	79	(AC004165) putative malonyl-CoA:Acyl carrier protein transacylase [Arabidopsis thaliana]
15219	GM_M02_B2_D09_MF	g2586081	BLASTX	188	5e-13	36	(U72725) receptor kinase-like protein [Oryza longistaminata]
15220	GM_M02_B2_D09_MR	g3033389	BLASTX	209	5e-15	39	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
15221	GM_M02_B2_E01_MF	g2130082	BLASTX	199	7e-14	40	protein kinase Xa21 (EC 2.7.1.-) - rice gi 1122443 (U37133) receptor kinase-like protein [Oryza sativa] gi 2586085 (U72723) receptor kinase-like protein [Oryza longistaminata] gi 1586408 prf 2203451A receptor kinase-like protein [Oryza sativa]
15222	GM_M02_B2_E03_MR	g3777526	BLASTN	465	5e-14	82	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15223	GM_M02_B2_E12_MR	g1931640	BLASTX	156	9e-10	72	(U95973) Serine carboxypeptidase isolog [Arabidopsis thaliana]
15224	GM_M02_B2_F04_MF	g4063760	BLASTX	194	3e-13	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15225	GM_M02_B2_F05_MF	g4063756	BLASTN	433	2e-12	66	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15226	GM_M02_B2_F07_MR	g3142328	BLASTN	1458	3e-59	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15227	GM_M02_B2_F08_MR	g4115365	BLASTX	228	8e-17	38	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
15228	GM_M02_B2_G02_MF	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
15229	GM_M02_B2_G11_MF	g3645899	BLASTX	153	1e-15	44	(U68408) 5' end not determined experimentally [Zea mays]
15230	GM_M02_B2_G12_MF	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15231	GM_M02_B2_G12_MR	g507910	BLASTN	406	1e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15232	GM_M02_B2_H01_MF	g3645899	BLASTX	314	4e-26	50	(U68408) 5' end not determined experimentally [Zea mays]
15233	GM_M02_B2_H03_MR	g3777527	BLASTX	246	1e-18	41	(AF053008) gag-pol polyprotein [Glycine max]
15234	GM_M02_B2_H05_MF	g2443320	BLASTX	287	4e-23	46	(D85597) polyprotein [Oryza australiensis]
15235	GM_M03_A1_A02_MR	g18559	BLASTN	672	2e-23	73	G.max gene for catalase
15236	GM_M03_A1_A05_MF	g4063760	BLASTX	477	2e-43	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15237	GM_M03_A1_B02_MF	g3046704	BLASTX	290	2e-23	43	(AL022223) putative protein [Arabidopsis thaliana]
15238	GM_M03_A1_B03_MF	g4006833	BLASTX	269	4e-21	42	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
15239	GM_M03_A1_B07_MF	g4063756	BLASTN	384	3e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15240	GM_M03_A1_B08_MR	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15241	GM_M03_A1_B11_MF	g2245031	BLASTN	399	6e-11	66	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 7
15242	GM_M03_A1_C02_MR	g3777527	BLASTX	193	6e-13	45	(AF053008) gag-pol polyprotein [Glycine max]
15243	GM_M03_A1_C03_MF	g4063760	BLASTX	298	2e-43	77	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15244	GM_M03_A1_C05_MF	g3522932	BLASTN	371	1e-09	64	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]
15245	GM_M03_A1_C06_MF	g3292817	BLASTX	99	7e-09	51	(AL031018) hypothetical protein [Arabidopsis thaliana]
15246	GM_M03_A1_C06_MR	g2493908	BLASTX	194	1e-20	52	CULLIN HOMOLOG 3 (CUL-3) gi 1381146 (U58089) Hs-CUL-3 [Homo sapiens]
15247	GM_M03_A1_C08_MR	g2443320	BLASTX	274	1e-21	48	(D85597) polyprotein [Oryza australiensis]
15248	GM_M03_A1_C09_MF	g3386534	BLASTX	360	3e-32	56	(AF078934) mariner transposase [Glycine max]
15249	GM_M03_A1_C11_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15250	GM_M03_A1_D01_MR	g4063760	BLASTX	511	4e-47	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15251	GM_M03_A1_D11_MR	g4063760	BLASTX	488	1e-44	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15252	GM_M03_A1_E01_MF	g3097320	BLASTN	842	4e-31	79	Glycine max gene for Bd 30K, complete cds
15253	GM_M03_A1_F03_MF	g507910	BLASTN	386	8e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15254	GM_M03_A1_F03_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15255	GM_M03_A1_F07_MF	g3097320	BLASTN	461	8e-14	70	Glycine max gene for Bd 30K, complete cds
15256	GM_M03_A1_F08_MF	g2769655	BLASTN	503	1e-15	65	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
15257	GM_M03_A1_F09_MF	g18559	BLASTN	882	6e-33	75	G.max gene for catalase
15258	GM_M03_A1_G02_MF	g4063760	BLASTX	492	5e-45	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15259	GM_M03_A1_G06_MF	g3777527	BLASTX	358	1e-30	97	(AF053008) gag-pol polyprotein [Glycine max]
15260	GM_M03_A1_G06_MR	g3983556	BLASTN	421	6e-12	62	Homo sapiens clone UWGC:r13c from 6p21, complete sequence [Homo sapiens]
15261	GM_M03_A1_G08_MR	g507910	BLASTN	579	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15262	GM_M03_A1_G09_MR	g3402747	BLASTN	352	7e-09	60	Arabidopsis thaliana DNA chromosome 4, BAC clone T6K22 (ESSAII project)
15263	GM_M03_A1_G11_MF	g3645899	BLASTX	203	2e-28	51	(U68408) 5' end not determined experimentally [Zea mays]
15264	GM_M03_A1_H03_MR	g1666236	BLASTX	187	1e-13	36	(U76261) unknown [Hordeum vulgare]
15265	GM_M03_A1_H04_MF	g3746069	BLASTX	178	1e-13	34	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
15266	GM_M03_A1_H04_MR	g3142328	BLASTN	563	2e-18	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15267	GM_M03_A1_H06_MF	g2129618	BLASTX	153	8e-14	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15268	GM_M03_A1_H07_MF	g507910	BLASTN	552	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15269	GM_M03_A1_H07_MR	g507910	BLASTN	362	9e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15270	GM_M03_A1_H10_MF	g507910	BLASTN	385	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15271	GM_M03_A1_H11_MF	g4063760	BLASTX	522	3e-48	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15272	GM_M03_A1_H12_MF	g2160189	BLASTX	234	1e-17	57	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this gene. [Arabidopsis thaliana]
15273	GM_M03_A2_A05_MR	g3142328	BLASTN	979	2e-37	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15274	GM_M03_A2_B05_MR	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15275	GM_M03_A2_B06_MR	g1785744	BLASTX	147	1e-09	50	(Y08502) orf158 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15276	GM_M03_A2_B07_MF	g507910	BLASTN	609	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15277	GM_M03_A2_B07_MR	g507910	BLASTN	554	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15278	GM_M03_A2_B10_MF	g507910	BLASTN	369	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
15279	GM_M03_A2_B12_MR	g507910	BLASTN	384	9e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15280	GM_M03_A2_C03_MF	g3777527	BLASTX	436	7e-39	55	(AF053008) gag-pol polyprotein [Glycine max]
15281	GM_M03_A2_C11_MF	g3650039	BLASTX	215	7e-16	38	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
15282	GM_M03_A2_D01_MR	g2384696	BLASTX	145	3e-15	62	(AF013216) acyl-CoA oxidase [Myxococcus xanthus]
15283	GM_M03_A2_D02_MF	g3746069	BLASTX	188	1e-15	32	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
15284	GM_M03_A2_D02_MR	g3142328	BLASTN	650	2e-22	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15285	GM_M03_A2_D08_MR	g18559	BLASTN	445	4e-13	75	G.max gene for catalase
15286	GM_M03_A2_D12_MF	g3688173	BLASTX	159	2e-09	51	(AL031804) putative protein [Arabidopsis thaliana]
15287	GM_M03_A2_E01_MR	g2129618	BLASTX	146	2e-09	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15288	GM_M03_A2_E02_MF	g3777527	BLASTX	154	7e-14	36	(AF053008) gag-pol polyprotein [Glycine max]
15289	GM_M03_A2_E04_MF	g3142328	BLASTN	482	8e-15	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15290	GM_M03_A2_E05_MF	g4063760	BLASTX	317	3e-26	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15291	GM_M03_A2_F01_MR	g2351071	BLASTN	358	4e-09	60	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MVA3
15292	GM_M03_A2_F04_MF	g507910	BLASTN	369	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15293	GM_M03_A2_F04_MR	g507910	BLASTN	360	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15294	GM_M03_A2_F05_MF	g2245104	BLASTX	401	3e-35	53	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
15295	GM_M03_A2_F07_MF	g479124	BLASTN	435	8e-13	65	C.parapsilosos mitochondrial DNA for right telomeric region and ATP6 gene
15296	GM_M03_A2_F08_MF	g1666236	BLASTX	145	7e-09	30	(U76261) unknown [Hordeum vulgare]
15297	GM_M03_A2_F11_MF	g3097320	BLASTN	386	2e-10	68	Glycine max gene for Bd 30K, complete cds
15298	GM_M03_A2_G03_MR	g1658457	BLASTX	363	1e-32	67	(U75248) reverse transcriptase [Gossypium barbadense]
15299	GM_M03_A2_G04_MR	g3292823	BLASTX	94	4e-10	30	(AL031018) putative protein [Arabidopsis thaliana]
15300	GM_M03_A2_G06_MF	g421954	BLASTX	289	3e-32	57	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
15301	GM_M03_A2_G12_MF	g3426334	BLASTN	382	3e-10	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
15302	GM_M03_A2_H04_MF	g3097320	BLASTN	435	1e-12	68	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15303	GM_M03_A2_H06_MF	g3319362	BLASTX	262	1e-20	53	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
15304	GM_M03_A2_H09_MR	g4063760	BLASTX	325	3e-27	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15305	GM_M03_A2_H10_MF	g3426334	BLASTN	373	7e-10	64	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
15306	GM_M03_A2_H12_MF	g587603	BLASTN	353	5e-09	63	P.falciparum gene for beta subunit RNA polymerase
15307	GM_M03_B1_A01_MF	g629693	BLASTX	216	1e-16	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
15308	GM_M03_B1_A04_MR	g3426334	BLASTN	569	9e-19	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
15309	GM_M03_B1_A05_MF	g1769897	BLASTX	149	7e-09	27	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15310	GM_M03_B1_A08_MF	g507910	BLASTN	358	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15311	GM_M03_B1_A09_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15312	GM_M03_B1_B03_MF	g507910	BLASTN	547	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15313	GM_M03_B1_B07_MF	g3097320	BLASTN	557	3e-18	76	Glycine max gene for Bd 30K, complete cds
15314	GM_M03_B1_B08_MR	g507910	BLASTN	567	5e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15315	GM_M03_B1_B09_MF	g507910	BLASTN	403	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15316	GM_M03_B1_B12_MR	g507910	BLASTN	381	1e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
15317	GM_M03_B1_C05_MF	g3845197	BLASTN	363	2e-09	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
15318	GM_M03_B1_C05_MR	g3687234	BLASTX	187	2e-12	42	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
15319	GM_M03_B1_C08_MF	g2522230	BLASTX	190	3e-14	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
15320	GM_M03_B1_C08_MR	g629693	BLASTX	222	3e-17	33	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
15321	GM_M03_B1_C09_MF	g100484	BLASTX	242	1e-18	41	hypothetical protein - garden snapdragon
15322	GM_M03_B1_C09_MR	g1142700	BLASTN	925	3e-35	88	Glycine max satellite STR120-A.2.
15323	GM_M03_B1_D01_MR	g3142328	BLASTN	901	7e-34	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15324	GM_M03_B1_D03_MR	g2970050	BLASTN	327	1e-15	77	Vigna radiata mRNA for ARG10, complete cds
15325	GM_M03_B1_D09_MR	g1809230	BLASTN	379	4e-10	66	Human BAC clone GS188P18, complete sequence [Homo sapiens]
15326	GM_M03_B1_E01_MF	g507910	BLASTN	402	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15327	GM_M03_B1_E02_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15328	GM_M03_B1_E08_MR	g18563	BLASTN	456	8e-14	63	G.max intergenic region DNA (between Gmachs1 and Gmachs3)
15329	GM_M03_B1_E09_MR	g2129503	BLASTX	186	1e-13	55	ACC oxidase (clone ACO2) oxidase - muskmelon gi 1183898 gnl PID e221405 (X95552) ACC oxidase [Cucumis melo]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15330	GM_M03_B1_E10_MR	g3645899	BLASTX	201	2e-23	37	(U68408) 5' end not determined experimentally [Zea mays]
15331	GM_M03_B1_F03_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15332	GM_M03_B1_F07_MF	g3820757	BLASTN	399	3e-11	61	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
15333	GM_M03_B1_F09_MF	g4115373	BLASTX	475	2e-43	72	(AC005967) receptor-like protein kinase [Arabidopsis thaliana]
15334	GM_M03_B1_F10_MF	g3953458	BLASTX	301	2e-25	80	(AC002328) F20N2.3 [Arabidopsis thaliana]
15335	GM_M03_B1_F12_MF	g18559	BLASTN	821	3e-30	75	G.max gene for catalase
15336	GM_M03_B1_G02_MR	g3645899	BLASTX	252	2e-19	42	(U68408) 5' end not determined experimentally [Zea mays]
15337	GM_M03_B1_G03_MR	g2462936	BLASTX	330	4e-29	46	(Y12321) open reading frame 2 [Brassica oleracea]
15338	GM_M03_B1_G07_MR	g2522228	BLASTX	335	1e-29	66	(AB007466) reverse transcriptase-like protein [Vicia faba]
15339	GM_M03_B1_G09_MF	g1769898	BLASTX	152	4e-09	31	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15340	GM_M03_B1_H03_MR	g3599418	BLASTN	861	5e-32	72	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
15341	GM_M03_B1_H06_MR	g2673917	BLASTX	445	1e-39	80	(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]
15342	GM_M03_B1_H08_MR	g1550659	BLASTX	116	8e-10	40	(Z80226) ptrBb [Mycobacterium tuberculosis]
15343	GM_M03_B2_A02_MR	g2522227	BLASTX	218	3e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
15344	GM_M03_B2_A03_MF	g3645899	BLASTX	168	6e-12	43	(U68408) 5' end not determined experimentally [Zea mays]
15345	GM_M03_B2_A05_MF	g3930515	BLASTX	121	1e-10	47	(AF059674) putative gag protein [Nicotiana tabacum]
15346	GM_M03_B2_A05_MR	g2194136	BLASTX	163	7e-10	35	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
15347	GM_M03_B2_B01_MF	g507910	BLASTN	432	6e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
15348	GM_M03_B2_B01_MR	g3777527	BLASTX	536	2e-49	94	(AF053008) gag-pol polyprotein [Glycine max]
15349	GM_M03_B2_B02_MR	g130582	BLASTX	251	3e-19	51	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
15350	GM_M03_B2_B09_MR	g905361	BLASTX	517	7e-49	88	(U22103) gag-protease polyprotein [Glycine max]
15351	GM_M03_B2_C02_MF	g2244803	BLASTX	298	1e-25	41	(Z97336) reverse transcriptase-like protein [Arabidopsis thaliana]
15352	GM_M03_B2_C04_MF	g170029	BLASTN	423	4e-12	82	Glycine max cv. Dare nodulin 26 gene fragment.
15353	GM_M03_B2_C05_MF	g480618	BLASTX	172	2e-12	50	ATAF1 protein - Arabidopsis thaliana (fragment) gi 1345506 gnl PID e85756 (X74755) ATAF1 gene product [Arabidopsis thaliana]
15354	GM_M03_B2_C08_MF	g3108248	BLASTN	801	6e-30	71	Gossypium barbadense clone pXP027 repetitive DNA sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15355	GM_M03_B2_C08_MR	g12212	BLASTN	1138	8e-51	86	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
15356	GM_M03_B2_C11_MF	g178858	BLASTN	403	9e-12	64	Human restriction fragment length polymorphism 3' to the apolipoprotein B gene.
15357	GM_M03_B2_D04_MF	g2429543	BLASTX	204	3e-14	43	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]
15358	GM_M03_B2_D04_MR	g294668	BLASTX	102	7e-09	48	(L13242) beta-ketoacyl-ACP synthase [Ricinus communis]
15359	GM_M03_B2_D09_MF	g100484	BLASTX	342	2e-29	58	hypothetical protein - garden snapdragon
15360	GM_M03_B2_E01_MF	g3097320	BLASTN	1036	7e-40	80	Glycine max gene for Bd 30K, complete cds
15361	GM_M03_B2_E12_MR	g2245116	BLASTX	204	9e-16	55	(Z97343) unnamed protein product [Arabidopsis thaliana]
15362	GM_M03_B2_F03_MF	g2493494	BLASTX	156	1e-17	46	SERINE CARBOXYPEPTIDASE II-2 PRECURSOR (CP-MII.2) gi 619351 bbs 153537 CP-MII.2=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 436 aa]
15363	GM_M03_B2_F03_MR	g3513747	BLASTX	146	1e-13	37	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
15364	GM_M03_B2_F06_MR	g3142328	BLASTN	624	3e-21	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15365	GM_M03_B2_F09_MR	g3777527	BLASTX	748	3e-72	94	(AF053008) gag-pol polyprotein [Glycine max]
15366	GM_M03_B2_F10_MR	g3097320	BLASTN	1271	2e-50	81	Glycine max gene for Bd 30K, complete cds
15367	GM_M03_B2_F12_MR	g3777527	BLASTX	726	8e-70	96	(AF053008) gag-pol polyprotein [Glycine max]
15368	GM_M03_B2_G01_MR	g3599418	BLASTN	354	5e-09	64	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
15369	GM_M03_B2_G04_MF	g2827699	BLASTX	483	3e-44	69	(AL021684) predicted protein [Arabidopsis thaliana]
15370	GM_M03_B2_G04_MR	g1172555	BLASTX	254	5e-21	54	34 KD OUTER MITOCHONDRIAL MEMBRANE PROTEIN PORIN (VOLTAGE-DEPENDENT ANION-SELECTIVE CHANNEL PROTEIN) (VDAC) (POM 34) gi 629720 pir S46936 34K porin - potato gi 1076682 pir A55364 porin (clone pPOM-34) - potato mitochondrion gi 516166 gnl PID e1188619 (X80386) 34 kDA porin [Solanum tuberosum]
15371	GM_M03_B2_G08_MR	g4063760	BLASTX	415	8e-37	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15372	GM_M03_B2_G09_MF	g3097320	BLASTN	475	2e-14	76	Glycine max gene for Bd 30K, complete cds
15373	GM_M03_B2_G10_MR	g3097320	BLASTN	567	1e-18	68	Glycine max gene for Bd 30K, complete cds
15374	GM_M03_B2_G11_MR	g507910	BLASTN	522	6e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15375	GM_M03_B2_G12_MR	g3319362	BLASTX	144	5e-10	45	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
15376	GM_M03_B2_H01_MF	g1666236	BLASTX	177	2e-12	28	(U76261) unknown [Hordeum vulgare]
15377	GM_M03_B2_H01_MR	g3777527	BLASTX	231	2e-20	51	(AF053008) gag-pol polyprotein [Glycine max]
15378	GM_M03_B2_H02_MF	g3142328	BLASTN	907	4e-34	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15379	GM_M03_B2_H03_MR	g2230959	BLASTX	397	2e-35	52	(Y10149) subtilisin-like protease [Lycopersicon esculentum]
15380	GM_M03_B2_H04_MF	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15381	GM_M03_B2_H04_MR	g3142379	BLASTX	157	7e-10	75	(AF053008) envelope-like [Glycine max]
15382	GM_M03_B2_H05_MF	g2708741	BLASTX	242	9e-18	86	(AC003952) hypothetical protein [Arabidopsis thaliana]
15383	GM_M03_B2_H05_MR	g2969943	BLASTN	365	2e-09	61	Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS
15384	GM_M03_B2_H06_MF	g18559	BLASTN	684	6e-24	73	G.max gene for catalase
15385	GM_M03_B2_H10_MF	g2288985	BLASTX	243	1e-18	56	(AC002335) hypothetical protein [Arabidopsis thaliana]
15386	GM_M04_A1_A02_MF	g4063760	BLASTX	426	5e-38	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15387	GM_M04_A1_B04_MF	g2924729	BLASTN	699	1e-24	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]
15388	GM_M04_A1_C02_MF	g507910	BLASTN	377	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15389	GM_M04_A1_C09_MF	g3646936	BLASTN	364	2e-09	61	Caenorhabditis elegans cosmid Y47D3B, complete sequence [Caenorhabditis elegans]
15390	GM_M04_A1_D03_MF	g4063760	BLASTX	430	2e-46	76	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15391	GM_M04_A1_E07_MF	g3928116	BLASTN	407	2e-11	74	, complete sequence [Homo sapiens]
15392	GM_M04_A1_E11_MF	g507910	BLASTN	384	9e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15393	GM_M04_A1_F02_MF	g905361	BLASTX	149	3e-10	83	(U22103) gag-protease polyprotein [Glycine max]
15394	GM_M04_A1_F03_MF	g2522230	BLASTX	159	5e-11	32	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
15395	GM_M04_A1_F04_MF	g2495209	BLASTX	191	2e-14	44	HYPOTHETICAL 12.9 KD PROTEIN SLR1417 gi 1651819 gnl PID d1017479 (D90900) hypothetical protein [Synechocystis sp.]
15396	GM_M04_A1_F08_MF	g4138583	BLASTX	233	8e-18	62	(Y10821) plastidic ATP/ADP-transporter [Solanum tuberosum]
15397	GM_M04_A1_F09_MF	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15398	GM_M04_A1_F11_MF	g2961370	BLASTN	383	3e-10	84	Arabidopsis thaliana DNA chromosome 4, BAC clone F23E13 (ESSAII project)
15399	GM_M04_A1_G05_MF	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15400	GM_M04_A1_G06_MF	g2995405	BLASTX	196	6e-22	47	(Y12432) polyprotein [Ananas comosus]
15401	GM_M04_A1_G07_MF	g507910	BLASTN	675	7e-24	85	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15402	GM_M04_A1_G12_MF	g4063770	BLASTX	193	2e-13	32	(AB004906) transposase [Ipomoea purpurea]
15403	GM_M04_A1_H03_MF	g18559	BLASTN	854	1e-31	78	G.max gene for catalase
15404	GM_M04_A1_H05_MF	g3142328	BLASTN	1237	4e-49	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15405	GM_M04_A1_H12_MF	g507910	BLASTN	401	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
15406	GM_M04_A2_A04_MF	g507910	BLASTN	536	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15407	GM_M04_A2_A08_MR	g2443320	BLASTX	220	6e-16	32	(D85597) polyprotein [Oryza australiensis]
15408	GM_M04_A2_A10_MR	g3264565	BLASTN	378	5e-10	60	Homo sapiens chromosome 17, clone hRPC.1037_O_7, complete sequence [Homo sapiens]
15409	GM_M04_A2_B02_MF	g507910	BLASTN	651	8e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
15410	GM_M04_A2_B03_MF	g2407790	BLASTX	165	2e-10	44	(AF019910) grr1 [Glycine max]
15411	GM_M04_A2_B05_MF	g3777527	BLASTX	312	1e-25	50	(AF053008) gag-pol polyprotein [Glycine max]
15412	GM_M04_A2_B07_MF	g4140712	BLASTX	113	9e-11	31	(AF110183) putative integrase [Oryza sativa]
15413	GM_M04_A2_B07_MR	g1769897	BLASTX	304	8e-26	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15414	GM_M04_A2_B09_MF	g507910	BLASTN	580	1e-19	86	Glycine max BSR-101 satellite SB92 genomic sequence.
15415	GM_M04_A2_B10_MF	g3777527	BLASTX	686	2e-65	91	(AF053008) gag-pol polyprotein [Glycine max]
15416	GM_M04_A2_B11_MR	g3777527	BLASTX	312	1e-25	47	(AF053008) gag-pol polyprotein [Glycine max]
15417	GM_M04_A2_B12_MR	g3193306	BLASTX	205	2e-14	29	(AF069300) contains similarity to Arabidopsis membrane-associated salt-inducible-like protein (GB:AL021637) [Arabidopsis thaliana]
15418	GM_M04_A2_C02_MF	g905361	BLASTX	597	2e-57	87	(U22103) gag-protease polyprotein [Glycine max]
15419	GM_M04_A2_C06_MR	g2522228	BLASTX	367	4e-40	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
15420	GM_M04_A2_C07_MF	g18559	BLASTN	974	4e-37	74	G.max gene for catalase
15421	GM_M04_A2_C08_MR	g1669680	BLASTN	472	3e-14	63	Human DNA sequence from PAC 293E14 contains ESTs, STS
15422	GM_M04_A2_C12_MF	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15423	GM_M04_A2_D04_MR	g905361	BLASTX	370	1e-32	89	(U22103) gag-protease polyprotein [Glycine max]
15424	GM_M04_A2_D05_MF	g507910	BLASTN	386	8e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15425	GM_M04_A2_D05_MR	g507910	BLASTN	396	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15426	GM_M04_A2_D06_MF	g2275186	BLASTN	403	4e-11	63	Human BAC clone RG020D02 from 7q22, complete sequence [Homo sapiens]
15427	GM_M04_A2_D07_MF	g3377848	BLASTX	107	1e-10	33	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
15428	GM_M04_A2_D07_MR	g4102839	BLASTX	180	3e-12	41	(AF016713) LeOPT1 [Lycopersicon esculentum]
15429	GM_M04_A2_E06_MR	g4063760	BLASTX	326	3e-27	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15430	GM_M04_A2_E08_MF	g905361	BLASTX	180	2e-14	36	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15431	GM_M04_A2_E11_MF	g2335100	BLASTX	432	4e-39	61	(AC002339) unknown protein [Arabidopsis thaliana]
15432	GM_M04_A2_F10_MR	g1840106	BLASTN	378	1e-10	64	Human fragile site locus (FRA16B) minisatellite repeat
15433	GM_M04_A2_G03_MR	g18559	BLASTN	433	1e-12	75	G.max gene for catalase
15434	GM_M04_A2_G06_MF	g1669374	BLASTN	362	3e-09	67	Human PAC clone 2G3A from 13q12-13q13, complete sequence [Homo sapiens]
15435	GM_M04_A2_G08_MF	g18559	BLASTN	368	1e-09	68	G.max gene for catalase
15436	GM_M04_A2_G10_MF	g3176795	BLASTN	421	1e-12	62	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
15437	GM_M04_A2_G11_MF	g2995405	BLASTX	338	8e-29	46	(Y12432) polyprotein [Ananas comosus]
15438	GM_M04_A2_G12_MR	g4063760	BLASTX	377	1e-32	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15439	GM_M04_A2_H02_MF	g629693	BLASTX	149	3e-09	30	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
15440	GM_M04_A2_H03_MR	g3043726	BLASTX	193	3e-13	35	(AB011173) KIAA0601 protein [Homo sapiens]
15441	GM_M04_A2_H05_MF	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15442	GM_M04_A2_H05_MR	g507910	BLASTN	445	2e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15443	GM_M04_B1_A01_MR	g2522227	BLASTX	189	4e-14	49	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
15444	GM_M04_B1_A03_MR	g3273118	BLASTN	361	3e-09	59	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-52, complete sequence [Plasmodium falciparum]
15445	GM_M04_B1_A04_MF	g4063760	BLASTX	211	5e-15	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15446	GM_M04_B1_A08_MR	g13536	BLASTN	347	7e-09	63	Yeast (S. cerevisiae) mitochondrial genes for several tRNAs (Thr(2), Cys(2) and His). >gi 343930 gb K00537 YSCMTTGO1 Yeast (S.cerevisiae) mitochondrial cap-oxi1 region: Thr-2, Cys-2 and His-tRNA genes.
15447	GM_M04_B1_B01_MR	g18559	BLASTN	916	2e-34	71	G.max gene for catalase
15448	GM_M04_B1_B04_MF	g629693	BLASTX	263	6e-22	60	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
15449	GM_M04_B1_B05_MF	g730526	BLASTX	190	4e-31	80	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis thaliana gi 404166 (X75162) BBC1 protein [Arabidopsis thaliana]
15450	GM_M04_B1_B08_MR	g18559	BLASTN	1013	6e-39	76	G.max gene for catalase
15451	GM_M04_B1_B10_MR	g4159707	BLASTN	683	8e-24	66	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MJK13, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15452	GM_M04_B1_B12_MR	g1076387	BLASTX	332	3e-42	83	protein kinase homolog - Arabidopsis thaliana gi 717180 (X79279) protein kinase homologous to shaggy and glycogen synthase kinase-3 [Arabidopsis thaliana]
15453	GM_M04_B1_C01_MF	g99922	BLASTX	520	3e-49	67	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
15454	GM_M04_B1_C01_MR	g99730	BLASTX	443	2e-43	57	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
15455	GM_M04_B1_C04_MF	g3777527	BLASTX	298	4e-24	48	(AF053008) gag-pol polyprotein [Glycine max]
15456	GM_M04_B1_C05_MR	g4063756	BLASTN	566	2e-18	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15457	GM_M04_B1_C08_MF	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15458	GM_M04_B1_C08_MR	g507910	BLASTN	522	6e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15459	GM_M04_B1_C11_MR	g3341679	BLASTX	298	7e-25	68	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]
15460	GM_M04_B1_C12_MR	g421954	BLASTX	220	2e-20	41	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
15461	GM_M04_B1_D07_MF	g507910	BLASTN	394	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15462	GM_M04_B1_D07_MR	g507910	BLASTN	353	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
15463	GM_M04_B1_D10_MR	g4063756	BLASTN	515	3e-16	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15464	GM_M04_B1_E03_MF	g507910	BLASTN	532	2e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15465	GM_M04_B1_E03_MR	g507910	BLASTN	552	2e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15466	GM_M04_B1_E05_MF	g3142379	BLASTX	284	5e-24	83	(AF053008) envelope-like [Glycine max]
15467	GM_M04_B1_F05_MR	g3522932	BLASTN	655	1e-22	65	Arabidopsis thaliana chromosome II BAC F14M4 genomic sequence, complete sequence [Arabidopsis thaliana]
15468	GM_M04_B1_G02_MR	g507910	BLASTN	579	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15469	GM_M04_B1_G06_MF	g550452	BLASTX	177	1e-17	79	(U08469) 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]
15470	GM_M04_B1_G07_MF	g4063760	BLASTX	207	1e-15	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15471	GM_M04_B1_G08_MF	g3810596	BLASTX	193	3e-13	36	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
15472	GM_M04_B1_G10_MR	g3097320	BLASTN	678	1e-23	70	Glycine max gene for Bd 30K, complete cds
15473	GM_M04_B1_H02_MF	g4063760	BLASTX	285	6e-23	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15474	GM_M04_B1_H02_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15475	GM_M04_B1_H04_MR	g3142328	BLASTN	598	4e-20	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15476	GM_M04_B1_H05_MF	g1905780	BLASTN	373	6e-10	61	D.discoideum genes enocoding cytochrome C oxidase, subunits VIIe & VIIs
15477	GM_M04_B1_H08_MF	g3777527	BLASTX	246	1e-18	46	(AF053008) gag-pol polyprotein [Glycine max]
15478	GM_M04_B1_H09_MF	g550452	BLASTX	331	1e-51	98	(U08469) 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]
15479	GM_M04_B1_H10_MF	g4063760	BLASTX	172	6e-12	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15480	GM_M04_B1_H12_MR	g3142328	BLASTN	722	5e-34	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15481	GM_M04_B2_A07_MF	g4063760	BLASTX	247	7e-19	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15482	GM_M04_B2_A07_MR	g507910	BLASTN	341	8e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
15483	GM_M04_B2_B03_MF	g507910	BLASTN	670	1e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
15484	GM_M04_B2_B03_MR	g507910	BLASTN	649	1e-22	86	Glycine max BSR-101 satellite SB92 genomic sequence.
15485	GM_M04_B2_B04_MF	g507910	BLASTN	388	6e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15486	GM_M04_B2_B05_MR	g4063760	BLASTX	372	3e-32	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15487	GM_M04_B2_B06_MF	g2462744	BLASTX	135	6e-09	32	(AC002292) Hypothetical protein [Arabidopsis thaliana]
15488	GM_M04_B2_B08_MF	g498931	BLASTX	103	1e-10	44	(Z12825) ORF167; homologous to reverse transcriptases from retroviral-like transposons TNT 1-94 from tobacco and COPIA from Drosophila [Beta vulgaris]
15489	GM_M04_B2_B09_MR	g4063760	BLASTX	358	1e-30	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15490	GM_M04_B2_B10_MR	g3142328	BLASTN	943	9e-36	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15491	GM_M04_B2_C03_MR	g3402749	BLASTX	252	3e-21	45	(AL031187) putative protein [Arabidopsis thaliana]
15492	GM_M04_B2_C04_MR	g1335862	BLASTX	313	1e-25	81	(U42608) clathrin heavy chain [Glycine max]
15493	GM_M04_B2_C05_MR	g3241921	BLASTN	457	1e-13	80	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCM23, complete sequence [Arabidopsis thaliana]
15494	GM_M04_B2_C10_MR	g507910	BLASTN	556	2e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
15495	GM_M04_B2_C11_MF	g507910	BLASTN	370	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15496	GM_M04_B2_C11_MR	g4063760	BLASTX	225	2e-16	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15497	GM_M04_B2_D01_MF	g905361	BLASTX	644	2e-62	96	(U22103) gag-protease polyprotein [Glycine max]
15498	GM_M04_B2_D01_MR	g4063760	BLASTX	518	8e-48	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15499	GM_M04_B2_D07_MR	g905361	BLASTX	204	1e-14	35	(U22103) gag-protease polyprotein [Glycine max]
15500	GM_M04_B2_D12_MF	g2462134	BLASTX	147	9e-09	32	(Y13368) reverse transcriptase [Beta vulgaris]
15501	GM_M04_B2_D12_MR	g3522943	BLASTX	183	8e-13	57	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15502	GM_M04_B2_E03_MR	g2244747	BLASTN	372	9e-10	70	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 0
15503	GM_M04_B2_E04_MR	g4063760	BLASTX	424	9e-38	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15504	GM_M04_B2_E08_MF	g1769897	BLASTX	294	1e-28	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15505	GM_M04_B2_E08_MR	g4063760	BLASTX	214	2e-15	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15506	GM_M04_B2_E09_MF	g507910	BLASTN	355	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15507	GM_M04_B2_F12_MR	g3687234	BLASTX	165	3e-10	49	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
15508	GM_M04_B2_G01_MF	g1755162	BLASTX	239	2e-19	72	(U75192) germin-like protein [Arabidopsis thaliana]
15509	GM_M04_B2_G03_MF	g507910	BLASTN	521	6e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15510	GM_M04_B2_G03_MR	g507910	BLASTN	527	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15511	GM_M04_B2_G04_MF	g507910	BLASTN	352	3e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
15512	GM_M04_B2_G05_MR	g3928116	BLASTN	426	3e-12	65	, complete sequence [Homo sapiens]
15513	GM_M04_B2_G06_MR	g3337395	BLASTN	416	9e-12	64	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
15514	GM_M04_B2_G08_MF	g4092470	BLASTN	369	1e-09	62	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
15515	GM_M04_B2_G11_MF	g4056503	BLASTX	148	8e-10	77	(AC005896) unknown protein [Arabidopsis thaliana]
15516	GM_M04_B2_H03_MR	g170029	BLASTN	389	1e-10	80	Glycine max cv. Dare nodulin 26 gene fragment.
15517	GM_M04_B2_H04_MR	g1769898	BLASTX	158	8e-10	30	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15518	GM_M04_B2_H05_MF	g4063760	BLASTX	384	2e-33	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15519	GM_M04_B2_H05_MR	g507910	BLASTN	514	1e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15520	GM_M04_B2_H12_MR	g3510505	BLASTX	166	3e-10	45	(AF030881) pol polyprotein [Fugu rubripes]
15521	GM_M05_A1_A02_MR	g3142379	BLASTX	338	6e-30	68	(AF053008) envelope-like [Glycine max]
15522	GM_M05_A1_A05_MR	g3319366	BLASTX	160	6e-11	46	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
15523	GM_M05_A1_B05_MR	g9825	BLASTN	391	1e-10	68	Plasmodium falciparum 11-1 gene part 1
15524	GM_M05_A1_B08_MR	g507910	BLASTN	340	9e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
15525	GM_M05_A1_B09_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15526	GM_M05_A1_D03_MR	g507910	BLASTN	559	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15527	GM_M05_A1_D06_MR	g3142379	BLASTX	217	2e-20	87	(AF053008) envelope-like [Glycine max]
15528	GM_M05_A1_D10_MR	g1272410	BLASTX	197	5e-15	97	(U52045) immunophilin precursor [Vicia faba]
15529	GM_M05_A1_G03_MR	g3152613	BLASTX	114	6e-13	36	(AC004482) hypothetical protein [Arabidopsis thaliana]
15530	GM_M05_A1_H03_MR	g3834390	BLASTX	117	9e-16	48	(AF039029) snurportin1 [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15531	GM_M05_A1_H04_MR	g462013	BLASTX	192	4e-25	88	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) gi 542022 pir S39558 HSP90 homolog - Madagascar periwinkle gi 348696 (L14594) heat shock protein 90 [Catharanthus roseus]
15532	GM_M05_B1_A07_MR	g4063760	BLASTX	172	7e-11	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15533	GM_M05_B1_A11_MR	g3641780	BLASTN	358	4e-09	61	Homo sapiens PAC clone DJ1159C10 from 7q34-q36, complete sequence [Homo sapiens]
15534	GM_M05_B1_A12_MR	g1142701	BLASTN	1388	2e-56	87	Glycine max satellite STR120-A.3.
15535	GM_M05_B1_D02_MR	g1589778	BLASTX	165	2e-15	76	(U62135) SPINDLY [Arabidopsis thaliana]
15536	GM_M05_B1_D04_MR	g4063760	BLASTX	145	3e-10	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15537	GM_M05_B1_D06_MR	g507910	BLASTN	419	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15538	GM_M05_B1_D11_MR	g99922	BLASTX	466	2e-43	78	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
15539	GM_M05_B1_E08_MR	g18559	BLASTN	672	2e-23	74	G.max gene for catalase
15540	GM_M05_B1_G09_MR	g968986	BLASTN	439	6e-13	84	Glycine max ferritin gene, nuclear gene encoding chloroplast protein, complete cds
15541	GM_M05_B1_G10_MR	g4063760	BLASTX	246	8e-19	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15542	GM_M05_B1_G12_MR	g1399304	BLASTN	394	6e-11	71	Glycine max phosphoinositide-specific phospholipase C P13 mRNA, complete cds.
15543	GM_M05_B1_H01_MR	g507910	BLASTN	394	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15544	GM_M05_B1_H03_MR	g3097320	BLASTN	369	1e-09	68	Glycine max gene for Bd 30K, complete cds
15545	GM_M05_B1_H06_MR	g178823	BLASTN	338	4e-09	62	Human apolipoprotein B gene hypervariable region, 3' flank.
15546	GM_M05_B2_A12_MF	g3805853	BLASTX	173	3e-11	60	(AL031986) putative protein [Arabidopsis thaliana]
15547	GM_M05_B2_B05_MF	g100484	BLASTX	374	6e-33	61	hypothetical protein - garden snapdragon
15548	GM_M05_B2_D02_MF	g2995405	BLASTX	408	2e-36	57	(Y12432) polyprotein [Ananas comosus]
15549	GM_M05_B2_D04_MF	g3142328	BLASTN	1530	2e-62	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15550	GM_M05_B2_D05_MF	g3777527	BLASTX	644	5e-61	92	(AF053008) gag-pol polyprotein [Glycine max]
15551	GM_M05_B2_E03_MF	g2541876	BLASTX	214	5e-16	36	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
15552	GM_M05_B2_E04_MF	g507910	BLASTN	388	6e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15553	GM_M05_B2_F05_MF	g2129618	BLASTX	233	1e-17	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15554	GM_M05_B2_F10_MF	g3142379	BLASTX	140	2e-14	52	(AF053008) envelope-like [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15555	GM_M05_B2_F12_MF	g2497820	BLASTX	181	1e-24	81	DNA REPLICATION LICENSING FACTOR MCM3 HOMOLOG (REPLICATION ORIGIN ACTIVATOR) (ROA PROTEIN) gi 1076823 pir S52247 probable replication origin activator protein ROA - maize (fragment) gi 609290 (Z29368) ROA protein [Zea mays]
15556	GM_M05_B2_G07_MF	g1170507	BLASTX	109	4e-11	67	EUKARYOTIC INITIATION FACTOR 4A-3 (EIF-4A-3) gi 100276 pir S22579 translation initiation factor eIF-4A - curled-leaved tobacco gi 19699 (X61206) nicotiana eukaryotic translation initiation factor 4A [Nicotiana plumbaginifolia]
15557	GM_M05_B2_G09_MF	g14293	BLASTN	374	9e-11	69	Yeast R0.54 mutant mitochondrial DNA lacking ori1 sequence recombination junction with tRNA-Pro and 15S rRNA genes
15558	GM_M05_B2_G12_MF	g3777527	BLASTX	650	1e-61	94	(AF053008) gag-pol polyprotein [Glycine max]
15559	GM_M05_B2_H11_MF	g4063760	BLASTX	221	3e-19	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15560	GM_M06_A1_A08_MR	g13597	BLASTN	293	1e-09	69	Yeast mitochondrial tRNA genes for tRNA-Ala, tRNA-Tyr and tRNA-Ile
15561	GM_M06_A1_A11_MR	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15562	GM_M06_A1_A12_MR	g4160362	BLASTN	378	5e-10	61	Saccharomyces cerevisiae complete mitochondrial genome
15563	GM_M06_A1_B11_MR	g3643085	BLASTX	465	2e-43	66	(AF075580) protein phosphatase-2C; PP2C [Mesembryanthemum crystallinum]
15564	GM_M06_A1_C08_MR	g507910	BLASTN	393	4e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15565	GM_M06_A1_C10_MR	g3402755	BLASTX	307	2e-26	51	(AL031187) putative transposable element [Arabidopsis thaliana]
15566	GM_M06_A1_C11_MR	g3777527	BLASTX	659	2e-65	94	(AF053008) gag-pol polyprotein [Glycine max]
15567	GM_M06_A1_D06_MR	g226407	BLASTX	119	4e-11	38	retrotransposon del1-46 [Lilium henryi]
15568	GM_M06_A1_D07_MR	g1769898	BLASTX	303	2e-32	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15569	GM_M06_A1_E01_MR	g2132242	BLASTX	272	1e-22	49	hypothetical protein YPL235w - yeast (Saccharomyces cerevisiae) gi 1061254 (Z67751) putative protein [Saccharomyces cerevisiae] gi 1181253 (X94561) ATP/GTP binding site motif A (P-loop) [Saccharomyces cerevisiae] gi 1370486 gnl PID e246945 (Z73591) ORF YPL235w [Saccharomyces cerevisiae]
15570	GM_M06_A1_E04_MR	g2522228	BLASTX	339	2e-38	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
15571	GM_M06_A1_E12_MR	g3309583	BLASTX	164	4e-19	96	(AF073830) fructose-6-phosphate 2-kinase/fructose-2,6-bisphosphatase [Solanum tuberosum]
15572	GM_M06_A1_G07_MR	g2129618	BLASTX	160	1e-09	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15573	GM_M06_A1_H01_MR	g4102181	BLASTN	388	2e-10	63	Mus musculus phosphoenolpyruvate carboxykinase (PEPCK) gene, complete cds
15574	GM_M06_A1_H04_MR	g507910	BLASTN	464	2e-14	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15575	GM_M06_A1_H06_MR	g507910	BLASTN	415	4e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15576	GM_M06_A1_H10_MR	g2129618	BLASTX	157	2e-09	32	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15577	GM_M06_A2_A05_MR	g629693	BLASTX	152	2e-09	31	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
15578	GM_M06_A2_A07_MR	g507910	BLASTN	543	6e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15579	GM_M06_A2_A09_MF	g2764526	BLASTN	443	5e-13	67	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
15580	GM_M06_A2_B11_MF	g18768	BLASTN	351	2e-09	70	Soybean Tgm6 transposable element 3' end
15581	GM_M06_A2_C02_MR	g3452140	BLASTX	357	6e-32	82	(AJ004901) resistance protein [Glycine max]
15582	GM_M06_A2_C04_MF	g2979597	BLASTN	453	2e-13	67	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
15583	GM_M06_A2_C09_MR	g4063760	BLASTX	116	2e-13	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15584	GM_M06_A2_D09_MR	g507910	BLASTN	380	1e-10	69	Glycine max BSR-101 satellite SB92 genomic sequence.
15585	GM_M06_A2_D10_MR	g905361	BLASTX	174	2e-11	28	(U22103) gag-protease polyprotein [Glycine max]
15586	GM_M06_A2_E01_MF	g2245021	BLASTX	144	7e-11	74	(Z97341) heat shock protein 110 homolog [Arabidopsis thaliana]
15587	GM_M06_A2_E04_MF	g3142328	BLASTN	685	3e-29	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15588	GM_M06_A2_E04_MR	g3492803	BLASTX	164	4e-11	48	(AJ002479) ENBP1 [Medicago truncatula]
15589	GM_M06_A2_F04_MR	g4063760	BLASTX	427	4e-38	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15590	GM_M06_A2_F06_MR	g3142328	BLASTN	944	8e-36	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15591	GM_M06_A2_F08_MF	g18559	BLASTN	552	5e-18	72	G.max gene for catalase
15592	GM_M06_A2_H01_MR	g1480927	BLASTN	461	6e-14	78	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
15593	GM_M06_A2_H11_MR	g2129618	BLASTX	151	1e-14	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15594	GM_M06_B1_A02_MF	g3033389	BLASTX	177	1e-11	38	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
15595	GM_M06_B1_A05_MF	g166884	BLASTN	609	3e-21	77	A.thaliana telomeric DNA. >gi 589934 gb I07744 Sequence 1 from Patent EP 0338266
15596	GM_M06_B1_A08_MF	g3142328	BLASTN	1101	6e-43	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15597	GM_M06_B1_A11_MR	g1167523	BLASTX	300	2e-24	54	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
15598	GM_M06_B1_A12_MF	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15599	GM_M06_B1_A12_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15600	GM_M06_B1_B10_MF	g507910	BLASTN	391	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15601	GM_M06_B1_B10_MR	g507910	BLASTN	350	3e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
15602	GM_M06_B1_B11_MF	g507910	BLASTN	403	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
15603	GM_M06_B1_B11_MR	g507910	BLASTN	394	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15604	GM_M06_B1_B12_MR	g1666236	BLASTX	169	1e-11	35	(U76261) unknown [Hordeum vulgare]
15605	GM_M06_B1_C06_MF	g1167523	BLASTX	172	8e-11	41	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
15606	GM_M06_B1_C09_MF	g3377856	BLASTX	283	9e-23	50	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 19.54) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 12.35) [Arabidopsis thaliana]
15607	GM_M06_B1_D04_MF	g1769898	BLASTX	130	4e-15	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15608	GM_M06_B1_D09_MF	g99922	BLASTX	285	2e-24	92	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
15609	GM_M06_B1_D10_MR	g3869075	BLASTN	400	5e-11	73	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence [Arabidopsis thaliana]
15610	GM_M06_B1_E02_MF	g2764526	BLASTN	393	1e-10	61	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
15611	GM_M06_B1_E07_MF	g2351060	BLASTX	488	7e-46	70	(AB006660) sucrose-phosphate synthase [Citrus unshiu]
15612	GM_M06_B1_E09_MF	g2979562	BLASTX	351	6e-31	54	(AC003680) unknown protein [Arabidopsis thaliana] gi 3386623 (AC004665) unknown protein [Arabidopsis thaliana]
15613	GM_M06_B1_E10_MR	g507910	BLASTN	556	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15614	GM_M06_B1_E11_MR	g4063760	BLASTX	205	2e-14	75	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15615	GM_M06_B1_F01_MF	g2995179	BLASTN	362	3e-09	63	Homo sapiens DNA sequence from PAC 262D12 on chromosome q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIK...
15616	GM_M06_B1_F06_MR	g3645899	BLASTX	245	1e-23	50	(U68408) 5' end not determined experimentally [Zea mays]
15617	GM_M06_B1_F12_MR	g4160362	BLASTN	443	6e-13	63	Saccharomyces cerevisiae complete mitochondrial genome
15618	GM_M06_B1_G12_MR	g4063760	BLASTX	497	1e-45	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15619	GM_M06_B1_H02_MF	g1769897	BLASTX	295	9e-25	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15620	GM_M06_B1_H06_MF	g3650026	BLASTN	425	4e-12	63	Arabidopsis thaliana chromosome II BAC T26I20 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15621	GM_M06_B1_H07_MF	g3176803	BLASTN	333	6e-09	59	Homo sapiens allele 15 fragile site locus (FRA10B) minisatellite sequence
15622	GM_M06_B1_H08_MF	g905361	BLASTX	698	4e-68	93	(U22103) gag-protease polyprotein [Glycine max]
15623	GM_M06_B1_H08_MR	g3142328	BLASTN	619	5e-21	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15624	GM_M06_B1_H11_MF	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15625	GM_M06_B1_H11_MR	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15626	GM_M06_B2_A10_MR	g18559	BLASTN	548	8e-18	74	G.max gene for catalase
15627	GM_M06_B2_A12_MR	g3687234	BLASTX	153	3e-14	60	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
15628	GM_M06_B2_B08_MR	g4063760	BLASTX	230	4e-17	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15629	GM_M06_B2_B12_MR	g728905	BLASTX	199	1e-13	42	PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC RETICULUM CA2+-ATPASE) gi 1078206 pir S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) gi 171114 (L01795) ATPase [Saccharomyces cerevisiae] gi 595560 (U12980) Drs2p: Membrane spanning Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae]
15630	GM_M06_B2_C04_MF	g3142328	BLASTN	655	1e-22	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15631	GM_M06_B2_C10_MF	g3142328	BLASTN	748	7e-27	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15632	GM_M06_B2_D09_MR	g507910	BLASTN	372	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
15633	GM_M06_B2_D12_MF	g3777527	BLASTX	528	1e-48	93	(AF053008) gag-pol polyprotein [Glycine max]
15634	GM_M06_B2_E10_MR	g3097320	BLASTN	683	7e-24	75	Glycine max gene for Bd 30K, complete cds
15635	GM_M06_B2_F08_MR	g507910	BLASTN	547	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15636	GM_M06_B2_F09_MF	g2342690	BLASTX	127	2e-16	58	(AC000106) Similar to Homo copine I (gb U83246). [Arabidopsis thaliana]
15637	GM_M06_B2_G01_MF	g3608154	BLASTX	167	4e-12	47	(AC005314) unknown protein [Arabidopsis thaliana]
15638	GM_M06_B2_G07_MF	g2995405	BLASTX	215	2e-26	49	(Y12432) polyprotein [Ananas comosus]
15639	GM_M06_B2_G12_MR	g507910	BLASTN	686	2e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
15640	GM_M06_B2_H05_MF	g3097320	BLASTN	836	8e-31	74	Glycine max gene for Bd 30K, complete cds
15641	GM_M06_B2_H08_MF	g3097320	BLASTN	372	8e-10	71	Glycine max gene for Bd 30K, complete cds
15642	GM_M07_A1_A03_MR	g4063760	BLASTX	419	3e-37	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15643	GM_M07_A1_A04_MF	g3142328	BLASTN	554	4e-18	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15644	GM_M07_A1_A05_MR	g2501565	BLASTX	104	3e-09	43	HYPOTHETICAL 40.2 KD PROTEIN IN CTF13-YPK2 INTERGENIC REGION gi 1078518 pir S55087 hypothetical protein YMR101c - yeast (Saccharomyces cerevisiae) gi 854438 (Z49807) unknown [Saccharomyces cerevisiae]
15645	GM_M07_A1_A07_MF	g169934	BLASTN	665	8e-24	80	G.max (soybean) atpH gene encoding CFO-ATPase subunit III, chloroplast gene encoding chloroplast protein, complete cds.
15646	GM_M07_A1_A07_MR	g2887437	BLASTX	128	2e-13	88	(AB007893) KIAA0433 [Homo sapiens]
15647	GM_M07_A1_A08_MR	g3513747	BLASTX	265	1e-20	47	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
15648	GM_M07_A1_A12_MR	g3097320	BLASTN	402	4e-11	68	Glycine max gene for Bd 30K, complete cds
15649	GM_M07_A1_B08_MR	g3928097	BLASTX	243	7e-20	73	(AC005770) unknown protein, 5' partial [Arabidopsis thaliana]
15650	GM_M07_A1_C02_MF	g4063760	BLASTX	225	1e-16	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15651	GM_M07_A1_C02_MR	g507910	BLASTN	577	2e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15652	GM_M07_A1_C07_MF	g2462753	BLASTX	137	2e-09	67	(AC002292) putative polygalacturonase [Arabidopsis thaliana]
15653	GM_M07_A1_C09_MR	g728905	BLASTX	181	8e-12	44	PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC RETICULUM CA2+-ATPASE) gi 1078206 pir S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) gi 171114 (L01795) ATPase [Saccharomyces cerevisiae] gi 595560 (U12980) Drs2p: Membrane spanning Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae]
15654	GM_M07_A1_C10_MF	g507910	BLASTN	461	3e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15655	GM_M07_A1_D02_MR	g3645899	BLASTX	222	6e-22	52	(U68408) 5' end not determined experimentally [Zea mays]
15656	GM_M07_A1_D03_MR	g3097320	BLASTN	785	2e-28	78	Glycine max gene for Bd 30K, complete cds
15657	GM_M07_A1_D10_MR	g2129618	BLASTX	170	8e-11	47	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15658	GM_M07_A1_E01_MF	g20854	BLASTN	400	3e-11	68	Pea rbcS-3A gene for ribulose 1.5-bisphosphate carboxylase (RBC) small subunit
15659	GM_M07_A1_F08_MR	g18559	BLASTN	365	2e-09	75	G.max gene for catalase
15660	GM_M07_A1_F12_MF	g2104945	BLASTN	651	2e-22	69	Glycine max copia-like retrotransposon Tgmr, complete sequence
15661	GM_M07_A1_G05_MF	g3193221	BLASTN	358	3e-09	77	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
15662	GM_M07_A1_G08_MR	g3426334	BLASTN	491	3e-15	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15663	GM_M07_A1_G09_MF	g2522228	BLASTX	187	5e-16	44	(AB007466) reverse transcriptase-like protein [Vicia faba]
15664	GM_M07_A1_G12_MF	g4063760	BLASTX	195	3e-13	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15665	GM_M07_A1_H01_MR	g4006828	BLASTX	182	4e-12	31	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
15666	GM_M07_A1_H02_MF	g2583128	BLASTX	367	5e-33	74	(AC002387) hypothetical protein [Arabidopsis thaliana]
15667	GM_M07_A1_H03_MF	g3930515	BLASTX	121	1e-11	47	(AF059674) putative gag protein [Nicotiana tabacum]
15668	GM_M07_A1_H09_MR	g507910	BLASTN	375	2e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
15669	GM_M07_A2_A07_MF	g729092	BLASTX	349	2e-30	64	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK) gi 477484 pir A49082 calcium-dependent protein kinase isoform AK1 - Arabidopsis thaliana gi 304105 (L14771) calcium-dependent protein kinase [Arabidopsis thaliana]
15670	GM_M07_A2_A09_MF	g100484	BLASTX	335	1e-28	58	hypothetical protein - garden snapdragon
15671	GM_M07_A2_B05_MR	g2129618	BLASTX	204	2e-14	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15672	GM_M07_A2_B10_MF	g422028	BLASTX	268	2e-22	73	transcription factor OBF3.1, ocs element-binding - maize gi 297020 (X69153) ocs-element binding factor 3.1 [Zea mays]
15673	GM_M07_A2_B12_MR	g1769899	BLASTX	261	8e-22	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15674	GM_M07_A2_C03_MR	g3142330	BLASTX	311	3e-32	89	(U96295) envelope-like [Glycine max]
15675	GM_M07_A2_C04_MR	g3738114	BLASTN	377	5e-10	62	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
15676	GM_M07_A2_C11_MR	g2462749	BLASTX	184	1e-12	66	(AC002292) Putative Serine/Threonine protein kinase [Arabidopsis thaliana]
15677	GM_M07_A2_D02_MR	g421955	BLASTX	148	2e-26	60	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
15678	GM_M07_A2_D08_MF	g18559	BLASTN	477	1e-14	69	G.max gene for catalase
15679	GM_M07_A2_D10_MF	g2462834	BLASTX	178	5e-13	44	(AF000657) hypothetical protein [Arabidopsis thaliana]
15680	GM_M07_A2_D12_MF	g2924781	BLASTX	144	3e-19	47	(AC002334) putative cellulose synthase [Arabidopsis thaliana]
15681	GM_M07_A2_E02_MR	g4038056	BLASTX	194	2e-13	38	(AC005897) putative transposon [Arabidopsis thaliana]
15682	GM_M07_A2_F04_MR	g2326372	BLASTX	167	2e-21	82	(Y14404) putative arabinose kinase [Arabidopsis thaliana]
15683	GM_M07_A2_F06_MR	g4063760	BLASTX	309	2e-25	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15684	GM_M07_A2_H03_MR	g18559	BLASTN	323	4e-11	70	G.max gene for catalase
15685	GM_M07_A2_H04_MR	g3033389	BLASTX	123	1e-10	43	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
15686	GM_M07_A2_H08_MR	g2522230	BLASTX	257	2e-21	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
15687	GM_M07_B1_A01_MF	g340797	BLASTN	339	4e-09	70	Figure 6. DNA sequence of three 3' apoB VNTR alleles.
15688	GM_M07_B1_B10_MF	g1769898	BLASTX	159	7e-10	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15689	GM_M07_B1_C06_MR	g4063760	BLASTX	405	1e-35	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15690	GM_M07_B1_C07_MR	g3845197	BLASTN	408	2e-11	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
15691	GM_M07_B1_C08_MF	g1165321	BLASTN	672	2e-23	80	Glycine max extensin (SbHRGP3) gene, complete cds
15692	GM_M07_B1_C08_MR	g3142328	BLASTN	1068	2e-41	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15693	GM_M07_B1_C09_MR	g4140712	BLASTX	118	9e-09	34	(AF110183) putative integrase [Oryza sativa]
15694	GM_M07_B1_D06_MR	g507910	BLASTN	627	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
15695	GM_M07_B1_D07_MR	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
15696	GM_M07_B1_E02_MF	g3928086	BLASTX	204	1e-15	54	(AC005770) unknown protein [Arabidopsis thaliana]
15697	GM_M07_B1_E06_MR	g3142328	BLASTN	433	1e-12	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15698	GM_M07_B1_F08_MF	g1040717	BLASTN	336	4e-09	65	D.polychroa microsatellite sequence (clone Dp ch1 F3)
15699	GM_M07_B1_G07_MF	g3091216	BLASTX	103	3e-18	58	(AF060192) putative resistance protein [Glycine max]
15700	GM_M07_B1_G09_MF	g100484	BLASTX	339	4e-29	57	hypothetical protein - garden snapdragon
15701	GM_M07_B1_G10_MR	g2921317	BLASTX	246	8e-37	83	(AF034108) beta-1,3-glucanase 3 [Glycine max]
15702	GM_M07_B1_G11_MR	g2864613	BLASTX	143	7e-11	55	(AL021811) S-receptor kinase -like protein [Arabidopsis thaliana]
15703	GM_M07_B1_G12_MF	g3142328	BLASTN	791	7e-29	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15704	GM_M07_B1_H05_MF	g507910	BLASTN	342	7e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15705	GM_M07_B1_H05_MR	g507910	BLASTN	412	5e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
15706	GM_M07_B1_H07_MF	g905360	BLASTN	381	3e-10	83	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
15707	GM_M07_B1_H07_MR	g507910	BLASTN	365	7e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15708	GM_M09_B1_A07_MF	g3282159	BLASTN	352	7e-09	63	Homo sapiens chromosome 20, BAC clone 99 (LBNL H80), complete sequence [Homo sapiens]
15709	GM_M09_B1_A09_MF	g3021268	BLASTX	169	1e-24	44	(AL022347) putative protein [Arabidopsis thaliana]
15710	GM_M09_B1_A11_MF	g3097320	BLASTN	755	4e-27	70	Glycine max gene for Bd 30K, complete cds
15711	GM_M09_B1_B06_MR	g4063760	BLASTX	344	3e-29	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15712	GM_M09_B1_B08_MF	g3097320	BLASTN	452	2e-13	78	Glycine max gene for Bd 30K, complete cds
15713	GM_M09_B1_B08_MR	g3947735	BLASTX	207	7e-15	37	(AJ009720) NL27 [Solanum tuberosum]
15714	GM_M09_B1_B09_MF	g4063756	BLASTN	481	1e-14	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15715	GM_M09_B1_C02_MR	g1666236	BLASTX	196	1e-14	32	(U76261) unknown [Hordeum vulgare]
15716	GM_M09_B1_C03_MR	g155854	BLASTN	347	6e-09	58	Babesia bigemina antigen (Bbg 1.1) mRNA, 3' end.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15717	GM_M09_B1_C11_MR	g3142328	BLASTN	678	1e-23	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15718	GM_M09_B1_D01_MR	g3834313	BLASTX	316	9e-34	69	(AC005679) Strong similarity to T16B12.3 gi 3746060 unknown protein from Arabidopsis thaliana BAC gb AC005311. [Arabidopsis thaliana]
15719	GM_M09_B1_D04_MF	g2894600	BLASTX	358	9e-31	59	(AL021889) putative protein [Arabidopsis thaliana]
15720	GM_M09_B1_D09_MF	g2522228	BLASTX	152	2e-09	30	(AB007466) reverse transcriptase-like protein [Vicia faba]
15721	GM_M09_B1_D10_MF	g2464905	BLASTX	228	3e-18	59	(Z99708) minor allergen [Arabidopsis thaliana]
15722	GM_M09_B1_D11_MF	g2811226	BLASTX	238	3e-18	86	(AF042669) fimbrin 2 [Arabidopsis thaliana] gi 2811232 (AF042671) fimbrin 2 [Arabidopsis thaliana]
15723	GM_M09_B1_E01_MR	g3080353	BLASTX	165	3e-11	66	(AL022580) cytochrome P450 [Arabidopsis thaliana]
15724	GM_M09_B1_E06_MR	g18559	BLASTN	1621	1e-66	91	G.max gene for catalase
15725	GM_M09_B1_E10_MF	g22102	BLASTN	442	5e-13	63	Zea mays A1 gene for 40.1kd A1 protein (NADPH-dependent reductase).
15726	GM_M09_B1_F01_MF	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15727	GM_M09_B1_F01_MR	g507910	BLASTN	635	4e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15728	GM_M09_B1_F07_MR	g3176804	BLASTN	334	6e-09	61	Homo sapiens allele 15 fragile site locus (FRA10B) minisatellite, 3' sequence
15729	GM_M09_B1_F09_MF	g130582	BLASTX	319	2e-26	47	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
15730	GM_M09_B1_G02_MF	g507910	BLASTN	449	1e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
15731	GM_M09_B1_G02_MR	g507910	BLASTN	412	5e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
15732	GM_M09_B1_G03_MR	g507910	BLASTN	562	9e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15733	GM_M09_B1_G05_MF	g3097320	BLASTN	671	2e-23	84	Glycine max gene for Bd 30K, complete cds
15734	GM_M09_B1_G05_MR	g100484	BLASTX	251	1e-19	50	hypothetical protein - garden snapdragon
15735	GM_M09_B1_G07_MR	g2995405	BLASTX	293	4e-24	58	(Y12432) polyprotein [Ananas comosus]
15736	GM_M09_B1_G08_MF	g1707644	BLASTX	179	2e-12	37	(X99514) mexE [Pseudomonas aeruginosa]
15737	GM_M09_B1_G09_MR	g2982257	BLASTX	144	8e-12	77	(AF051211) probable calcium dependent protein kinase [Picea mariana]
15738	GM_M09_B1_G11_MF	g3738114	BLASTN	373	8e-10	64	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
15739	GM_M09_B1_H01_MR	g507910	BLASTN	415	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15740	GM_M09_B1_H08_MR	g3135274	BLASTX	218	2e-16	56	(AC003058) putative beta-1,3-endoglucanase [Arabidopsis thaliana]
15741	GM_M09_B1_H11_MF	g18559	BLASTN	658	8e-23	70	G.max gene for catalase
15742	GM_M10_A1_A09_MR	g3645899	BLASTX	216	1e-15	52	(U68408) 5' end not determined experimentally [Zea mays]
15743	GM_M10_A1_B05_MR	g3777526	BLASTN	552	6e-18	86	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
15744	GM_M10_A1_B09_MR	g4063760	BLASTX	179	5e-13	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15745	GM_M10_A1_C09_MR	g507910	BLASTN	566	6e-19	86	Glycine max BSR-101 satellite SB92 genomic sequence.
15746	GM_M10_A1_C10_MR	g3785999	BLASTX	175	5e-15	84	(AC005499) putative peptidyl-prolyl cis-trans isomerase [Arabidopsis thaliana]
15747	GM_M10_A1_D03_MR	g1076763	BLASTX	153	1e-11	44	AWJL218 protein - wheat gi 551212 (X81369) AWJL218 gene product [Triticum aestivum]
15748	GM_M10_A1_D07_MR	g3142328	BLASTN	499	1e-15	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15749	GM_M10_A1_D08_MR	g3033389	BLASTX	147	5e-15	39	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
15750	GM_M10_A1_F03_MR	g2129618	BLASTX	193	3e-13	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15751	GM_M10_A1_F06_MR	g4063756	BLASTN	350	9e-09	66	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15752	GM_M10_A1_G01_MR	g3097320	BLASTN	1281	5e-51	81	Glycine max gene for Bd 30K, complete cds
15753	GM_M10_A1_G04_MR	g4092471	BLASTN	401	4e-11	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
15754	GM_M10_A2_A02_MF	g226407	BLASTX	246	1e-18	64	retrotransposon del1-46 [Lilium henryi]
15755	GM_M10_A2_B03_MF	g2408029	BLASTX	187	9e-13	66	(Z99162) hypothetical protein [Schizosaccharomyces pombe]
15756	GM_M10_A2_B05_MF	g3283026	BLASTX	164	9e-12	39	putative transposase [Arabidopsis thaliana]
15757	GM_M10_A2_B09_MF	g3834317	BLASTX	331	6e-29	91	(AC005679) Similar to CDC16 protein gb U18291 (CDC16Hs) from Homo sapiens. [Arabidopsis thaliana]
15758	GM_M10_A2_C09_MF	g507910	BLASTN	603	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15759	GM_M10_A2_E01_MF	g3930515	BLASTX	122	2e-13	47	(AF059674) putative gag protein [Nicotiana tabacum]
15760	GM_M10_A2_E02_MF	g507910	BLASTN	540	8e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
15761	GM_M10_A2_E09_MF	g4092471	BLASTN	457	1e-13	71	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
15762	GM_M10_A2_F01_MF	g1666236	BLASTX	148	3e-09	31	(U76261) unknown [Hordeum vulgare]
15763	GM_M10_A2_F04_MF	g1272349	BLASTX	247	1e-19	50	(U51740) secreted glycoprotein 3 [Ipomoea trifida]
15764	GM_M10_A2_F05_MF	g3097320	BLASTN	520	2e-16	77	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15765	GM_M10_A2_F07_MF	g3687234	BLASTX	170	1e-10	42	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
15766	GM_M10_A2_F10_MF	g4063760	BLASTX	432	1e-38	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15767	GM_M10_A2_G01_MF	g3097320	BLASTN	460	8e-14	71	Glycine max gene for Bd 30K, complete cds
15768	GM_M10_A2_H02_MF	g730526	BLASTX	242	6e-36	90	60S RIBOSOMAL PROTEIN L13 (BBC1 PROTEIN HOMOLOG) gi 480787 pir S37271 ribosomal protein L13 - Arabidopsis thaliana gi 404166 (X75162) BBC1 protein [Arabidopsis thaliana]
15769	GM_M10_A2_H05_MF	g1769898	BLASTX	213	1e-15	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15770	GM_M10_A2_H08_MF	g2865427	BLASTX	170	1e-10	38	(AF039372) polyprotein [Arabidopsis thaliana]
15771	GM_M10_A2_H12_MF	g2522227	BLASTX	222	1e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
15772	GM_M10_B1_A06_MF	g2764526	BLASTN	355	5e-09	63	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
15773	GM_M10_B1_A07_MF	g3097320	BLASTN	601	9e-22	76	Glycine max gene for Bd 30K, complete cds
15774	GM_M10_B1_B01_MF	g3645899	BLASTX	369	5e-32	51	(U68408) 5' end not determined experimentally [Zea mays]
15775	GM_M10_B1_B03_MF	g99922	BLASTX	316	2e-37	73	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
15776	GM_M10_B1_B05_MF	g507910	BLASTN	556	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15777	GM_M10_B1_B10_MF	g507910	BLASTN	533	2e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15778	GM_M10_B1_B10_MR	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15779	GM_M10_B1_B11_MF	g2586082	BLASTX	206	2e-25	58	(U72725) retrofit [Oryza longistaminata]
15780	GM_M10_B1_C02_MR	g1666236	BLASTX	128	5e-09	37	(U76261) unknown [Hordeum vulgare]
15781	GM_M10_B1_C11_MR	g2129618	BLASTX	204	2e-14	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15782	GM_M10_B1_D09_MF	g2335061	BLASTN	423	4e-12	60	Homo sapiens chromosome 16 BAC clone CIT987SK-334D11 complete sequence [Homo sapiens]
15783	GM_M10_B1_D09_MR	g3510505	BLASTX	172	9e-14	35	(AF030881) pol polyprotein [Fugu rubripes]
15784	GM_M10_B1_D10_MR	g2995405	BLASTX	346	1e-29	50	(Y12432) polyprotein [Ananas comosus]
15785	GM_M10_B1_E01_MF	g3097320	BLASTN	336	1e-15	83	Glycine max gene for Bd 30K, complete cds
15786	GM_M10_B1_E03_MR	g320569	BLASTX	226	4e-18	50	transposon TNT1 - Arabidopsis thaliana (fragment)
15787	GM_M10_B1_E05_MR	g173088	BLASTX	180	1e-11	35	has homology to retroviral pol genes; ORF2 TYB3-2 (5' end of coding region not precisely determined)

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15788	GM_M10_B1_E10_MR	g13767	BLASTN	431	2e-13	62	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
15789	GM_M10_B1_E11_MF	g2129618	BLASTX	200	5e-14	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15790	GM_M10_B1_F01_MF	g3142328	BLASTN	649	2e-22	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15791	GM_M10_B1_F02_MR	g2522227	BLASTX	154	5e-10	39	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
15792	GM_M10_B1_F05_MF	g3142328	BLASTN	1772	1e-73	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15793	GM_M10_B1_F05_MR	g507910	BLASTN	647	1e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
15794	GM_M10_B1_F07_MR	g3845287	BLASTN	357	4e-09	60	Plasmodium falciparum chromosome 2, section 57 of 73 of the complete sequence
15795	GM_M10_B1_F11_MF	g2129618	BLASTX	160	9e-10	37	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
15796	GM_M10_B1_F12_MR	g3319372	BLASTX	257	1e-21	42	(AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]
15797	GM_M10_B1_G03_MF	g4063760	BLASTX	360	6e-31	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15798	GM_M10_B1_G06_MF	g3599418	BLASTN	391	1e-10	73	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
15799	GM_M10_B1_H04_MR	g2462058	BLASTX	156	2e-21	38	(Y13389) reverse transcriptase [Antirrhinum majus]
15800	GM_M10_B1_H06_MF	g2801423	BLASTN	474	2e-14	68	Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence [Homo sapiens]
15801	GM_M10_B1_H11_MR	g905361	BLASTX	739	2e-72	97	(U22103) gag-protease polyprotein [Glycine max]
15802	GM_M10_B1_H12_MF	g4063760	BLASTX	430	2e-38	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15803	GM_M10_B2_A03_MF	g3097320	BLASTN	448	3e-13	72	Glycine max gene for Bd 30K, complete cds
15804	GM_M10_B2_A05_MR	g4063760	BLASTX	232	3e-17	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15805	GM_M10_B2_A06_MF	g4063756	BLASTN	530	7e-17	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15806	GM_M10_B2_A09_MF	g2443320	BLASTX	242	3e-18	42	(D85597) polyprotein [Oryza australiensis]
15807	GM_M10_B2_A09_MR	g1769898	BLASTX	208	3e-15	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15808	GM_M10_B2_B08_MF	g170288	BLASTN	517	2e-16	67	Nicotiana plumbaginifolia plasma-membrane H+ ATPase (pma1) gene, complete cds.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15809	GM_M10_B2_B09_MR	g905361	BLASTX	515	1e-48	97	(U22103) gag-protease polyprotein [Glycine max]
15810	GM_M10_B2_C02_MR	g3599418	BLASTN	405	3e-11	65	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
15811	GM_M10_B2_C11_MF	g3097320	BLASTN	362	2e-09	80	Glycine max gene for Bd 30K, complete cds
15812	GM_M10_B2_D04_MR	g507910	BLASTN	460	4e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15813	GM_M10_B2_D07_MF	g170606	BLASTN	782	6e-29	69	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
15814	GM_M10_B2_D08_MR	g128405	BLASTX	258	1e-21	65	NODULIN 21 (N-21) gi 99942 pir S08632 nodulin-21 - soybean gi 18694 (X16488) nodulin-21 (AA 1-201) [Glycine max]
15815	GM_M10_B2_D11_MF	g3695294	BLASTN	430	2e-12	85	Glycine max nodule-specific glutamine synthetase gene, complete cds
15816	GM_M10_B2_E06_MR	g3097320	BLASTN	367	1e-09	69	Glycine max gene for Bd 30K, complete cds
15817	GM_M10_B2_E07_MR	g18559	BLASTN	800	3e-29	76	G.max gene for catalase
15818	GM_M10_B2_E08_MR	g100226	BLASTX	207	5e-15	37	hypothetical protein - tomato gi 19275 (Z12127) protein of unknown function [Lycopersicon esculentum] gi 445619 prf 1909366A Leu zipper protein [Lycopersicon esculentum]
15819	GM_M10_B2_E09_MR	g2522228	BLASTX	189	2e-13	77	(AB007466) reverse transcriptase-like protein [Vicia faba]
15820	GM_M10_B2_E12_MR	g3142328	BLASTN	935	2e-35	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15821	GM_M10_B2_F01_MR	g2109275	BLASTX	158	3e-09	38	(U97106) downy mildew resistance protein RPP5 [Arabidopsis thaliana]
15822	GM_M10_B2_F02_MF	g100484	BLASTX	134	1e-10	37	hypothetical protein - garden snapdragon
15823	GM_M10_B2_F04_MR	g1769898	BLASTX	154	2e-09	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15824	GM_M10_B2_F05_MR	g2497540	BLASTX	241	3e-19	47	PYRUVATE KINASE, CHLOROPLAST ISOZYME G
15825	GM_M10_B2_G01_MR	g3063459	BLASTX	176	2e-11	69	(AC003981) F22O13.21 [Arabidopsis thaliana]
15826	GM_M10_B2_G02_MF	g18559	BLASTN	356	4e-09	73	G.max gene for catalase
15827	GM_M10_B2_G03_MR	g3831448	BLASTN	785	2e-28	76	Arabidopsis thaliana chromosome II BAC T32F6 genomic sequence, complete sequence [Arabidopsis thaliana]
15828	GM_M10_B2_G06_MF	g2995405	BLASTX	443	4e-40	61	(Y12432) polyprotein [Ananas comosus]
15829	GM_M10_B2_G07_MR	g1769898	BLASTX	312	2e-26	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15830	GM_M10_B2_G11_MF	g3273122	BLASTN	359	3e-09	60	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-53, complete sequence [Plasmodium falciparum]
15831	GM_M10_B2_G12_MR	g3650035	BLASTX	233	2e-17	45	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
15832	GM_M10_B2_H02_MF	g3097320	BLASTN	1165	1e-45	84	Glycine max gene for Bd 30K, complete cds
15833	GM_M10_B2_H04_MR	g507910	BLASTN	575	2e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15834	GM_M10_B2_H09_MF	g4063760	BLASTX	280	2e-22	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15835	GM_M10_B2_H09_MR	g507910	BLASTN	684	3e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
15836	GM_M10_B2_H11_MF	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15837	GM_M10_B2_H11_MR	g507910	BLASTN	518	8e-17	77	Glycine max BSR-101 satellite SB92 genomic sequence.
15838	GM_M13_A1_A07_MF	g3142328	BLASTN	1355	2e-54	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15839	GM_M13_A1_A09_MR	g3746069	BLASTX	243	2e-18	37	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
15840	GM_M13_A1_A11_MR	g3738114	BLASTN	594	8e-20	67	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
15841	GM_M13_A1_B01_MF	g507910	BLASTN	350	3e-09	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15842	GM_M13_A1_B01_MR	g3142379	BLASTX	213	5e-16	55	(AF053008) envelope-like [Glycine max]
15843	GM_M13_A1_B02_MF	g507910	BLASTN	387	7e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15844	GM_M13_A1_B05_MF	g2522228	BLASTX	222	4e-17	74	(AB007466) reverse transcriptase-like protein [Vicia faba]
15845	GM_M13_A1_B06_MF	g507910	BLASTN	502	4e-16	77	Glycine max BSR-101 satellite SB92 genomic sequence.
15846	GM_M13_A1_B06_MR	g4063760	BLASTX	427	4e-38	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15847	GM_M13_A1_B08_MF	g3645899	BLASTX	286	4e-23	56	(U68408) 5' end not determined experimentally [Zea mays]
15848	GM_M13_A1_B10_MF	g3513747	BLASTX	307	4e-25	53	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
15849	GM_M13_A1_C01_MR	g4115365	BLASTX	111	1e-10	42	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
15850	GM_M13_A1_C03_MR	g4050011	BLASTN	584	2e-19	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
15851	GM_M13_A1_C10_MF	g3777527	BLASTX	119	4e-10	39	(AF053008) gag-pol polyprotein [Glycine max]
15852	GM_M13_A1_D02_MF	g1431738	BLASTN	528	5e-17	88	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
15853	GM_M13_A1_D04_MF	g3319351	BLASTX	211	5e-15	43	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
15854	GM_M13_A1_D09_MF	g3695395	BLASTX	284	2e-23	37	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
15855	GM_M13_A1_D09_MR	g2462134	BLASTX	194	8e-14	37	(Y13368) reverse transcriptase [Beta vulgaris]
15856	GM_M13_A1_D12_MF	g507910	BLASTN	402	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15857	GM_M13_A1_D12_MR	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15858	GM_M13_A1_E02_MF	g507910	BLASTN	350	3e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15859	GM_M13_A1_E04_MR	g3142328	BLASTN	1020	3e-39	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15860	GM_M13_A1_E10_MF	g3513747	BLASTX	230	9e-19	45	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
15861	GM_M13_A1_F01_MR	g18559	BLASTN	329	4e-10	78	G.max gene for catalase
15862	GM_M13_A1_F02_MR	g2522228	BLASTX	119	8e-14	76	(AB007466) reverse transcriptase-like protein [Vicia faba]
15863	GM_M13_A1_F03_MF	g507910	BLASTN	538	1e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15864	GM_M13_A1_F03_MR	g507910	BLASTN	556	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15865	GM_M13_A1_F04_MF	g3152629	BLASTN	361	3e-09	62	Homo sapiens PAC clone DJ0807C15 from 7q34-q36, complete sequence [Homo sapiens]
15866	GM_M13_A1_F12_MF	g2443320	BLASTX	231	4e-17	38	(D85597) polyprotein [Oryza australiensis]
15867	GM_M13_A1_G01_MR	g3142379	BLASTX	280	2e-23	63	(AF053008) envelope-like [Glycine max]
15868	GM_M13_A1_G10_MF	g4063760	BLASTX	199	9e-14	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15869	GM_M13_A1_G10_MR	g4038056	BLASTX	298	2e-24	53	(AC005897) putative transposon [Arabidopsis thaliana]
15870	GM_M13_A1_G11_MF	g3063445	BLASTX	169	1e-10	36	(AC003981) F22O13.7 [Arabidopsis thaliana]
15871	GM_M13_A1_H02_MF	g3738133	BLASTN	442	6e-13	63	Human DNA sequence from clone 409O10 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence [Homo sapiens]
15872	GM_M13_A1_H06_MF	g4038056	BLASTX	203	2e-14	37	(AC005897) putative transposon [Arabidopsis thaliana]
15873	GM_M13_A1_H08_MF	g3777527	BLASTX	709	5e-68	94	(AF053008) gag-pol polyprotein [Glycine max]
15874	GM_M13_A1_H08_MR	g507910	BLASTN	563	8e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15875	GM_M13_A2_A08_MR	g944837	BLASTN	358	3e-09	65	P.elliotii DNA for repeat region
15876	GM_M13_A2_A09_MF	g2578038	BLASTN	396	7e-11	65	Human DNA sequence from PAC 106H14 on chromosome Xq21.1-21.33. Contains STS
15877	GM_M13_A2_A10_MF	g507910	BLASTN	404	1e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15878	GM_M13_A2_A10_MR	g507910	BLASTN	398	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15879	GM_M13_A2_B02_MF	g3142328	BLASTN	1351	2e-54	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15880	GM_M13_A2_B02_MR	g507910	BLASTN	376	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
15881	GM_M13_A2_B07_MF	g3097320	BLASTN	739	2e-26	78	Glycine max gene for Bd 30K, complete cds
15882	GM_M13_A2_B10_MR	g1785699	BLASTX	170	4e-12	42	(Y08501) orf145a [Arabidopsis thaliana]
15883	GM_M13_A2_C10_MR	g4126312	BLASTN	349	1e-08	62	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
15884	GM_M13_A2_D02_MF	g3777527	BLASTX	511	7e-47	94	(AF053008) gag-pol polyprotein [Glycine max]
15885	GM_M13_A2_D04_MF	g1769897	BLASTX	107	8e-12	34	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15886	GM_M13_A2_D12_MR	g507910	BLASTN	466	2e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15887	GM_M13_A2_F01_MR	g421955	BLASTX	142	2e-12	55	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
15888	GM_M13_A2_F05_MR	g3097320	BLASTN	637	8e-22	77	Glycine max gene for Bd 30K, complete cds
15889	GM_M13_A2_F06_MF	g2500026	BLASTX	354	1e-31	70	ADENYLOSUCCINATE SYNTHETASE PRECURSOR (IMP--ASPARTATE LIGASE) gi 1616657 (U49389) adenylosuccinate synthetase [Arabidopsis thaliana]
15890	GM_M13_A2_F10_MR	g905361	BLASTX	244	5e-19	72	(U22103) gag-protease polyprotein [Glycine max]
15891	GM_M13_A2_G02_MF	g1142701	BLASTN	1021	8e-40	83	Glycine max satellite STR120-A.3.
15892	GM_M13_A2_G03_MR	g1813979	BLASTX	249	2e-20	52	(Y10860) hypothetical protein [Musa acuminata]
15893	GM_M13_A2_G05_MF	g4063760	BLASTX	505	2e-46	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15894	GM_M13_A2_G07_MR	g2981130	BLASTN	396	7e-11	67	Populus balsamifera subsp. trichocarpa AGAMOUS homolog (PTAG1) gene, complete cds
15895	GM_M13_A2_G10_MF	g549100	BLASTX	456	2e-41	95	TRANSPOSASE FOR INSERTION SEQUENCE ELEMENT IS1071 IN TRANSPOSON TN5271 >gi 95495 pir A41290 probable transposase (IS1071) - Alcaligenes sp. transposon Tn5271 >gi 141982 (M65135) transposase [Alcaligenes sp.]
15896	GM_M13_A2_H03_MF	g1769897	BLASTX	329	2e-28	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15897	GM_M13_A2_H07_MR	g3142328	BLASTN	604	2e-20	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15898	GM_M13_A2_H10_MR	g3645899	BLASTX	110	6e-14	38	(U68408) 5' end not determined experimentally [Zea mays]
15899	GM_M13_B1_A02_MF	g3176791	BLASTN	443	8e-14	65	Homo sapiens allele 11 fragile site locus (FRA10B) minisatellite, 5' sequence
15900	GM_M13_B1_A04_MF	g2832901	BLASTN	1190	6e-47	79	Cajanus cajan copia-like retrotransposon,Panzee
15901	GM_M13_B1_A08_MF	g3789709	BLASTN	442	6e-13	64	Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence [Homo sapiens]
15902	GM_M13_B1_B02_MR	g454847	BLASTN	489	4e-15	77	Glycine max ribosomal protein S11 gene, complete cds
15903	GM_M13_B1_B04_MF	g4063760	BLASTX	176	2e-11	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15904	GM_M13_B1_B05_MR	g18559	BLASTN	389	1e-10	72	G.max gene for catalase
15905	GM_M13_B1_B09_MR	g18683	BLASTN	475	1e-14	66	G.max N-20t gene
15906	GM_M13_B1_B10_MF	g2244793	BLASTX	500	2e-45	73	(Z97336) TMV resistance protein homolog [Arabidopsis thaliana]
15907	GM_M13_B1_B12_MF	g522302	BLASTX	193	4e-13	45	(L35053) endonuclease [Magnaporthe grisea]
15908	GM_M13_B1_C01_MR	g4056480	BLASTX	254	5e-21	65	(AC005896) putative adenylate kinase [Arabidopsis thaliana]
15909	GM_M13_B1_C03_MF	g2995405	BLASTX	261	7e-36	61	(Y12432) polyprotein [Ananas comosus]
15910	GM_M13_B1_C04_MR	g2995405	BLASTX	369	4e-32	50	(Y12432) polyprotein [Ananas comosus]
15911	GM_M13_B1_C05_MR	g3021268	BLASTX	273	1e-21	57	(AL022347) putative protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15912	GM_M13_B1_C08_MF	g4063756	BLASTN	441	7e-13	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15913	GM_M13_B1_C12_MR	g507910	BLASTN	513	1e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
15914	GM_M13_B1_D04_MR	g4063756	BLASTN	387	2e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
15915	GM_M13_B1_D07_MR	g400531	BLASTN	610	1e-20	71	V.sativa mRNA for NADPH-ferrihemoprotein reductase.
15916	GM_M13_B1_D11_MR	g3643604	BLASTX	314	4e-26	57	(AC005395) receptor-like protein kinase [Arabidopsis thaliana]
15917	GM_M13_B1_D12_MF	g18559	BLASTN	352	6e-09	71	G.max gene for catalase
15918	GM_M13_B1_E02_MF	g1769898	BLASTX	126	2e-11	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15919	GM_M13_B1_E03_MR	g3924609	BLASTX	189	1e-12	36	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
15920	GM_M13_B1_E08_MF	g18559	BLASTN	546	1e-17	73	G.max gene for catalase
15921	GM_M13_B1_F01_MF	g3513747	BLASTX	315	6e-26	53	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
15922	GM_M13_B1_F07_MF	g13767	BLASTN	374	9e-11	63	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
15923	GM_M13_B1_F11_MF	g3176788	BLASTN	345	2e-09	63	Homo sapiens allele 8 fragile site locus (FRA10B) minisatellite sequence
15924	GM_M13_B1_G01_MF	g3323609	BLASTX	175	4e-12	57	(AF064093) KE04p [Homo sapiens]
15925	GM_M13_B1_G03_MF	g3319362	BLASTX	231	2e-17	37	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
15926	GM_M13_B1_G06_MF	g2160161	BLASTX	164	2e-10	31	(AC000132) F21M12.7 gene product [Arabidopsis thaliana]
15927	GM_M13_B1_G11_MF	g1142702	BLASTN	510	1e-16	78	Glycine max satellite STR120-A.4.
15928	GM_M13_B1_H01_MF	g1871190	BLASTX	311	5e-27	51	(U90439) Ser/Thr kinase isolog [Arabidopsis thaliana]
15929	GM_M13_B1_H03_MR	g2522230	BLASTX	355	1e-31	45	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
15930	GM_M13_B1_H04_MR	g3402671	BLASTN	640	7e-22	72	Arabidopsis thaliana chromosome II BAC T16B24 genomic sequence, complete sequence [Arabidopsis thaliana]
15931	GM_M13_B1_H07_MF	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
15932	GM_M13_B1_H07_MR	g507910	BLASTN	618	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15933	GM_M13_B1_H10_MF	g507910	BLASTN	379	2e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
15934	GM_M13_B1_H11_MF	g4063760	BLASTX	274	8e-22	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15935	GM_M13_B2_A06_MR	g4063760	BLASTX	406	8e-36	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15936	GM_M13_B2_B10_MF	g3777527	BLASTX	205	3e-14	90	(AF053008) gag-pol polyprotein [Glycine max]
15937	GM_M13_B2_C10_MR	g2326264	BLASTN	376	5e-10	68	Arabidopsis thaliana DNA for CCT alpha/TCP-1, complete cds.
15938	GM_M13_B2_C12_MR	g13768	BLASTN	334	5e-09	60	Torulopsis glabrata mitochondrial DNA for tRNA-Thr,-His and -Glu upstream of cytochrome b gene >gi 343951 gb M11856 YSLMTIG01 Yeast (T.glabrata) mitochondrial DNA between L rRNA and cytochrome b genes.
15939	GM_M13_B2_D02_MR	g2995405	BLASTX	243	1e-18	42	(Y12432) polyprotein [Ananas comosus]
15940	GM_M13_B2_D07_MR	g2995405	BLASTX	279	2e-22	60	(Y12432) polyprotein [Ananas comosus]
15941	GM_M13_B2_D11_MR	g3777527	BLASTX	652	6e-62	94	(AF053008) gag-pol polyprotein [Glycine max]
15942	GM_M13_B2_E06_MR	g3097320	BLASTN	536	3e-17	72	Glycine max gene for Bd 30K, complete cds
15943	GM_M13_B2_E10_MR	g1769897	BLASTX	166	7e-11	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15944	GM_M13_B2_F07_MR	g3935164	BLASTX	234	2e-19	53	(AC004557) F17L21.7 [Arabidopsis thaliana]
15945	GM_M13_B2_F11_MR	g226407	BLASTX	170	1e-10	33	retrotransposon del1-46 [Lilium henryi]
15946	GM_M13_B2_G01_MR	g320569	BLASTX	215	7e-17	50	transposon TNT1 - Arabidopsis thaliana (fragment)
15947	GM_M13_B2_G02_MR	g4063760	BLASTX	276	5e-22	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15948	GM_M13_B2_G03_MR	g3645899	BLASTX	306	3e-25	47	(U68408) 5' end not determined experimentally [Zea mays]
15949	GM_M13_B2_G08_MR	g3142379	BLASTX	154	1e-09	44	(AF053008) envelope-like [Glycine max]
15950	GM_M13_B2_H03_MR	g1769897	BLASTX	164	1e-10	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15951	GM_M14_A1_B08_MF	g2626751	BLASTN	386	2e-10	62	Triticum aestivum retrotransposon Tar1, partial sequence.
15952	GM_M14_A1_B09_MR	g4092470	BLASTN	355	5e-09	63	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
15953	GM_M14_A1_D07_MF	g170605	BLASTN	354	3e-09	66	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
15954	GM_M14_A1_F01_MF	g3777527	BLASTX	297	5e-24	69	(AF053008) gag-pol polyprotein [Glycine max]
15955	GM_M14_A1_F12_MF	g1769897	BLASTX	189	3e-13	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15956	GM_M14_A1_G05_MR	g1840106	BLASTN	413	2e-12	68	Human fragile site locus (FRA16B) minisatellite repeat
15957	GM_M14_A1_G10_MF	g225242	BLASTX	245	9e-19	80	ORF 1708 [Nicotiana tabacum]
15958	GM_M14_A1_G12_MF	g905361	BLASTX	429	2e-39	93	(U22103) gag-protease polyprotein [Glycine max]
15959	GM_M14_A1_H04_MF	g18559	BLASTN	325	1e-14	75	G.max gene for catalase
15960	GM_M14_A2_A03_MF	g3142379	BLASTX	390	2e-35	68	(AF053008) envelope-like [Glycine max]
15961	GM_M14_A2_A03_MR	g3097320	BLASTN	728	6e-26	77	Glycine max gene for Bd 30K, complete cds
15962	GM_M14_A2_A08_MR	g3097320	BLASTN	847	3e-31	74	Glycine max gene for Bd 30K, complete cds
15963	GM_M14_A2_A09_MR	g507910	BLASTN	420	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
15964	GM_M14_A2_A10_MR	g3777527	BLASTX	378	7e-55	97	(AF053008) gag-pol polyprotein [Glycine max]
15965	GM_M14_A2_B04_MF	g1946265	BLASTX	139	4e-15	77	(Y11414) myb [Oryza sativa]
15966	GM_M14_A2_B05_MF	g1946265	BLASTX	114	6e-12	80	(Y11414) myb [Oryza sativa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15967	GM_M14_A2_B07_MF	g3777527	BLASTX	556	1e-51	93	(AF053008) gag-pol polyprotein [Glycine max]
15968	GM_M14_A2_B07_MR	g507910	BLASTN	371	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
15969	GM_M14_A2_B10_MF	g3461840	BLASTX	270	3e-21	41	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
15970	GM_M14_A2_C02_MR	g507910	BLASTN	587	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
15971	GM_M14_A2_C06_MF	g507910	BLASTN	641	2e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
15972	GM_M14_A2_C07_MF	g2499465	BLASTX	145	9e-12	49	PHOSPHOENOLPYRUVATE CARBOXYLASE (PEPCASE) gi 1166373 (L49175) C4 photosynthetic phosphoenolpyruvate carboxylase [Amaranthus hypochondriacus] gi 1181197 gnl PID e211616 (Z68125) C4 photosynthetic phosphoenolpyruvate carboxylase [Amaranthus hypochondriacus]
15973	GM_M14_A2_D03_MR	g3142328	BLASTN	843	3e-31	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15974	GM_M14_A2_D05_MR	g1076763	BLASTX	111	7e-12	42	AWJL218 protein - wheat gi 551212 (X81369) AWJL218 gene product [Triticum aestivum]
15975	GM_M14_A2_D06_MF	g3868800	BLASTX	201	4e-14	77	(AB013603) topoisomerase III beta [Mus musculus]
15976	GM_M14_A2_D06_MR	g587603	BLASTN	371	8e-10	63	P.falciparum gene for beta subunit RNA polymerase
15977	GM_M14_A2_D08_MF	g4063760	BLASTX	234	3e-24	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
15978	GM_M14_A2_D11_MR	g2194136	BLASTX	185	3e-12	37	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
15979	GM_M14_A2_E01_MR	g18559	BLASTN	823	3e-30	77	G.max gene for catalase
15980	GM_M14_A2_E02_MR	g18559	BLASTN	909	3e-34	73	G.max gene for catalase
15981	GM_M14_A2_E04_MF	g4033838	BLASTX	277	7e-23	69	(Y18550) sigma-like factor [Arabidopsis thaliana]
15982	GM_M14_A2_E04_MR	g2443320	BLASTX	174	5e-11	33	(D85597) polyprotein [Oryza australiensis]
15983	GM_M14_A2_E05_MF	g1402883	BLASTX	148	7e-17	50	(X98130) unknown [Arabidopsis thaliana] gi 1495263 gnl PID e242837 (X97487) orf09 [Arabidopsis thaliana]
15984	GM_M14_A2_E05_MR	g3645899	BLASTX	186	1e-15	40	(U68408) 5' end not determined experimentally [Zea mays]
15985	GM_M14_A2_E11_MF	g2443320	BLASTX	186	4e-14	43	(D85597) polyprotein [Oryza australiensis]
15986	GM_M14_A2_F05_MF	g3142328	BLASTN	649	2e-22	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
15987	GM_M14_A2_F12_MR	g3777527	BLASTX	138	3e-16	44	(AF053008) gag-pol polyprotein [Glycine max]
15988	GM_M14_A2_G05_MR	g3777527	BLASTX	595	8e-56	98	(AF053008) gag-pol polyprotein [Glycine max]
15989	GM_M14_A2_G07_MR	g3421096	BLASTX	112	2e-10	91	(AF043528) 20S proteasome subunit PAG1 [Arabidopsis thaliana]
15990	GM_M14_A2_G09_MF	g507910	BLASTN	452	8e-14	80	Glycine max BSR-101 satellite SB92 genomic sequence.
15991	GM_M14_A2_G11_MR	g2129618	BLASTX	192	4e-13	37	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
15992	GM_M14_A2_H03_MF	g1769898	BLASTX	308	6e-26	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
15993	GM_M14_A2_H03_MR	g556344	BLASTN	482	8e-16	78	Pisum sativum histone H1 (H1-41) mRNA, complete cds.
15994	GM_M14_A2_H04_MF	g3777527	BLASTX	556	1e-51	95	(AF053008) gag-pol polyprotein [Glycine max]
15995	GM_M14_A2_H07_MR	g2522227	BLASTX	216	5e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
15996	GM_M14_A2_H12_MF	g2252863	BLASTX	161	3e-10	54	(AF013294) similar to nucleolin protein [Arabidopsis thaliana]
15997	GM_M14_B2_A01_MF	g3402703	BLASTX	200	8e-15	80	(AC004261) hypothetical protein [Arabidopsis thaliana]
15998	GM_M14_B2_A01_MR	g3779030	BLASTX	222	1e-17	33	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
15999	GM_M14_B2_A03_MF	g1666236	BLASTX	145	7e-09	32	(U76261) unknown [Hordeum vulgare]
16000	GM_M14_B2_A04_MR	g629693	BLASTX	165	6e-11	32	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
16001	GM_M14_B2_A05_MR	g3688808	BLASTX	148	9e-09	52	(AF084104) AcsA [Bacillus firmus]
16002	GM_M14_B2_A08_MF	g18559	BLASTN	1065	3e-41	75	G.max gene for catalase
16003	GM_M14_B2_A10_MF	g507910	BLASTN	348	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
16004	GM_M14_B2_B02_MF	g1514643	BLASTX	166	3e-16	75	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
16005	GM_M14_B2_B06_MF	g4063760	BLASTX	438	3e-39	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16006	GM_M14_B2_B06_MR	g3777527	BLASTX	326	4e-27	46	(AF053008) gag-pol polyprotein [Glycine max]
16007	GM_M14_B2_B07_MF	g2586083	BLASTX	295	4e-24	49	(U72725) receptor kinase-like protein [Oryza longistaminata]
16008	GM_M14_B2_B07_MR	g3777527	BLASTX	185	4e-12	35	(AF053008) gag-pol polyprotein [Glycine max]
16009	GM_M14_B2_B09_MR	g100484	BLASTX	303	3e-25	57	hypothetical protein - garden snapdragon
16010	GM_M14_B2_B11_MF	g2462134	BLASTX	208	2e-15	35	(Y13368) reverse transcriptase [Beta vulgaris]
16011	GM_M14_B2_B12_MF	g3169169	BLASTN	399	6e-11	80	Arabidopsis thaliana chromosome II BAC F21P24 genomic sequence, complete sequence [Arabidopsis thaliana]
16012	GM_M14_B2_C05_MF	g3176798	BLASTN	395	1e-11	65	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite, 5' sequence
16013	GM_M14_B2_C08_MF	g3097320	BLASTN	993	6e-38	78	Glycine max gene for Bd 30K, complete cds
16014	GM_M14_B2_C08_MR	g3142328	BLASTN	537	2e-27	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16015	GM_M14_B2_D02_MF	g507910	BLASTN	354	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16016	GM_M14_B2_D02_MR	g4063760	BLASTX	478	2e-43	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16017	GM_M14_B2_D06_MR	g2605619	BLASTX	179	4e-13	65	(D88618) OSMYB2 [Oryza sativa]
16018	GM_M14_B2_D07_MF	g507910	BLASTN	586	7e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16019	GM_M14_B2_D11_MF	g730558	BLASTX	182	2e-13	65	60S RIBOSOMAL PROTEIN L34 gi 1076636 pir S48027 ribosomal protein L34 - common tobacco gi 2129964 pir S48028 ribosomal protein L34.e, cytosolic - common tobacco gi 436030 (L27089) 60S ribosomal protein L34 [Nicotiana tabacum] gi 436032 (L27107) 60S ribosomal protein L34 [Nicotiana tabacum]
16020	GM_M14_B2_D11_MR	g3757516	BLASTX	108	2e-10	47	(AC005167) putative TMV resistance protein [Arabidopsis thaliana]
16021	GM_M14_B2_E05_MR	g507910	BLASTN	587	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
16022	GM_M14_B2_E06_MR	g3779026	BLASTX	272	2e-21	45	(AC005171) putative retrotransposon [Arabidopsis thaliana]
16023	GM_M14_B2_E08_MR	g2522230	BLASTX	189	4e-14	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
16024	GM_M14_B2_E09_MF	g3097320	BLASTN	434	1e-12	72	Glycine max gene for Bd 30K, complete cds
16025	GM_M14_B2_F03_MF	g1142701	BLASTN	1220	8e-49	82	Glycine max satellite STR120-A.3.
16026	GM_M14_B2_F05_MF	g905361	BLASTX	141	4e-10	26	(U22103) gag-protease polyprotein [Glycine max]
16027	GM_M14_B2_F05_MR	g3097320	BLASTN	886	4e-33	74	Glycine max gene for Bd 30K, complete cds
16028	GM_M14_B2_F06_MF	g1666236	BLASTX	150	2e-09	26	(U76261) unknown [Hordeum vulgare]
16029	GM_M14_B2_F12_MF	g3319362	BLASTX	384	1e-33	51	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
16030	GM_M14_B2_G03_MR	g3721856	BLASTX	96	1e-10	72	(AB014057) beta-Amyrin Synthase [Panax ginseng]
16031	GM_M14_B2_G06_MR	g505129	BLASTN	463	5e-14	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
16032	GM_M14_B2_G12_MF	g507910	BLASTN	377	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16033	GM_M14_B2_G12_MR	g507910	BLASTN	382	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16034	GM_M14_B2_H01_MF	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16035	GM_M14_B2_H01_MR	g507910	BLASTN	593	3e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
16036	GM_M14_B2_H02_MR	g2842477	BLASTX	151	4e-09	74	(AL021749) copper-binding protein-like [Arabidopsis thaliana]
16037	GM_M14_B2_H03_MF	g2995405	BLASTX	451	5e-41	63	(Y12432) polyprotein [Ananas comosus]
16038	GM_M14_B2_H04_MF	g1666236	BLASTX	185	2e-13	28	(U76261) unknown [Hordeum vulgare]
16039	GM_M14_B2_H06_MF	g2827621	BLASTX	168	1e-10	45	(AL021636) putative protein [Arabidopsis thaliana]
16040	GM_M14_B2_H06_MR	g2864611	BLASTX	149	4e-09	57	(AL021811) putative protein [Arabidopsis thaliana]
16041	GM_M14_B2_H07_MR	g2708743	BLASTX	154	7e-09	35	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
16042	GM_M14_B2_H08_MR	g99721	BLASTX	381	4e-33	54	retrovirus-related polyprotein - Arabidopsis thaliana retrotransposon Ta1-3 gi 16534 (X13291) polyprotein [Arabidopsis thaliana]
16043	GM_M14_B2_H10_MR	g3522952	BLASTX	166	1e-11	73	(AC004411) putative alcohol dehydrogenase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16044	GM_M15_A1_A02_MR	g2129618	BLASTX	166	2e-10	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16045	GM_M15_A1_B01_MR	g4063760	BLASTX	400	3e-46	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16046	GM_M15_A1_B03_MF	g3953461	BLASTX	155	1e-09	58	(AC002328) F20N2.6 [Arabidopsis thaliana]
16047	GM_M15_A1_B05_MR	g4063760	BLASTX	263	1e-20	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16048	GM_M15_A1_B08_MF	g18559	BLASTN	1107	3e-43	84	G.max gene for catalase
16049	GM_M15_A1_C01_MF	g2769655	BLASTN	395	8e-11	63	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
16050	GM_M15_A1_C02_MF	g4063760	BLASTX	398	5e-35	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16051	GM_M15_A1_C03_MR	g4063760	BLASTX	248	5e-19	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16052	GM_M15_A1_C06_MR	g629693	BLASTX	97	3e-11	33	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
16053	GM_M15_A1_C07_MF	g507910	BLASTN	403	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16054	GM_M15_A1_C07_MR	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16055	GM_M15_A1_C10_MR	g14227	BLASTN	414	2e-12	63	Yeast cytochrome c oxidase transcription initiation region subunit 1 (COX1) from mitochondrial DNA
16056	GM_M15_A1_D02_MR	g2443320	BLASTX	224	5e-27	48	(D85597) polyprotein [Oryza australiensis]
16057	GM_M15_A1_D04_MF	g3201625	BLASTX	152	9e-10	46	(AC004669) hypothetical protein [Arabidopsis thaliana]
16058	GM_M15_A1_D04_MR	g3445210	BLASTX	406	3e-37	51	(AC004786) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]
16059	GM_M15_A1_D05_MF	g1142701	BLASTN	263	6e-20	76	Glycine max satellite STR120-A.3.
16060	GM_M15_A1_D07_MR	g3142328	BLASTN	961	1e-36	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16061	GM_M15_A1_D10_MR	g3367519	BLASTX	253	1e-27	57	(AC004392) Contains similarity to gb U51898 Ca2+-independent phospholipase A2 from Rattus norvegicus. [Arabidopsis thaliana]
16062	GM_M15_A1_D12_MF	g170606	BLASTN	664	2e-23	65	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
16063	GM_M15_A1_D12_MR	g2811226	BLASTX	310	4e-26	65	(AF042669) fimbrin 2 [Arabidopsis thaliana] gi 2811232 (AF042671) fimbrin 2 [Arabidopsis thaliana]
16064	GM_M15_A1_E05_MR	g255578	BLASTN	929	6e-36	95	small auxin up RNA gene cluster: orf X10A [Glycine max=soybeans, cv. Wayne, Genomic, 666 nt]
16065	GM_M15_A1_E10_MR	g3142328	BLASTN	1952	8e-82	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16066	GM_M15_A1_F02_MR	g2522227	BLASTX	223	1e-17	36	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
16067	GM_M15_A1_F04_MR	g4063760	BLASTX	542	2e-50	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16068	GM_M15_A1_F09_MR	g1769898	BLASTX	340	2e-29	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16069	GM_M15_A1_G04_MF	g507910	BLASTN	380	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16070	GM_M15_A1_G04_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16071	GM_M15_A1_G05_MR	g2739369	BLASTX	334	4e-29	66	(AC002505) putative pectinesterase [Arabidopsis thaliana]
16072	GM_M15_A1_G09_MR	g343344	BLASTN	455	5e-18	81	Soybean chloroplast 16S rRNA (3' end), 18S rRNA (5' end), Ile-tRNA, and Ala-tRNA genes.
16073	GM_M15_A1_G10_MR	g1769898	BLASTX	452	5e-42	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16074	GM_M15_A1_H03_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16075	GM_M15_A1_H06_MR	g1769898	BLASTX	177	2e-24	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16076	GM_M15_A2_A02_MF	g1076668	BLASTX	656	1e-63	96	NADH dehydrogenase (EC 1.6.99.3) - potato gi 639834 (X83999) NADH dehydrogenase [Solanum tuberosum]
16077	GM_M15_A2_A05_MR	g2522230	BLASTX	306	2e-26	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
16078	GM_M15_A2_A07_MF	g728695	BLASTX	245	5e-25	86	(Z48618) DNA helicase type protein [Saccharomyces cerevisiae]
16079	GM_M15_A2_A07_MR	g3645899	BLASTX	365	1e-31	53	(U68408) 5' end not determined experimentally [Zea mays]
16080	GM_M15_A2_A08_MR	g2811226	BLASTX	252	7e-20	89	(AF042669) fimbrin 2 [Arabidopsis thaliana] gi 2811232 (AF042671) fimbrin 2 [Arabidopsis thaliana]
16081	GM_M15_A2_A11_MF	g18559	BLASTN	888	3e-33	77	G.max gene for catalase
16082	GM_M15_A2_B01_MR	g905361	BLASTX	589	6e-59	84	(U22103) gag-protease polyprotein [Glycine max]
16083	GM_M15_A2_B04_MF	g2708743	BLASTX	154	7e-09	41	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
16084	GM_M15_A2_B06_MF	g130582	BLASTX	243	1e-19	43	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
16085	GM_M15_A2_B07_MR	g507910	BLASTN	538	1e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
16086	GM_M15_A2_B12_MR	g992916	BLASTN	631	2e-21	76	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
16087	GM_M15_A2_C07_MR	g4006831	BLASTX	158	2e-09	36	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
16088	GM_M15_A2_C08_MF	g4063760	BLASTX	371	4e-32	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16089	GM_M15_A2_C09_MR	g3142328	BLASTN	793	6e-29	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16090	GM_M15_A2_C11_MR	g1769898	BLASTX	377	2e-33	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16091	GM_M15_A2_C12_MF	g3777527	BLASTX	609	3e-57	98	(AF053008) gag-pol polyprotein [Glycine max]
16092	GM_M15_A2_C12_MR	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
16093	GM_M15_A2_D01_MF	g4063760	BLASTX	380	5e-33	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16094	GM_M15_A2_D02_MF	g100484	BLASTX	354	9e-31	60	hypothetical protein - garden snapdragon
16095	GM_M15_A2_D05_MR	g2827992	BLASTX	509	5e-48	65	(AF034743) UDP-glucuronosyltransferase [Pisum sativum]
16096	GM_M15_A2_D08_MR	g2462134	BLASTX	195	6e-14	39	(Y13368) reverse transcriptase [Beta vulgaris]
16097	GM_M15_A2_D10_MR	g4063770	BLASTX	182	3e-12	38	(AB004906) transposase [Ipomoea purpurea]
16098	GM_M15_A2_E01_MR	g2708743	BLASTX	246	1e-18	35	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
16099	GM_M15_A2_E05_MF	g507910	BLASTN	354	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
16100	GM_M15_A2_E05_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16101	GM_M15_A2_E06_MF	g2443320	BLASTX	166	3e-10	35	(D85597) polyprotein [Oryza australiensis]
16102	GM_M15_A2_E09_MF	g3777527	BLASTX	301	4e-42	76	(AF053008) gag-pol polyprotein [Glycine max]
16103	GM_M15_A2_E12_MF	g2708743	BLASTX	154	7e-09	41	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
16104	GM_M15_A2_F01_MR	g2121303	BLASTN	376	6e-10	62	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
16105	GM_M15_A2_F02_MF	g2244802	BLASTX	355	3e-30	54	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
16106	GM_M15_A2_F09_MF	g4063760	BLASTX	349	9e-30	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16107	GM_M15_A2_F10_MF	g2244802	BLASTX	382	4e-33	56	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
16108	GM_M15_A2_G01_MF	g3930515	BLASTX	166	7e-11	32	(AF059674) putative gag protein [Nicotiana tabacum]
16109	GM_M15_A2_G05_MR	g3645899	BLASTX	233	5e-28	52	(U68408) 5' end not determined experimentally [Zea mays]
16110	GM_M15_A2_G09_MR	g507910	BLASTN	350	3e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
16111	GM_M15_A2_G10_MR	g2522228	BLASTX	274	4e-23	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
16112	GM_M15_A2_H01_MF	g4063760	BLASTX	210	6e-15	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16113	GM_M15_A2_H01_MR	g4063760	BLASTX	198	1e-15	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16114	GM_M15_A2_H04_MR	g3287270	BLASTX	164	6e-10	45	(Y09533) involved in starch metabalism [Solanum tuberosum]
16115	GM_M15_A2_H08_MF	g2656024	BLASTN	366	2e-09	60	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K15E6

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16116	GM_M15_A2_H10_MR	g2194124	BLASTX	194	4e-14	62	(AC002062) Similar to Glycine metalloendoproteinase (gb U63725). [Arabidopsis thaliana]
16117	GM_M15_A2_H11_MF	g3582067	BLASTN	383	4e-11	72	Rattus norvegicus repeat; map end-D8Wox18
16118	GM_M15_A2_H11_MR	g2194136	BLASTX	185	3e-12	39	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
16119	GM_M15_B1_A05_MR	g4063760	BLASTX	265	7e-21	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16120	GM_M15_B1_A07_MR	g2522230	BLASTX	185	9e-14	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
16121	GM_M15_B1_B04_MR	g1402881	BLASTX	266	3e-23	43	(X98130) non-ltr retrotransposon reverse transcriptase-like protein [Arabidopsis thaliana]
16122	GM_M15_B1_B06_MR	g4063760	BLASTX	250	2e-35	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16123	GM_M15_B1_C03_MR	g99922	BLASTX	551	5e-59	81	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
16124	GM_M15_B1_C04_MR	g2829611	BLASTX	144	6e-09	47	HEMK PROTEIN HOMOLOG >gi 1653158 gnl PID d1018807 (D90911) protoporphyrinogen oxidase [Synechocystis sp.]
16125	GM_M15_B1_C12_MR	g3184508	BLASTN	453	2e-13	66	Homo sapiens chromosome 17, clone HRPC41C23, complete sequence [Homo sapiens]
16126	GM_M15_B1_D05_MR	g18559	BLASTN	477	1e-14	66	G.max gene for catalase
16127	GM_M15_B1_D09_MR	g3738114	BLASTN	357	4e-09	62	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
16128	GM_M15_B1_E01_MR	g507910	BLASTN	570	4e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
16129	GM_M15_B1_E04_MR	g1326016	BLASTX	157	4e-19	34	TY3-2 orfB
16130	GM_M15_B1_E08_MR	g3097320	BLASTN	411	1e-11	73	Glycine max gene for Bd 30K, complete cds
16131	GM_M15_B1_E09_MR	g478218	BLASTX	220	2e-17	60	reverse transcriptase (copia-like retrotransposon) - maize (fragment) gi 168449 (M94482) reverse transcriptase [Zea mays]
16132	GM_M15_B1_F01_MR	g4056482	BLASTX	233	3e-17	58	(AC005896) putative ABC transporter [Arabidopsis thaliana]
16133	GM_M15_B1_F03_MR	g1769898	BLASTX	385	2e-34	70	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16134	GM_M15_B1_G01_MR	g2194136	BLASTX	192	6e-13	33	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
16135	GM_M15_B1_H05_MR	g2367392	BLASTX	177	1e-11	30	(U82513) random slug cDNA25 protein [Dictyostelium discoideum]
16136	GM_M15_B1_H10_MR	g18559	BLASTN	364	2e-09	73	G.max gene for catalase
16137	GM_M15_B1_H11_MR	g2583130	BLASTX	107	7e-09	53	(AC002387) putative reverse transcriptase [Arabidopsis thaliana]
16138	GM_M15_B2_A03_MR	g3142328	BLASTN	985	1e-37	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16139	GM_M15_B2_A09_MR	g3645899	BLASTX	209	3e-17	43	(U68408) 5' end not determined experimentally [Zea mays]
16140	GM_M15_B2_A12_MF	g3142328	BLASTN	763	1e-27	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16141	GM_M15_B2_B02_MF	g3426334	BLASTN	362	2e-09	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
16142	GM_M15_B2_B04_MR	g2605911	BLASTX	208	8e-22	86	(AF029258) plasma membrane H+-ATPase [Kosteletzkya virginica]
16143	GM_M15_B2_B05_MF	g3386621	BLASTX	208	2e-18	71	(AC004665) unknown protein [Arabidopsis thaliana]
16144	GM_M15_B2_B07_MF	g2443320	BLASTX	348	1e-29	53	(D85597) polyprotein [Oryza australiensis]
16145	GM_M15_B2_B07_MR	g3779030	BLASTX	171	3e-12	32	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
16146	GM_M15_B2_B11_MR	g2462134	BLASTX	155	1e-09	44	(Y13368) reverse transcriptase [Beta vulgaris]
16147	GM_M15_B2_C01_MF	g4038056	BLASTX	360	4e-31	52	(AC005897) putative transposon [Arabidopsis thaliana]
16148	GM_M15_B2_C02_MR	g18559	BLASTN	1097	1e-42	77	G.max gene for catalase
16149	GM_M15_B2_C08_MF	g18559	BLASTN	797	4e-29	73	G.max gene for catalase
16150	GM_M15_B2_C09_MR	g3549678	BLASTX	155	2e-09	87	(AL031394) putative aspartate--tRNA ligase [Arabidopsis thaliana]
16151	GM_M15_B2_C12_MF	g905361	BLASTX	429	2e-39	95	(U22103) gag-protease polyprotein [Glycine max]
16152	GM_M15_B2_D01_MF	g3810596	BLASTX	194	2e-13	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
16153	GM_M15_B2_D01_MR	g2981494	BLASTX	116	6e-10	62	(AF053473) kinesin heavy chain [Mus musculus]
16154	GM_M15_B2_D04_MF	g3930515	BLASTX	121	4e-12	47	(AF059674) putative gag protein [Nicotiana tabacum]
16155	GM_M15_B2_D04_MR	g2129709	BLASTX	306	4e-25	46	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
16156	GM_M15_B2_D05_MF	g3142328	BLASTN	1676	4e-69	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16157	GM_M15_B2_D06_MR	g629693	BLASTX	160	3e-19	69	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
16158	GM_M15_B2_D10_MR	g507910	BLASTN	420	2e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16159	GM_M15_B2_D11_MF	g3930515	BLASTX	100	7e-09	42	(AF059674) putative gag protein [Nicotiana tabacum]
16160	GM_M15_B2_D11_MR	g4038056	BLASTX	325	2e-27	48	(AC005897) putative transposon [Arabidopsis thaliana]
16161	GM_M15_B2_E01_MF	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16162	GM_M15_B2_E01_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16163	GM_M15_B2_E02_MR	g4038056	BLASTX	400	2e-35	54	(AC005897) putative transposon [Arabidopsis thaliana]
16164	GM_M15_B2_E03_MF	g3777527	BLASTX	232	4e-17	40	(AF053008) gag-pol polyprotein [Glycine max]
16165	GM_M15_B2_E06_MF	g100484	BLASTX	214	1e-15	44	hypothetical protein - garden snapdragon
16166	GM_M15_B2_E10_MF	g507910	BLASTN	602	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16167	GM_M15_B2_E11_MR	g4038056	BLASTX	372	2e-32	52	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16168	GM_M15_B2_E12_MF	g3645899	BLASTX	293	7e-28	64	(U68408) 5' end not determined experimentally [Zea mays]
16169	GM_M15_B2_F04_MF	g1769897	BLASTX	168	6e-11	32	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16170	GM_M15_B2_F05_MR	g3650039	BLASTX	311	3e-26	46	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
16171	GM_M15_B2_F07_MF	g3695395	BLASTX	97	3e-13	39	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
16172	GM_M15_B2_F08_MR	g100484	BLASTX	364	7e-32	53	hypothetical protein - garden snapdragon
16173	GM_M15_B2_F10_MF	g2429543	BLASTX	170	1e-10	38	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]
16174	GM_M15_B2_G05_MF	g507910	BLASTN	414	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16175	GM_M15_B2_G05_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16176	GM_M15_B2_G06_MR	g3645899	BLASTX	217	5e-32	60	(U68408) 5' end not determined experimentally [Zea mays]
16177	GM_M15_B2_G07_MF	g18559	BLASTN	380	3e-10	71	G.max gene for catalase
16178	GM_M15_B2_G07_MR	g2995405	BLASTX	283	5e-25	43	(Y12432) polyprotein [Ananas comosus]
16179	GM_M15_B2_G12_MF	g3935164	BLASTX	379	9e-33	52	(AC004557) F17L21.7 [Arabidopsis thaliana]
16180	GM_M15_B2_H08_MF	g507910	BLASTN	475	7e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
16181	GM_M15_B2_H08_MR	g507910	BLASTN	547	4e-18	82	Glycine max BSR-101 satellite SB92 genomic sequence.
16182	GM_M15_B2_H09_MR	g2114242	BLASTN	378	5e-10	65	Human (lambda) DNA for immunoglobulin light chain
16183	GM_M15_B2_H10_MF	g507910	BLASTN	364	8e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16184	GM_M15_B2_H10_MR	g905361	BLASTX	677	7e-66	94	(U22103) gag-protease polyprotein [Glycine max]
16185	GM_M16_A1_A07_MR	g2275207	BLASTX	295	2e-25	52	(AC002337) hypothetical protein [Arabidopsis thaliana]
16186	GM_M16_A1_A11_MF	g2522227	BLASTX	164	4e-11	46	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
16187	GM_M16_A1_B01_MF	g507910	BLASTN	415	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16188	GM_M16_A1_B01_MR	g3777527	BLASTX	709	5e-68	97	(AF053008) gag-pol polyprotein [Glycine max]
16189	GM_M16_A1_B05_MR	g2506938	BLASTX	171	4e-17	62	NADH-PLASTOQUINONE OXIDOREDUCTASE CHAIN 4, CHLOROPLAST
16190	GM_M16_A1_B07_MR	g2995405	BLASTX	307	2e-25	52	(Y12432) polyprotein [Ananas comosus]
16191	GM_M16_A1_C01_MR	g507910	BLASTN	587	6e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16192	GM_M16_A1_C03_MR	g4063760	BLASTX	238	6e-18	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16193	GM_M16_A1_C08_MR	g454847	BLASTN	377	4e-10	69	Glycine max ribosomal protein S11 gene, complete cds
16194	GM_M16_A1_C09_MR	g4063760	BLASTX	500	7e-46	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16195	GM_M16_A1_D08_MR	g3650039	BLASTX	280	7e-23	44	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16196	GM_M16_A1_D10_MF	g507910	BLASTN	403	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16197	GM_M16_A1_D10_MR	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16198	GM_M16_A1_D12_MF	g507910	BLASTN	662	3e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
16199	GM_M16_A1_D12_MR	g507910	BLASTN	395	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16200	GM_M16_A1_E02_MF	g2522228	BLASTX	97	9e-10	65	(AB007466) reverse transcriptase-like protein [Vicia faba]
16201	GM_M16_A1_E03_MF	g3142328	BLASTN	428	2e-12	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16202	GM_M16_A1_E05_MR	g2344891	BLASTX	167	6e-11	37	(AC002388) hypothetical protein [Arabidopsis thaliana]
16203	GM_M16_A1_E06_MF	g3885341	BLASTX	149	2e-10	32	(AC005623) unknown protein [Arabidopsis thaliana]
16204	GM_M16_A1_E10_MF	g2618704	BLASTX	170	3e-11	83	(AC002510) putative thioredoxin reductase [Arabidopsis thaliana]
16205	GM_M16_A1_E12_MR	g507910	BLASTN	406	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16206	GM_M16_A1_G02_MF	g3869069	BLASTN	636	1e-21	68	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MEB5, complete sequence [Arabidopsis thaliana]
16207	GM_M16_A1_G10_MR	g4038056	BLASTX	201	3e-30	58	(AC005897) putative transposon [Arabidopsis thaliana]
16208	GM_M16_A1_G12_MF	g218269	BLASTX	364	1e-32	85	(D12839) reverse transcriptase [Glycine max]
16209	GM_M16_A1_G12_MR	g2462056	BLASTX	284	3e-24	49	(Y13388) reverse transcriptase [Antirrhinum majus]
16210	GM_M16_A1_H02_MR	g3142328	BLASTN	527	7e-17	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16211	GM_M16_A1_H03_MF	g4063756	BLASTN	468	4e-14	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
16212	GM_M16_A1_H03_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16213	GM_M16_A1_H05_MF	g3449327	BLASTN	378	5e-10	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCA23, complete sequence [Arabidopsis thaliana]
16214	GM_M16_A1_H05_MR	g1737492	BLASTX	147	1e-10	62	(U81318) poly(A)-binding protein [Triticum aestivum]
16215	GM_M16_A1_H08_MF	g3319362	BLASTX	266	5e-21	42	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
16216	GM_M16_A1_H09_MR	g4038056	BLASTX	393	1e-34	54	(AC005897) putative transposon [Arabidopsis thaliana]
16217	GM_M16_A1_H10_MR	g3930515	BLASTX	121	4e-13	47	(AF059674) putative gag protein [Nicotiana tabacum]
16218	GM_M16_A1_H11_MF	g2191130	BLASTX	162	3e-10	40	(AF007269) A_IG002N01.7 gene product [Arabidopsis thaliana]
16219	GM_M16_A2_A04_MF	g1708710	BLASTX	272	6e-23	45	(U60069) 11.pep [Solanum tuberosum]
16220	GM_M16_A2_A04_MR	g2244866	BLASTX	187	3e-12	41	(Z97337) hypothetical protein [Arabidopsis thaliana]
16221	GM_M16_A2_A07_MR	g507910	BLASTN	575	2e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
16222	GM_M16_A2_A10_MF	g2129618	BLASTX	179	8e-12	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16223	GM_M16_A2_A10_MR	g629693	BLASTX	287	1e-27	54	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
16224	GM_M16_A2_A11_MF	g507910	BLASTN	475	7e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
16225	GM_M16_A2_B04_MR	g2570066	BLASTN	259	4e-11	78	Pisum sativum mRNA for second sucrose synthase.
16226	GM_M16_A2_B06_MR	g1236949	BLASTX	354	1e-41	83	(U50075) lipoxygenase L-5 [Glycine max]
16227	GM_M16_A2_B09_MR	g3930515	BLASTX	105	5e-09	47	(AF059674) putative gag protein [Nicotiana tabacum]
16228	GM_M16_A2_B10_MF	g130582	BLASTX	353	4e-30	60	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
16229	GM_M16_A2_B10_MR	g4063760	BLASTX	376	1e-32	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16230	GM_M16_A2_B12_MF	g507910	BLASTN	591	4e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
16231	GM_M16_A2_C02_MF	g130582	BLASTX	297	4e-24	53	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
16232	GM_M16_A2_C05_MF	g4038056	BLASTX	305	3e-25	50	(AC005897) putative transposon [Arabidopsis thaliana]
16233	GM_M16_A2_C07_MF	g3777527	BLASTX	599	3e-56	95	(AF053008) gag-pol polyprotein [Glycine max]
16234	GM_M16_A2_C07_MR	g507910	BLASTN	357	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
16235	GM_M16_A2_C12_MR	g3142328	BLASTN	1678	3e-69	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16236	GM_M16_A2_D02_MR	g1666236	BLASTX	200	5e-15	30	(U76261) unknown [Hordeum vulgare]
16237	GM_M16_A2_D04_MR	g507910	BLASTN	601	1e-20	84	Glycine max BSR-101 satellite SB92 genomic sequence.
16238	GM_M16_A2_D07_MR	g3142328	BLASTN	973	4e-37	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16239	GM_M16_A2_D11_MR	g2809243	BLASTX	150	5e-10	59	(AC002560) F21B7.12 [Arabidopsis thaliana]
16240	GM_M16_A2_D12_MF	g4038056	BLASTX	351	3e-30	55	(AC005897) putative transposon [Arabidopsis thaliana]
16241	GM_M16_A2_E01_MF	g2801423	BLASTN	383	3e-10	65	Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence [Homo sapiens]
16242	GM_M16_A2_E04_MF	g18559	BLASTN	885	4e-33	76	G.max gene for catalase
16243	GM_M16_A2_E06_MF	g3935141	BLASTX	159	4e-10	56	(AC005106) T25N20.5 [Arabidopsis thaliana]
16244	GM_M16_A2_E08_MR	g2995405	BLASTX	212	2e-15	44	(Y12432) polyprotein [Ananas comosus]
16245	GM_M16_A2_E12_MF	g2914706	BLASTX	135	4e-16	55	(AC003974) putative homeobox protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16246	GM_M16_A2_F01_MF	g2443320	BLASTX	242	3e-18	42	(D85597) polyprotein [Oryza australiensis]
16247	GM_M16_A2_F02_MF	g3063469	BLASTX	182	5e-12	47	(AC003981) F22O13.31 [Arabidopsis thaliana]
16248	GM_M16_A2_F03_MF	g3599418	BLASTN	512	3e-16	72	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
16249	GM_M16_A2_F04_MR	g3176673	BLASTX	110	4e-15	77	(AC003671) Similar to serine/threonine kinase gb Y12531 from Brassica oleracea. [Arabidopsis thaliana]
16250	GM_M16_A2_F06_MF	g3142328	BLASTN	672	2e-23	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16251	GM_M16_A2_F07_MF	g2708743	BLASTX	154	7e-09	41	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
16252	GM_M16_A2_F10_MR	g2655098	BLASTX	283	2e-23	73	(AF023472) peptide transporter [Hordeum vulgare]
16253	GM_M16_A2_F11_MF	g2522226	BLASTN	568	9e-19	64	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
16254	GM_M16_A2_G01_MR	g2522227	BLASTX	210	2e-16	41	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
16255	GM_M16_A2_G02_MF	g1769898	BLASTX	284	2e-23	75	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16256	GM_M16_A2_G05_MF	g3287696	BLASTX	309	8e-26	46	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]
16257	GM_M16_A2_G12_MF	g3777527	BLASTX	595	8e-56	97	(AF053008) gag-pol polyprotein [Glycine max]
16258	GM_M16_A2_H02_MF	g1769898	BLASTX	132	8e-11	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16259	GM_M16_A2_H05_MF	g4063760	BLASTX	162	7e-10	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16260	GM_M16_A2_H07_MF	g100484	BLASTX	355	7e-31	60	hypothetical protein - garden snapdragon
16261	GM_M16_A2_H09_MR	g1853970	BLASTX	268	2e-21	62	(D88122) CPRD46 protein [Vigna unguiculata]
16262	GM_M16_B1_A05_MR	g3510505	BLASTX	266	7e-21	39	(AF030881) pol polyprotein [Fugu rubripes]
16263	GM_M16_B1_B01_MR	g130592	BLASTX	184	2e-12	40	ENZYMATIC POLYPROTEIN [CONTAINS: ASPARTIC PROTEASE ; ENDONUCLEASE; REVERSE TRANSCRIPTASE] >gi 75491 pir QQCV5 hypothetical protein 5 - cauliflower mosaic virus (strains Strasbourg, CM1841 and D/H) >gi 58826 (V00141) reading frame (V) [Cauliflower mosaic virus]
16264	GM_M16_B1_B11_MR	g3776007	BLASTX	103	7e-09	53	(AJ010467) RNA helicase [Arabidopsis thaliana]
16265	GM_M16_B1_C04_MR	g2924257	BLASTN	398	6e-11	66	Tobacco chloroplast genome DNA
16266	GM_M16_B1_C08_MR	g1666236	BLASTX	179	1e-12	30	(U76261) unknown [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16267	GM_M16_B1_C11_MR	g3650039	BLASTX	235	5e-18	39	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
16268	GM_M16_B1_D02_MR	g2827535	BLASTX	246	4e-20	51	(AL021633) hypothetical protein [Arabidopsis thaliana]
16269	GM_M16_B1_D11_MR	g3021268	BLASTX	369	7e-32	54	(AL022347) putative protein [Arabidopsis thaliana]
16270	GM_M16_B1_E01_MR	g507910	BLASTN	371	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16271	GM_M16_B1_E03_MR	g507910	BLASTN	620	2e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
16272	GM_M16_B1_F01_MR	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
16273	GM_M16_B1_F07_MR	g2129709	BLASTX	171	1e-10	36	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
16274	GM_M16_B1_G02_MR	g3142328	BLASTN	984	1e-37	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16275	GM_M16_B1_G06_MR	g507910	BLASTN	394	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16276	GM_M16_B1_G07_MR	g3947839	BLASTN	558	4e-18	66	Human DNA sequence from clone 569D19 on chromosome 22q13.1. Contains a novel gene similar to mouse Ras, Dexamethasone-induced 1 (Ras-related protein, RASD1, DEXRAS1) and the last exon of the MB gene for Myoglobin. Cont...
16277	GM_M16_B1_H03_MR	g3777527	BLASTX	593	1e-55	94	(AF053008) gag-pol polyprotein [Glycine max]
16278	GM_M16_B1_H06_MR	g3930515	BLASTX	125	2e-13	50	(AF059674) putative gag protein [Nicotiana tabacum]
16279	GM_M16_B1_H07_MR	g507910	BLASTN	633	5e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16280	GM_M16_B2_A04_MF	g507910	BLASTN	379	2e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16281	GM_M16_B2_A04_MR	g507910	BLASTN	352	3e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16282	GM_M16_B2_A07_MR	g3386620	BLASTX	346	4e-30	58	(AC004665) hypothetical protein [Arabidopsis thaliana]
16283	GM_M16_B2_A11_MR	g4063760	BLASTX	329	2e-35	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16284	GM_M16_B2_B02_MF	g4063770	BLASTX	126	7e-11	35	(AB004906) transposase [Ipomoea purpurea]
16285	GM_M16_B2_B06_MR	g629693	BLASTX	181	3e-16	41	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
16286	GM_M16_B2_C02_MR	g3142328	BLASTN	1143	7e-45	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16287	GM_M16_B2_C05_MF	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16288	GM_M16_B2_C09_MF	g507910	BLASTN	442	2e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
16289	GM_M16_B2_C09_MR	g507910	BLASTN	435	5e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
16290	GM_M16_B2_C10_MR	g3283026	BLASTX	270	1e-21	40	putative transposase [Arabidopsis thaliana]
16291	GM_M16_B2_C12_MF	g3777527	BLASTX	276	8e-22	44	(AF053008) gag-pol polyprotein [Glycine max]
16292	GM_M16_B2_D02_MF	g4063760	BLASTX	192	5e-13	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16293	GM_M16_B2_D05_MF	g629693	BLASTX	374	9e-34	53	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
16294	GM_M16_B2_D05_MR	g3377834	BLASTX	151	6e-09	29	(AF075598) No definition line found [Arabidopsis thaliana]
16295	GM_M16_B2_E05_MF	g905361	BLASTX	124	3e-10	32	(U22103) gag-protease polyprotein [Glycine max]
16296	GM_M16_B2_E05_MR	g13563	BLASTN	388	1e-10	64	Yeast mitochondrial aap1 gene for ATPase subunit 8
16297	GM_M16_B2_E06_MR	g3510505	BLASTX	135	1e-12	34	(AF030881) pol polyprotein [Fugu rubripes]
16298	GM_M16_B2_E12_MR	g2827715	BLASTX	240	3e-18	40	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
16299	GM_M16_B2_F03_MR	g2194136	BLASTX	259	4e-20	39	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
16300	GM_M16_B2_F06_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16301	GM_M16_B2_F09_MF	g3645899	BLASTX	197	8e-18	47	(U68408) 5' end not determined experimentally [Zea mays]
16302	GM_M16_B2_F10_MR	g3777527	BLASTX	684	3e-65	94	(AF053008) gag-pol polyprotein [Glycine max]
16303	GM_M16_B2_G04_MF	g18559	BLASTN	1549	3e-63	90	G.max gene for catalase
16304	GM_M16_B2_G04_MR	g2708743	BLASTX	123	6e-11	33	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
16305	GM_M16_B2_G05_MR	g507910	BLASTN	417	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16306	GM_M16_B2_G06_MF	g3810596	BLASTX	129	1e-13	34	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
16307	GM_M16_B2_G06_MR	g18559	BLASTN	990	7e-38	76	G.max gene for catalase
16308	GM_M16_B2_G07_MF	g507910	BLASTN	387	7e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16309	GM_M16_B2_G10_MR	g18559	BLASTN	1201	2e-47	86	G.max gene for catalase
16310	GM_M16_B2_G11_MR	g3810596	BLASTX	215	1e-15	40	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
16311	GM_M16_B2_H01_MR	g3810596	BLASTX	320	7e-28	54	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
16312	GM_M16_B2_H02_MF	g4115559	BLASTX	251	4e-20	41	(AB013596) UDP-glucose:anthocysnin 5-O-glucosyltransferase [Perilla frutescens]
16313	GM_M16_B2_H02_MR	g2522230	BLASTX	304	3e-26	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
16314	GM_M16_B2_H11_MF	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16315	GM_M16_B2_H11_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16316	GM_M17_A1_B01_MF	g719291	BLASTX	404	2e-35	59	(U19134) unknown [Arabidopsis thaliana] gi 1095007 prf 2107236A SABRE gene [Arabidopsis thaliana]
16317	GM_M17_A1_B02_MF	g2145358	BLASTX	161	4e-21	68	(Y10922) HD-Zip protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16318	GM_M17_A1_C03_MF	g3777527	BLASTX	236	2e-17	37	(AF053008) gag-pol polyprotein [Glycine max]
16319	GM_M17_A1_C04_MF	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
16320	GM_M17_A1_C10_MF	g507910	BLASTN	597	2e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
16321	GM_M17_A1_D02_MF	g3510347	BLASTN	441	7e-13	66	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]
16322	GM_M17_A1_D06_MF	g2815245	BLASTN	400	5e-18	80	C.arietinum mRNA for class I type 2 metallothionein (clone: CanMT-2)
16323	GM_M17_A1_D10_MF	g1142702	BLASTN	457	4e-14	74	Glycine max satellite STR120-A.4.
16324	GM_M17_A1_D12_MF	g507910	BLASTN	588	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
16325	GM_M17_A1_E06_MF	g3097320	BLASTN	483	8e-15	73	Glycine max gene for Bd 30K, complete cds
16326	GM_M17_A1_E07_MF	g2351062	BLASTN	729	7e-26	70	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAH20
16327	GM_M17_A1_E12_MF	g4063760	BLASTX	225	1e-16	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16328	GM_M17_A1_F01_MF	g719291	BLASTX	445	6e-40	63	(U19134) unknown [Arabidopsis thaliana] gi 1095007 prf 2107236A SABRE gene [Arabidopsis thaliana]
16329	GM_M17_A1_F02_MF	g130582	BLASTX	391	3e-34	60	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
16330	GM_M17_A1_F03_MF	g3777527	BLASTX	234	2e-42	71	(AF053008) gag-pol polyprotein [Glycine max]
16331	GM_M17_A1_G02_MF	g3777527	BLASTX	655	3e-62	98	(AF053008) gag-pol polyprotein [Glycine max]
16332	GM_M17_A1_G03_MF	g507910	BLASTN	412	5e-12	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16333	GM_M17_A1_G05_MF	g3097320	BLASTN	424	4e-12	67	Glycine max gene for Bd 30K, complete cds
16334	GM_M17_A1_G07_MF	g3935148	BLASTX	220	2e-19	59	(AC005106) T25N20.12 [Arabidopsis thaliana]
16335	GM_M17_A1_G09_MF	g2264320	BLASTN	419	7e-12	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
16336	GM_M17_A1_G10_MF	g3249098	BLASTX	225	4e-18	44	(AC003114) ESTs gb T04610, gb N38459, gb T45174, gb R30481 and gb N64971 come from this gene. [Arabidopsis thaliana]
16337	GM_M17_A1_H07_MF	g1370171	BLASTN	591	1e-20	77	L.japonicus mRNA for small GTP-binding protein, RAB1X.
16338	GM_M17_A1_H08_MF	g4063756	BLASTN	461	9e-14	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
16339	GM_M17_A2_A01_MF	g2995405	BLASTX	145	4e-10	37	(Y12432) polyprotein [Ananas comosus]
16340	GM_M17_A2_A07_MR	g2995405	BLASTX	258	3e-24	54	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16341	GM_M17_A2_A09_MR	g3142328	BLASTN	1138	1e-44	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16342	GM_M17_A2_A10_MR	g3281850	BLASTX	276	1e-22	94	(AL031004) monogalactosyldiacylglycerol synthase - like protein [Arabidopsis thaliana]
16343	GM_M17_A2_A11_MR	g3510264	BLASTX	378	4e-34	55	(AC005310) hypothetical protein, 5' partial [Arabidopsis thaliana]
16344	GM_M17_A2_B03_MR	g2769655	BLASTN	463	7e-14	64	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
16345	GM_M17_A2_B05_MR	g4063760	BLASTX	198	1e-13	35	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16346	GM_M17_A2_B06_MF	g2443357	BLASTX	294	7e-28	70	(AB004293) SigB [Arabidopsis thaliana] gi 2597831 gnl PID e1169752 (Y15362) sigma factor [Arabidopsis thaliana] gi 2879922 gnl PID d1025747 (AB004820) plastid RNA polymerase sigma-subunit [Arabidopsis thaliana] gi 3063440 (AC003981) F22O13.2 [Arabidopsis thaliana]
16347	GM_M17_A2_B08_MF	g507910	BLASTN	498	7e-16	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16348	GM_M17_A2_B11_MF	g507910	BLASTN	738	1e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
16349	GM_M17_A2_B11_MR	g507910	BLASTN	588	6e-20	85	Glycine max BSR-101 satellite SB92 genomic sequence.
16350	GM_M17_A2_B12_MF	g1066857	BLASTX	258	4e-42	87	(L48995) acetyl-CoA carboxylase [Glycine max]
16351	GM_M17_A2_C01_MF	g2769655	BLASTN	381	4e-10	66	Human DNA sequence from PAC 127L4 on chromosome 22. Contains last exon (15) of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter). Conta...
16352	GM_M17_A2_C01_MR	g2792208	BLASTX	217	4e-17	44	(AF032682) NBS-LRR type resistance protein [Hordeum vulgare]
16353	GM_M17_A2_C05_MF	g100484	BLASTX	364	7e-32	61	hypothetical protein - garden snapdragon
16354	GM_M17_A2_C08_MR	g3746069	BLASTX	173	6e-11	37	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
16355	GM_M17_A2_C09_MR	g100484	BLASTX	260	1e-27	55	hypothetical protein - garden snapdragon
16356	GM_M17_A2_C10_MR	g2764526	BLASTN	466	5e-14	66	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
16357	GM_M17_A2_D02_MR	g2582971	BLASTX	164	7e-18	66	(D83711) TKRP125 [Nicotiana tabacum]
16358	GM_M17_A2_D04_MF	g3947439	BLASTX	151	6e-09	26	(AC005034) gc-rich sequence dna-binding factor [Homo sapiens]
16359	GM_M17_A2_D06_MF	g3097320	BLASTN	1123	8e-44	80	Glycine max gene for Bd 30K, complete cds
16360	GM_M17_A2_D09_MF	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16361	GM_M17_A2_D09_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16362	GM_M17_A2_D10_MF	g130582	BLASTX	366	2e-31	53	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
16363	GM_M17_A2_E04_MR	g2914758	BLASTN	361	3e-09	63	Homo sapiens wbscr1 (WBSCR1) and replication factor C subunit 2 (RFC2) genes, complete cds
16364	GM_M17_A2_E05_MF	g507910	BLASTN	547	4e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
16365	GM_M17_A2_E05_MR	g905361	BLASTX	528	4e-50	78	(U22103) gag-protease polyprotein [Glycine max]
16366	GM_M17_A2_E07_MR	g130582	BLASTX	381	4e-33	60	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
16367	GM_M17_A2_E08_MF	g1666236	BLASTX	169	1e-11	30	(U76261) unknown [Hordeum vulgare]
16368	GM_M17_A2_E10_MF	g3142328	BLASTN	1688	1e-69	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16369	GM_M17_A2_E11_MF	g3142328	BLASTN	651	2e-22	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16370	GM_M17_A2_F01_MF	g2316016	BLASTX	239	7e-18	75	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
16371	GM_M17_A2_F05_MR	g131754	BLASTX	144	2e-09	49	PPLZ02 PROTEIN gi 99973 pir S11881 hypothetical protein (clone pPLZ2) - large-leaved lupine gi 19507 (X51767) put. pPLZ2 product (AA 1-164) [Lupinus polyphyllus]
16372	GM_M17_A2_F08_MR	g1663551	BLASTX	216	5e-17	39	(U55810) disease resistance protein homolog [Glycine max]
16373	GM_M17_A2_G02_MR	g507910	BLASTN	486	2e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
16374	GM_M17_A2_G03_MF	g2213598	BLASTX	200	1e-13	34	(AC000348) T7N9.18 [Arabidopsis thaliana]
16375	GM_M17_A2_G03_MR	g3970928	BLASTN	320	2e-09	62	Homo sapiens chromosome 19, cosmid F14319, complete sequence [Homo sapiens]
16376	GM_M17_A2_G04_MR	g1663537	BLASTX	131	2e-16	46	(U55803) disease resistance protein homolog [Glycine max]
16377	GM_M17_A2_G11_MF	g3777527	BLASTX	192	7e-13	38	(AF053008) gag-pol polyprotein [Glycine max]
16378	GM_M17_A2_H02_MR	g507910	BLASTN	486	2e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
16379	GM_M17_A2_H04_MF	g507910	BLASTN	556	2e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
16380	GM_M17_A2_H10_MF	g18695	BLASTN	449	2e-13	76	Soybean nodulin 22 gene

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16381	GM_M17_B1_A05_MR	g1297184	BLASTN	482	1e-14	66	Arabidopsis thaliana chromosome I cosmid g8261 DNA (cytosine-5-) methyltransferase, zinc finger protein 1, nucleoporin 98, poly A+ RNA export protein, plasma membrane ATPase 2, and serine/threonine protein kinase genes, complete cds.
16382	GM_M17_B1_A08_MF	g2760167	BLASTN	479	1e-14	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCO15, complete sequence [Arabidopsis thaliana]
16383	GM_M17_B1_A09_MF	g3645899	BLASTX	206	6e-24	50	(U68408) 5' end not determined experimentally [Zea mays]
16384	GM_M17_B1_B02_MF	g18559	BLASTN	814	7e-30	73	G.max gene for catalase
16385	GM_M17_B1_B03_MF	g507910	BLASTN	547	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
16386	GM_M17_B1_B04_MF	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
16387	GM_M17_B1_B08_MF	g1066857	BLASTX	228	4e-36	89	(L48995) acetyl-CoA carboxylase [Glycine max]
16388	GM_M17_B1_C12_MR	g4063760	BLASTX	366	1e-31	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16389	GM_M17_B1_E01_MF	g507910	BLASTN	419	3e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
16390	GM_M17_B1_E01_MR	g905361	BLASTX	329	3e-28	77	(U22103) gag-protease polyprotein [Glycine max]
16391	GM_M17_B1_E02_MF	g2654868	BLASTX	177	3e-20	83	(AF015301) RbohAp108 [Arabidopsis thaliana]
16392	GM_M17_B1_E02_MR	g2979574	BLASTN	465	6e-14	66	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence [Homo sapiens]
16393	GM_M17_B1_E03_MF	g4063760	BLASTX	294	7e-24	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16394	GM_M17_B1_E04_MR	g4063760	BLASTX	164	5e-10	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16395	GM_M17_B1_E09_MF	g18559	BLASTN	648	2e-22	72	G.max gene for catalase
16396	GM_M17_B1_E12_MF	g2655227	BLASTN	509	3e-16	74	Zea mays Ty3/gypsy-type retrotransposon reverse transcriptase/integrase polyprotein pseudogene, partial sequence.
16397	GM_M17_B1_F01_MF	g18559	BLASTN	952	4e-36	77	G.max gene for catalase
16398	GM_M17_B1_F04_MF	g4063760	BLASTX	237	8e-18	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16399	GM_M17_B1_F06_MF	g905361	BLASTX	183	2e-12	35	(U22103) gag-protease polyprotein [Glycine max]
16400	GM_M17_B1_F06_MR	g99922	BLASTX	298	7e-34	59	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
16401	GM_M17_B1_F07_MF	g2245104	BLASTX	199	8e-19	39	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
16402	GM_M17_B1_F07_MR	g2129618	BLASTX	226	8e-17	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16403	GM_M17_B1_F09_MR	g170606	BLASTN	438	5e-13	68	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
16404	GM_M17_B1_F11_MR	g2979597	BLASTN	388	2e-10	63	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
16405	GM_M17_B1_G12_MF	g3377813	BLASTX	224	7e-18	69	(AF076275) No definition line found [Arabidopsis thaliana]
16406	GM_M17_B2_A01_MF	g3935157	BLASTX	269	9e-29	75	(AC005106) T25N20.21 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16407	GM_M17_B2_A02_MF	g3142328	BLASTN	435	1e-12	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16408	GM_M17_B2_A04_MR	g905361	BLASTX	287	1e-23	71	(U22103) gag-protease polyprotein [Glycine max]
16409	GM_M17_B2_A06_MF	g507910	BLASTN	368	5e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16410	GM_M17_B2_A06_MR	g507910	BLASTN	398	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16411	GM_M17_B2_A08_MF	g1663537	BLASTX	333	2e-29	54	(U55803) disease resistance protein homolog [Glycine max]
16412	GM_M17_B2_A12_MF	g905361	BLASTX	498	7e-47	91	(U22103) gag-protease polyprotein [Glycine max]
16413	GM_M17_B2_A12_MR	g3142328	BLASTN	977	3e-37	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16414	GM_M17_B2_B05_MR	g18695	BLASTN	427	2e-12	71	Soybean nodulin 22 gene
16415	GM_M17_B2_B10_MF	g3319362	BLASTX	332	4e-28	52	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
16416	GM_M17_B2_B12_MR	g629693	BLASTX	139	9e-12	48	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
16417	GM_M17_B2_C05_MF	g507910	BLASTN	571	3e-19	79	Glycine max BSR-101 satellite SB92 genomic sequence.
16418	GM_M17_B2_C05_MR	g4092471	BLASTN	493	3e-15	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
16419	GM_M17_B2_C06_MR	g18559	BLASTN	1171	4e-46	81	G.max gene for catalase
16420	GM_M17_B2_C09_MR	g3378224	BLASTX	334	2e-29	73	(AJ001213) reverse transcriptase [Lycopersicon chilense]
16421	GM_M17_B2_D01_MR	g3777527	BLASTX	207	7e-17	33	(AF053008) gag-pol polyprotein [Glycine max]
16422	GM_M17_B2_D03_MF	g3142328	BLASTN	1013	6e-39	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16423	GM_M17_B2_D03_MR	g3097320	BLASTN	664	5e-23	78	Glycine max gene for Bd 30K, complete cds
16424	GM_M17_B2_D05_MF	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16425	GM_M17_B2_D05_MR	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16426	GM_M17_B2_E04_MF	g3142328	BLASTN	890	2e-33	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16427	GM_M17_B2_E04_MR	g2864621	BLASTX	163	1e-10	33	hypothetical protein [Arabidopsis thaliana]
16428	GM_M17_B2_E11_MF	g2252823	BLASTN	364	2e-09	66	Arabidopsis thaliana BAC IG005I10
16429	GM_M17_B2_E12_MF	g18559	BLASTN	527	7e-17	86	G.max gene for catalase
16430	GM_M17_B2_F07_MR	g3097320	BLASTN	1312	2e-52	81	Glycine max gene for Bd 30K, complete cds
16431	GM_M17_B2_F10_MR	g4115912	BLASTN	350	9e-09	64	Arabidopsis thaliana BAC F3H7
16432	GM_M17_B2_F12_MF	g3845074	BLASTN	406	3e-11	63	Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence
16433	GM_M17_B2_G04_MF	g4063760	BLASTX	427	4e-38	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16434	GM_M17_B2_G05_MF	g3142328	BLASTN	1777	8e-74	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16435	GM_M17_B2_G06_MR	g905361	BLASTX	684	1e-66	95	(U22103) gag-protease polyprotein [Glycine max]
16436	GM_M17_B2_G07_MF	g2995405	BLASTX	296	2e-24	56	(Y12432) polyprotein [Ananas comosus]
16437	GM_M17_B2_G10_MR	g507910	BLASTN	442	2e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
16438	GM_M17_B2_G11_MF	g507910	BLASTN	442	2e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16439	GM_M17_B2_H01_MF	g3599418	BLASTN	356	4e-09	70	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
16440	GM_M17_B2_H03_MF	g3645899	BLASTX	146	1e-13	41	(U68408) 5' end not determined experimentally [Zea mays]
16441	GM_M17_B2_H09_MR	g2995405	BLASTX	374	1e-32	57	(Y12432) polyprotein [Ananas comosus]
16442	GM_M18_A1_A02_MF	g18559	BLASTN	879	8e-33	77	G.max gene for catalase
16443	GM_M18_A1_A02_MR	g2642158	BLASTX	179	2e-12	44	(AC003000) hypothetical protein [Arabidopsis thaliana]
16444	GM_M18_A1_A05_MR	g3142328	BLASTN	661	6e-23	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16445	GM_M18_A1_A07_MF	g13774	BLASTN	363	1e-09	63	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
16446	GM_M18_A1_A09_MR	g131754	BLASTX	150	5e-10	49	PPLZ02 PROTEIN gi 99973 pir S11881 hypothetical protein (clone pPLZ2) - large-leaved lupine gi 19507 (X51767) put. pPLZ2 product (AA 1-164) [Lupinus polyphyllus]
16447	GM_M18_A1_A10_MF	g4038056	BLASTX	222	2e-16	41	(AC005897) putative transposon [Arabidopsis thaliana]
16448	GM_M18_A1_A12_MR	g1142701	BLASTN	1358	5e-55	86	Glycine max satellite STR120-A.3.
16449	GM_M18_A1_B01_MR	g3097320	BLASTN	983	2e-37	76	Glycine max gene for Bd 30K, complete cds
16450	GM_M18_A1_B05_MR	g20861	BLASTN	362	2e-09	66	P.sativum retrotransposon
16451	GM_M18_A1_B07_MR	g4006827	BLASTX	301	4e-25	52	(AC005970) subtilisin-like protease [Arabidopsis thaliana]
16452	GM_M18_A1_C02_MR	g1167523	BLASTX	109	1e-11	35	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
16453	GM_M18_A1_D01_MF	g1871182	BLASTX	189	4e-22	64	(U90439) phospholipase D isolog [Arabidopsis thaliana]
16454	GM_M18_A1_D05_MR	g507910	BLASTN	615	4e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
16455	GM_M18_A1_D10_MR	g3319351	BLASTX	415	1e-36	65	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
16456	GM_M18_A1_D11_MF	g421960	BLASTX	161	3e-11	91	small nuclear ribonucleoprotein U2B" - potato gi 169589 (M72892) spliceosomal protein [Solanum tuberosum]
16457	GM_M18_A1_D11_MR	g100226	BLASTX	243	6e-19	44	hypothetical protein - tomato gi 19275 (Z12127) protein of unknown function [Lycopersicon esculentum] gi 445619 prf 1909366A Leu zipper protein [Lycopersicon esculentum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16458	GM_M18_A1_E08_MF	g2702273	BLASTX	150	5e-17	59	(AC003033) carrot B2 protein-like [Arabidopsis thaliana]
16459	GM_M18_A1_F06_MF	g4063770	BLASTX	178	9e-12	41	(AB004906) transposase [Ipomoea purpurea]
16460	GM_M18_A1_F07_MR	g1142701	BLASTN	1235	2e-49	85	Glycine max satellite STR120-A.3.
16461	GM_M18_A1_F08_MF	g4096078	BLASTN	362	3e-09	70	Arabidopsis thaliana chromosome I BAC T5A14 genomic sequence, complete sequence [Arabidopsis thaliana]
16462	GM_M18_A1_F08_MR	g4063760	BLASTX	235	1e-18	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16463	GM_M18_A1_G08_MR	g131150	BLASTX	140	1e-15	66	PHOTOSYSTEM I P700 CHLOROPHYLL A APOPROTEIN A2 gi 81515 pir S00445 photosystem I protein A2 - spinach chloroplast gi 12271 (X04131) psaB gene product (aa 1-734) P700 chlorophyll a apoprotein [Spinacia oleracea] gi 225422 prf 1303218B gene psaB [Spinacia oleracea]
16464	GM_M18_A1_G11_MR	g1769898	BLASTX	368	2e-32	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16465	GM_M18_A1_H04_MF	g507910	BLASTN	379	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16466	GM_M18_A1_H07_MR	g2995405	BLASTX	524	6e-49	69	(Y12432) polyprotein [Ananas comosus]
16467	GM_M18_A1_H09_MR	g18559	BLASTN	709	4e-25	72	G.max gene for catalase
16468	GM_M18_A1_H10_MR	g2443320	BLASTX	305	5e-25	50	(D85597) polyprotein [Oryza australiensis]
16469	GM_M18_A1_H11_MR	g99729	BLASTX	138	2e-14	40	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
16470	GM_M18_A2_A02_MR	g131754	BLASTX	150	5e-10	49	PPLZ02 PROTEIN gi 99973 pir S11881 hypothetical protein (clone pPLZ2) - large-leaved lupine gi 19507 (X51767) put. pPLZ2 product (AA 1-164) [Lupinus polyphyllus]
16471	GM_M18_A2_B02_MR	g2462058	BLASTX	335	1e-29	48	(Y13389) reverse transcriptase [Antirrhinum majus]
16472	GM_M18_A2_B04_MF	g3097320	BLASTN	1002	2e-38	77	Glycine max gene for Bd 30K, complete cds
16473	GM_M18_A2_B09_MR	g3097320	BLASTN	579	4e-19	77	Glycine max gene for Bd 30K, complete cds
16474	GM_M18_A2_B10_MR	g905361	BLASTX	185	1e-12	30	(U22103) gag-protease polyprotein [Glycine max]
16475	GM_M18_A2_B12_MR	g4063760	BLASTX	287	4e-23	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16476	GM_M18_A2_C03_MF	g1066857	BLASTX	239	6e-35	97	(L48995) acetyl-CoA carboxylase [Glycine max]
16477	GM_M18_A2_C10_MF	g4063760	BLASTX	208	9e-15	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16478	GM_M18_A2_C10_MR	g4038056	BLASTX	202	3e-14	53	(AC005897) putative transposon [Arabidopsis thaliana]
16479	GM_M18_A2_C12_MR	g507910	BLASTN	394	3e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
16480	GM_M18_A2_D05_MR	g1666236	BLASTX	212	2e-16	34	(U76261) unknown [Hordeum vulgare]
16481	GM_M18_A2_D06_MR	g3142328	BLASTN	1736	6e-72	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16482	GM_M18_A2_D10_MR	g3688600	BLASTX	107	2e-12	84	(AB009030) beta-Amyrin Synthase [Panax ginseng]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16483	GM_M18_A2_E03_MR	g18559	BLASTN	976	3e-37	77	G.max gene for catalase
16484	GM_M18_A2_E04_MF	g3645899	BLASTX	138	3e-09	60	(U68408) 5' end not determined experimentally [Zea mays]
16485	GM_M18_A2_E04_MR	g2129618	BLASTX	256	5e-20	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16486	GM_M18_A2_E10_MR	g3548808	BLASTX	439	1e-40	61	(AC005313) unknown protein [Arabidopsis thaliana]
16487	GM_M18_A2_E11_MF	g507910	BLASTN	569	4e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
16488	GM_M18_A2_F01_MF	g4063760	BLASTX	221	3e-17	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16489	GM_M18_A2_F02_MF	g3645899	BLASTX	334	3e-28	53	(U68408) 5' end not determined experimentally [Zea mays]
16490	GM_M18_A2_F04_MF	g1944188	BLASTN	625	9e-22	71	Soybean DNA for nodulin 35, partial cds
16491	GM_M18_A2_F06_MF	g1066857	BLASTX	215	2e-26	93	(L48995) acetyl-CoA carboxylase [Glycine max]
16492	GM_M18_A2_G02_MF	g3097320	BLASTN	530	6e-17	74	Glycine max gene for Bd 30K, complete cds
16493	GM_M18_A2_G04_MR	g18559	BLASTN	727	6e-26	86	G.max gene for catalase
16494	GM_M18_A2_G05_MF	g4038056	BLASTX	294	4e-24	54	(AC005897) putative transposon [Arabidopsis thaliana]
16495	GM_M18_A2_G06_MR	g2995405	BLASTX	236	2e-31	46	(Y12432) polyprotein [Ananas comosus]
16496	GM_M18_A2_G07_MF	g1431738	BLASTN	654	9e-23	75	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
16497	GM_M18_A2_G09_MF	g1769898	BLASTX	399	5e-36	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16498	GM_M18_A2_G11_MR	g2605909	BLASTX	162	4e-14	80	(AF029257) plasma membrane H+-ATPase [Kosteletzkya virginica]
16499	GM_M18_A2_G12_MR	g3777527	BLASTX	689	7e-66	97	(AF053008) gag-pol polyprotein [Glycine max]
16500	GM_M18_A2_H02_MR	g3776579	BLASTX	156	5e-09	64	(AC005388) Strong similarity to F22O13.22 gi 3063460 myosin homolog from A. thaliana BAC gb AC003981. [Arabidopsis thaliana]
16501	GM_M18_A2_H06_MR	g1813704	BLASTX	275	7e-22	43	(U82559) aldehyde oxidase 1 homolog [Lycopersicon esculentum]
16502	GM_M18_A2_H07_MR	g2088652	BLASTX	324	2e-28	78	(AF002109) 26S proteasome regulatory subunit S12 isolog [Arabidopsis thaliana] gi 2351376 (U54561) eIF3-p47 homolog; homolog of human translation initiation factor eIF3 p47 subunit [Arabidopsis thaliana]
16503	GM_M18_A2_H11_MF	g3097320	BLASTN	703	8e-25	73	Glycine max gene for Bd 30K, complete cds
16504	GM_M18_A2_H12_MR	g3777527	BLASTX	687	1e-65	97	(AF053008) gag-pol polyprotein [Glycine max]
16505	GM_M18_B1_A02_MR	g3599418	BLASTN	988	8e-38	79	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
16506	GM_M18_B1_A03_MR	g2129618	BLASTX	198	8e-14	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16507	GM_M18_B1_A10_MF	g3445238	BLASTX	239	2e-19	63	(AL022347) putative protein [Arabidopsis thaliana] gi 3451059 gnl PID e1316746 (AL031326) putative protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16508	GM_M18_B1_A10_MR	g3913067	BLASTX	199	5e-15	55	ALTERNATIVE OXIDASE 2 PRECURSOR >gi 1946336 (U87906) alternative oxidase [Glycine max]
16509	GM_M18_B1_B01_MF	g3142328	BLASTN	534	2e-33	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16510	GM_M18_B1_B03_MR	g507910	BLASTN	557	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
16511	GM_M18_B1_B04_MF	g99729	BLASTX	212	2e-26	49	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
16512	GM_M18_B1_B05_MF	g4063760	BLASTX	166	6e-14	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16513	GM_M18_B1_B05_MR	g507910	BLASTN	702	4e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
16514	GM_M18_B1_B06_MF	g1170606	BLASTX	167	5e-21	68	ADENYLATE KINASE, CHLOROPLAST (ATP-AMP TRANSPHOSPHORYLASE) gi 629863 pir S45634 adenylate kinase (EC 2.7.4.3), chloroplast - maize gi 3114421 pdb 1ZAK A Chain A, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a) Atp:amp-Phosphotransferase, Transferase Mol_id: 1; Molecule: Adenylate Kinase; Chain: A, B; Ec: 2.7.4.3; Biological_u... gi 3114422 pdb 1ZAK B Chain B, Adenylate Kinase From Maize In Complex With The Inhibitor P1,P5-Bis(Adenosine-5'-)pentaphosphate (Ap5a) Atp:amp-Phosphotransferase, Transferase Mol_id: 1; Molecule: Adenylate Kinase; Chain: A, B; Ec: 2.7.4.3; Biological_u...
16515	GM_M18_B1_B07_MF	g2626751	BLASTN	387	1e-19	63	Triticum aestivum retrotransposon Tar1, partial sequence.
16516	GM_M18_B1_B07_MR	g3695393	BLASTX	102	1e-09	47	(AF096371) contains similarity to retroviral aspartyl proteases (Pfam: rvp.hmm, score: 11.80) [Arabidopsis thaliana]
16517	GM_M18_B1_B08_MF	g3758836	BLASTN	349	1e-08	71	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
16518	GM_M18_B1_C02_MF	g3845268	BLASTN	374	7e-10	64	Plasmodium falciparum chromosome 2, section 53 of 73 of the complete sequence
16519	GM_M18_B1_C07_MF	g343022	BLASTN	620	4e-21	80	Pea chloroplast photosystem II gene encoding the D2 and 44kd chlorophyll a-binding proteins, complete cds.
16520	GM_M18_B1_C07_MR	g3645899	BLASTX	333	4e-28	58	(U68408) 5' end not determined experimentally [Zea mays]
16521	GM_M18_B1_C08_MF	g2244749	BLASTX	211	1e-15	74	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
16522	GM_M18_B1_C09_MF	g2121303	BLASTN	473	3e-14	67	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
16523	GM_M18_B1_C12_MF	g3777527	BLASTX	507	2e-46	85	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16524	GM_M18_B1_D03_MR	g507910	BLASTN	602	1e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
16525	GM_M18_B1_D04_MF	g3142328	BLASTN	983	1e-37	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16526	GM_M18_B1_D05_MR	g18695	BLASTN	377	4e-10	68	Soybean nodulin 22 gene
16527	GM_M18_B1_D08_MR	g18559	BLASTN	923	8e-35	74	G.max gene for catalase
16528	GM_M18_B1_D10_MF	g4063756	BLASTN	441	7e-13	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
16529	GM_M18_B1_D10_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16530	GM_M18_B1_D11_MF	g3269288	BLASTX	351	3e-31	70	(AL030978) putative protein [Arabidopsis thaliana]
16531	GM_M18_B1_E02_MF	g3097320	BLASTN	582	3e-19	73	Glycine max gene for Bd 30K, complete cds
16532	GM_M18_B1_E06_MF	g2129698	BLASTX	98	4e-15	70	protein kinase ATN1 (EC 2.7.1.-) - Arabidopsis thaliana gi 1054633 (X92728) protein kinase [Arabidopsis thaliana]
16533	GM_M18_B1_E07_MR	g905361	BLASTX	226	4e-17	41	(U22103) gag-protease polyprotein [Glycine max]
16534	GM_M18_B1_E10_MR	g3252807	BLASTX	239	2e-18	60	(AC004705) hypothetical protein [Arabidopsis thaliana]
16535	GM_M18_B1_F05_MF	g4063760	BLASTX	396	8e-35	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16536	GM_M18_B1_F07_MF	g3097320	BLASTN	874	2e-32	79	Glycine max gene for Bd 30K, complete cds
16537	GM_M18_B1_G01_MR	g2522227	BLASTX	213	1e-16	53	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
16538	GM_M18_B1_G09_MF	g1346387	BLASTX	188	2e-13	87	KNOTTED-LIKE HOMEOBOX PROTEIN 3 gi 1045042 (X92392) KNAT3 homeobox protein [Arabidopsis thaliana]
16539	GM_M18_B1_G10_MF	g3097320	BLASTN	378	4e-10	72	Glycine max gene for Bd 30K, complete cds
16540	GM_M18_B1_G10_MR	g3645899	BLASTX	205	1e-23	51	(U68408) 5' end not determined experimentally [Zea mays]
16541	GM_M18_B1_G11_MF	g3947735	BLASTX	268	2e-21	49	(AJ009720) NL27 [Solanum tuberosum]
16542	GM_M18_B1_G12_MR	g4050011	BLASTN	436	1e-12	63	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
16543	GM_M18_B1_H01_MF	g1750376	BLASTX	201	5e-14	75	(U80808) ubiquitin activating enzyme [Arabidopsis thaliana] gi 3150409 (AC004165) ubiquitin activating enzyme (UBA1) [Arabidopsis thaliana]
16544	GM_M18_B1_H03_MR	g2443320	BLASTX	241	9e-20	43	(D85597) polyprotein [Oryza australiensis]
16545	GM_M18_B1_H08_MF	g4038056	BLASTX	331	4e-28	51	(AC005897) putative transposon [Arabidopsis thaliana]
16546	GM_M18_B2_A02_MF	g2129618	BLASTX	200	5e-14	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16547	GM_M18_B2_A03_MR	g1769897	BLASTX	158	2e-20	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16548	GM_M18_B2_A05_MF	g18559	BLASTN	605	7e-26	75	G.max gene for catalase
16549	GM_M18_B2_A06_MF	g507910	BLASTN	373	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16550	GM_M18_B2_A07_MR	g2129618	BLASTX	156	2e-09	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16551	GM_M18_B2_A08_MR	g2252864	BLASTX	174	6e-12	55	(AF013294) Similar to receptor kinase [Arabidopsis thaliana]
16552	GM_M18_B2_B04_MF	g4038056	BLASTX	300	9e-25	46	(AC005897) putative transposon [Arabidopsis thaliana]
16553	GM_M18_B2_B07_MR	g2522226	BLASTN	509	4e-16	65	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
16554	GM_M18_B2_B12_MF	g2213632	BLASTX	179	2e-12	53	(AC000103) F21J9.24 [Arabidopsis thaliana]
16555	GM_M18_B2_C03_MF	g2497574	BLASTX	173	2e-12	41	THYMIDINE KINASE, MITOCHONDRIAL >gi 1905969 (U77088) thymidine kinase 2 [Homo sapiens]
16556	GM_M18_B2_C06_MR	g226407	BLASTX	177	3e-11	32	retrotransposon del1-46 [Lilium henryi]
16557	GM_M18_B2_C09_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16558	GM_M18_B2_C11_MR	g3097836	BLASTN	418	8e-12	66	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
16559	GM_M18_B2_D05_MR	g2618698	BLASTX	128	1e-12	81	(AC002510) unknown protein [Arabidopsis thaliana]
16560	GM_M18_B2_D11_MF	g507910	BLASTN	430	8e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16561	GM_M18_B2_F01_MF	g3319362	BLASTX	229	4e-17	46	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
16562	GM_M18_B2_F10_MR	g3142328	BLASTN	993	5e-38	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16563	GM_M18_B2_F11_MR	g1171046	BLASTX	156	1e-10	60	METALLOTHIONEIN-LIKE PROTEIN B gi 480753 pir S37240 metallothionein-like protein - white clover gi 403329 (Z26493) metallothionein-like protein [Trifolium repens]
16564	GM_M18_B2_F12_MF	g3645899	BLASTX	235	3e-34	57	(U68408) 5' end not determined experimentally [Zea mays]
16565	GM_M18_B2_G02_MF	g18559	BLASTN	729	5e-26	77	G.max gene for catalase
16566	GM_M18_B2_G04_MR	g2522228	BLASTX	235	3e-36	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
16567	GM_M18_B2_G05_MR	g18559	BLASTN	410	1e-11	67	G.max gene for catalase
16568	GM_M18_B2_G06_MR	g3894201	BLASTX	240	1e-19	80	(AC005662) phosphatidylinositol-4-phosphate-5-kinase, 5' partial [Arabidopsis thaliana]
16569	GM_M18_B2_G12_MR	g3142328	BLASTN	1984	3e-83	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16570	GM_M18_B2_H01_MR	g3097320	BLASTN	1178	3e-46	82	Glycine max gene for Bd 30K, complete cds
16571	GM_M18_B2_H02_MF	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
16572	GM_M18_B2_H02_MR	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16573	GM_M18_B2_H04_MF	g3097320	BLASTN	445	4e-13	72	Glycine max gene for Bd 30K, complete cds
16574	GM_M18_B2_H04_MR	g507910	BLASTN	615	4e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16575	GM_M18_B2_H05_MF	g507910	BLASTN	374	3e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16576	GM_M18_B2_H07_MF	g294042	BLASTN	423	4e-12	65	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
16577	GM_M18_B2_H10_MR	g18559	BLASTN	1074	1e-41	76	G.max gene for catalase
16578	GM_M18_B2_H11_MF	g507910	BLASTN	367	6e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16579	GM_M18_B2_H11_MR	g4063760	BLASTX	393	2e-34	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16580	GM_M18_B2_H12_MR	g507910	BLASTN	395	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16581	GM_M19_A1_A07_MR	g905361	BLASTX	176	1e-11	30	(U22103) gag-protease polyprotein [Glycine max]
16582	GM_M19_A1_A12_MR	g169313	BLASTN	354	5e-09	58	Phaseolus vulgaris arcelin (arc) gene, complete cds.
16583	GM_M19_A1_B02_MF	g3445210	BLASTX	115	9e-14	57	(AC004786) putative flavonol 3-o-glucosyltransferase [Arabidopsis thaliana]
16584	GM_M19_A1_B05_MF	g4063760	BLASTX	490	8e-45	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16585	GM_M19_A1_B05_MR	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
16586	GM_M19_A1_B09_MF	g4063760	BLASTX	209	6e-16	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16587	GM_M19_A1_B10_MF	g4063760	BLASTX	275	7e-22	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16588	GM_M19_A1_B10_MR	g3046855	BLASTN	352	7e-09	71	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSL1, complete sequence [Arabidopsis thaliana]
16589	GM_M19_A1_B11_MF	g342964	BLASTN	346	2e-09	59	paramecium species 5,311 mt dna dimer: replication init. region.
16590	GM_M19_A1_C03_MR	g905361	BLASTX	193	2e-13	30	(U22103) gag-protease polyprotein [Glycine max]
16591	GM_M19_A1_C05_MF	g3777527	BLASTX	672	4e-64	97	(AF053008) gag-pol polyprotein [Glycine max]
16592	GM_M19_A1_C06_MR	g3033389	BLASTX	233	1e-17	38	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
16593	GM_M19_A1_C10_MF	g1769897	BLASTX	341	5e-33	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16594	GM_M19_A1_D02_MR	g3415116	BLASTN	367	1e-09	69	Arabidopsis thaliana villin 3 (VLN3) mRNA, complete cds
16595	GM_M19_A1_D03_MR	g1769898	BLASTX	387	1e-34	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16596	GM_M19_A1_D05_MF	g343801	BLASTN	304	5e-11	60	Yeast (S.cerevisiae) mitochondrial apocytochrome b gene, 5' flank.
16597	GM_M19_A1_D07_MF	g4063760	BLASTX	207	2e-16	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16598	GM_M19_A1_D08_MF	g531389	BLASTX	297	4e-24	50	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
16599	GM_M19_A1_D08_MR	g4038037	BLASTX	233	2e-17	35	(AC005936) hypothetical protein [Arabidopsis thaliana]
16600	GM_M19_A1_E01_MF	g505129	BLASTN	354	5e-09	61	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
16601	GM_M19_A1_E05_MR	g2522228	BLASTX	445	3e-41	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
16602	GM_M19_A1_E07_MF	g905361	BLASTX	269	1e-21	64	(U22103) gag-protease polyprotein [Glycine max]
16603	GM_M19_A1_E07_MR	g3777527	BLASTX	555	2e-51	84	(AF053008) gag-pol polyprotein [Glycine max]
16604	GM_M19_A1_E09_MR	g4063760	BLASTX	354	3e-33	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16605	GM_M19_A1_E12_MF	g2522228	BLASTX	190	1e-13	53	(AB007466) reverse transcriptase-like protein [Vicia faba]
16606	GM_M19_A1_E12_MR	g2244802	BLASTX	389	7e-34	50	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
16607	GM_M19_A1_F05_MF	g992916	BLASTN	384	3e-10	71	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
16608	GM_M19_A1_F06_MF	g3097320	BLASTN	1084	5e-42	83	Glycine max gene for Bd 30K, complete cds
16609	GM_M19_A1_F08_MF	g3810596	BLASTX	209	5e-15	32	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
16610	GM_M19_A1_F11_MF	g3319345	BLASTX	159	1e-09	33	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
16611	GM_M19_A1_G04_MF	g3297823	BLASTX	182	4e-12	53	(AL031032) putative protein [Arabidopsis thaliana]
16612	GM_M19_A1_G05_MR	g3319351	BLASTX	305	5e-25	42	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
16613	GM_M19_A1_G06_MR	g1142701	BLASTN	263	9e-20	76	Glycine max satellite STR120-A.3.
16614	GM_M19_A1_G09_MF	g4063760	BLASTX	252	2e-19	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16615	GM_M19_A1_G11_MR	g3142328	BLASTN	1262	3e-50	83	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16616	GM_M19_A1_H01_MR	g3319351	BLASTX	311	1e-25	43	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
16617	GM_M19_A1_H04_MF	g18683	BLASTN	393	8e-11	69	G.max N-20t gene
16618	GM_M19_A1_H04_MR	g100484	BLASTX	386	3e-34	55	hypothetical protein - garden snapdragon
16619	GM_M19_A1_H05_MR	g4063770	BLASTX	230	9e-29	54	(AB004906) transposase [Ipomoea purpurea]
16620	GM_M19_A1_H06_MF	g3894387	BLASTX	216	9e-16	46	(AF053995) Hcr2-0B [Lycopersicon esculentum]
16621	GM_M19_A1_H07_MF	g3283026	BLASTX	109	9e-19	38	putative transposase [Arabidopsis thaliana]
16622	GM_M19_A1_H10_MF	g2462056	BLASTX	285	3e-24	49	(Y13388) reverse transcriptase [Antirrhinum majus]
16623	GM_M19_A1_H10_MR	g18768	BLASTN	509	1e-16	66	Soybean Tgm6 transposable element 3' end
16624	GM_M19_A1_H11_MR	g3097320	BLASTN	469	3e-14	71	Glycine max gene for Bd 30K, complete cds
16625	GM_M19_A2_A03_MF	g170080	BLASTN	424	3e-12	70	Soybean seed lectin gene transposable element tgm1.
16626	GM_M19_A2_A07_MR	g2995405	BLASTX	302	5e-25	44	(Y12432) polyprotein [Ananas comosus]
16627	GM_M19_A2_A08_MR	g2995405	BLASTX	297	2e-24	45	(Y12432) polyprotein [Ananas comosus]
16628	GM_M19_A2_A11_MF	g4063760	BLASTX	376	1e-32	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16629	GM_M19_A2_B02_MF	g1707020	BLASTX	185	9e-15	36	(U78721) hypothetical protein [Arabidopsis thaliana]
16630	GM_M19_A2_B07_MF	g1931642	BLASTX	397	9e-36	61	(U95973) Ser/Thr protein kinase isolog [Arabidopsis thaliana]
16631	GM_M19_A2_B07_MR	g2501850	BLASTX	173	1e-11	91	(AF012823) GDP dissociation inhibitor [Nicotiana tabacum]
16632	GM_M19_A2_C01_MF	g3860247	BLASTX	249	3e-29	95	(AC005824) unknown protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16633	GM_M19_A2_C01_MR	g2586082	BLASTX	259	9e-33	57	(U72725) retrofit [Oryza longistaminata]
16634	GM_M19_A2_C08_MR	g18559	BLASTN	939	2e-35	74	G.max gene for catalase
16635	GM_M19_A2_D03_MF	g2522226	BLASTN	447	3e-13	62	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
16636	GM_M19_A2_D04_MR	g2522228	BLASTX	492	3e-46	63	(AB007466) reverse transcriptase-like protein [Vicia faba]
16637	GM_M19_A2_D05_MR	g3033389	BLASTX	225	1e-16	36	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
16638	GM_M19_A2_D06_MF	g2264320	BLASTN	496	2e-15	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
16639	GM_M19_A2_D07_MF	g18559	BLASTN	329	3e-10	70	G.max gene for catalase
16640	GM_M19_A2_D12_MF	g2114040	BLASTN	372	2e-10	69	Vigna vexillata DNA for TY1-copia-like retrotransposable element
16641	GM_M19_A2_E06_MF	g507910	BLASTN	390	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16642	GM_M19_A2_E07_MF	g3142328	BLASTN	882	5e-33	83	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16643	GM_M19_A2_F02_MR	g18559	BLASTN	1030	1e-39	75	G.max gene for catalase
16644	GM_M19_A2_F03_MF	g2764526	BLASTN	375	6e-10	65	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
16645	GM_M19_A2_F03_MR	g100484	BLASTX	264	4e-21	49	hypothetical protein - garden snapdragon
16646	GM_M19_A2_F04_MF	g3449326	BLASTN	429	2e-12	64	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K19M22, complete sequence [Arabidopsis thaliana]
16647	GM_M19_A2_F05_MF	g2522228	BLASTX	458	1e-42	69	(AB007466) reverse transcriptase-like protein [Vicia faba]
16648	GM_M19_A2_F06_MF	g1431738	BLASTN	564	1e-18	79	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
16649	GM_M19_A2_F10_MF	g2462828	BLASTX	358	9e-31	57	(AF000657) hypothetical protein [Arabidopsis thaliana]
16650	GM_M19_A2_F11_MF	g507910	BLASTN	365	7e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
16651	GM_M19_A2_F11_MR	g507910	BLASTN	380	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16652	GM_M19_A2_G01_MR	g3319351	BLASTX	328	2e-27	48	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
16653	GM_M19_A2_G03_MF	g507910	BLASTN	408	8e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16654	GM_M19_A2_G03_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
16655	GM_M19_A2_G04_MR	g1769898	BLASTX	125	9e-10	41	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16656	GM_M19_A2_G06_MF	g2317901	BLASTX	141	5e-21	72	(U89959) Similar to vesicle transport protein, PIR Accession Number A55931 [Arabidopsis thaliana]
16657	GM_M19_A2_G11_MR	g3777527	BLASTX	253	3e-23	47	(AF053008) gag-pol polyprotein [Glycine max]
16658	GM_M19_A2_H02_MF	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16659	GM_M19_A2_H02_MR	g507910	BLASTN	354	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16660	GM_M19_A2_H05_MF	g1142703	BLASTN	301	1e-17	77	Glycine max satellite STR120-B.1.
16661	GM_M19_B1_A03_MR	g508826	BLASTN	470	3e-14	67	Drosophila melanogaster Oregon-R mitochondrial A+T region.
16662	GM_M19_B1_A10_MF	g4115365	BLASTX	215	6e-25	48	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
16663	GM_M19_B1_B01_MR	g3142328	BLASTN	1614	2e-66	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16664	GM_M19_B1_B04_MF	g1167523	BLASTX	257	2e-21	43	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
16665	GM_M19_B1_B09_MF	g1769898	BLASTX	186	8e-13	52	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16666	GM_M19_B1_B12_MF	g505129	BLASTN	357	3e-09	61	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
16667	GM_M19_B1_C01_MF	g100226	BLASTX	173	2e-25	79	hypothetical protein - tomato gi 19275 (Z12127) protein of unknown function [Lycopersicon esculentum] gi 445619 prf 1909366A Leu zipper protein [Lycopersicon esculentum]
16668	GM_M19_B1_C08_MF	g4063770	BLASTX	179	7e-12	39	(AB004906) transposase [Ipomoea purpurea]
16669	GM_M19_B1_C09_MR	g1769898	BLASTX	372	5e-33	56	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16670	GM_M19_B1_C12_MF	g3688193	BLASTX	112	5e-11	67	(AJ010091) MAP3K alpha 1 protein kinase [Brassica napus]
16671	GM_M19_B1_D01_MF	g507910	BLASTN	555	2e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
16672	GM_M19_B1_D04_MR	g3894387	BLASTX	240	3e-18	40	(AF053995) Hcr2-0B [Lycopersicon esculentum]
16673	GM_M19_B1_D06_MF	g3005576	BLASTX	167	6e-11	57	(AF047718) putative high affinity nitrate transporter; GmNRT2 [Glycine max]
16674	GM_M19_B1_D07_MR	g2995405	BLASTX	286	3e-23	53	(Y12432) polyprotein [Ananas comosus]
16675	GM_M19_B1_D10_MR	g3142328	BLASTN	1960	3e-82	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16676	GM_M19_B1_E01_MR	g3097320	BLASTN	458	1e-13	71	Glycine max gene for Bd 30K, complete cds
16677	GM_M19_B1_E02_MR	g1490417	BLASTX	405	6e-36	57	(U45025) 89B helicase [Drosophila melanogaster]
16678	GM_M19_B1_E03_MR	g3142328	BLASTN	498	1e-15	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16679	GM_M19_B1_E05_MR	g4063756	BLASTN	519	2e-16	62	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
16680	GM_M19_B1_E07_MR	g170605	BLASTN	402	2e-11	60	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
16681	GM_M19_B1_E08_MR	g475598	BLASTX	444	8e-44	88	(U08382) BiP isoform C [Glycine max]
16682	GM_M19_B1_E10_MR	g4063760	BLASTX	289	2e-23	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16683	GM_M19_B1_E11_MR	g3142328	BLASTN	1627	6e-67	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16684	GM_M19_B1_F03_MR	g2980806	BLASTX	205	3e-21	62	(AL022197) putative protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16685	GM_M19_B1_F04_MF	g1769899	BLASTX	320	5e-28	74	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16686	GM_M19_B1_F04_MR	g2827715	BLASTX	290	1e-23	44	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
16687	GM_M19_B1_F05_MR	g2708743	BLASTX	269	4e-21	41	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
16688	GM_M19_B1_F07_MR	g3645899	BLASTX	315	3e-26	53	(U68408) 5' end not determined experimentally [Zea mays]
16689	GM_M19_B1_F11_MR	g1142703	BLASTN	283	2e-15	77	Glycine max satellite STR120-B.1.
16690	GM_M19_B1_G04_MF	g3386533	BLASTN	1555	8e-64	97	Glycine max mariner element Soymar1 transposase gene, complete cds
16691	GM_M19_B1_G07_MR	g1769897	BLASTX	189	2e-26	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16692	GM_M19_B1_G09_MF	g507910	BLASTN	345	6e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16693	GM_M19_B1_H03_MR	g2979597	BLASTN	431	2e-12	61	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
16694	GM_M19_B1_H05_MR	g3319351	BLASTX	297	4e-24	43	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
16695	GM_M19_B1_H10_MR	g18559	BLASTN	613	5e-23	73	G.max gene for catalase
16696	GM_M19_B1_H12_MF	g3329366	BLASTX	378	6e-34	56	(AF031243) nodule-specific protein Nlj70 [Lotus japonicus]
16697	GM_M19_B2_A02_MR	g3930515	BLASTX	89	9e-09	40	(AF059674) putative gag protein [Nicotiana tabacum]
16698	GM_M19_B2_A03_MF	g3135269	BLASTX	131	3e-11	55	(AC003058) unknown protein [Arabidopsis thaliana]
16699	GM_M19_B2_A03_MR	g3097836	BLASTN	618	7e-21	68	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
16700	GM_M19_B2_A04_MR	g1769898	BLASTX	250	6e-26	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16701	GM_M19_B2_A05_MR	g3097320	BLASTN	437	9e-13	70	Glycine max gene for Bd 30K, complete cds
16702	GM_M19_B2_A06_MR	g170606	BLASTN	770	2e-28	69	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
16703	GM_M19_B2_A08_MF	g1769898	BLASTX	300	4e-25	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16704	GM_M19_B2_A08_MR	g905361	BLASTX	197	6e-14	32	(U22103) gag-protease polyprotein [Glycine max]
16705	GM_M19_B2_A10_MR	g2104945	BLASTN	520	1e-16	64	Glycine max copia-like retrotransposon Tgmr, complete sequence
16706	GM_M19_B2_B02_MF	g99922	BLASTX	489	6e-46	74	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
16707	GM_M19_B2_B05_MF	g4063760	BLASTX	238	6e-18	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16708	GM_M19_B2_B05_MR	g2129618	BLASTX	206	1e-14	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16709	GM_M19_B2_B06_MF	g507910	BLASTN	385	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16710	GM_M19_B2_B06_MR	g507910	BLASTN	358	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16711	GM_M19_B2_B07_MF	g4063760	BLASTX	217	1e-15	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16712	GM_M19_B2_B12_MR	g3786000	BLASTX	178	5e-12	47	(AC005499) hypothetical protein [Arabidopsis thaliana]
16713	GM_M19_B2_C01_MR	g18559	BLASTN	1011	8e-39	75	G.max gene for catalase
16714	GM_M19_B2_C02_MF	g99922	BLASTX	327	3e-42	83	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
16715	GM_M19_B2_C02_MR	g2160694	BLASTX	202	1e-14	75	(U73528) B' regulatory subunit of PP2A [Arabidopsis thaliana]
16716	GM_M19_B2_C03_MR	g2996647	BLASTN	446	4e-13	62	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
16717	GM_M19_B2_C04_MF	g2129618	BLASTX	232	2e-17	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16718	GM_M19_B2_C11_MF	g2463654	BLASTN	476	2e-14	66	Petunia vein clearing virus, complete genome
16719	GM_M19_B2_D01_MR	g2921211	BLASTX	158	3e-17	93	(AF026149) beta-ketoacyl-ACP synthase II [Perilla frutescens]
16720	GM_M19_B2_D02_MR	g18559	BLASTN	1024	2e-39	71	G.max gene for catalase
16721	GM_M19_B2_D04_MR	g3193292	BLASTX	111	2e-17	87	(AF069298) similar to ATPases associated with various cellular activites (Pfam: AAA.hmm, score: 230.91) [Arabidopsis thaliana]
16722	GM_M19_B2_D05_MR	g3513747	BLASTX	380	7e-33	53	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
16723	GM_M19_B2_D12_MR	g507910	BLASTN	638	3e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16724	GM_M19_B2_E02_MF	g2522230	BLASTX	268	1e-22	41	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
16725	GM_M19_B2_E02_MR	g18559	BLASTN	755	3e-27	74	G.max gene for catalase
16726	GM_M19_B2_E03_MF	g13096	BLASTN	354	5e-09	60	Leishmania tarentolae maxicircle DNA fragment
16727	GM_M19_B2_E05_MR	g4038056	BLASTX	235	2e-33	54	(AC005897) putative transposon [Arabidopsis thaliana]
16728	GM_M19_B2_E08_MF	g2995405	BLASTX	199	2e-26	59	(Y12432) polyprotein [Ananas comosus]
16729	GM_M19_B2_E09_MR	g4063760	BLASTX	302	3e-26	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16730	GM_M19_B2_E10_MF	g3777527	BLASTX	184	5e-13	75	(AF053008) gag-pol polyprotein [Glycine max]
16731	GM_M19_B2_E12_MF	g4092471	BLASTN	428	3e-12	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
16732	GM_M19_B2_F06_MR	g2529665	BLASTX	179	2e-15	62	(AC002535) putative ribosomal protein L7A [Arabidopsis thaliana]
16733	GM_M19_B2_G01_MF	g3097320	BLASTN	1217	4e-48	81	Glycine max gene for Bd 30K, complete cds
16734	GM_M19_B2_G02_MF	g2995405	BLASTX	459	7e-42	68	(Y12432) polyprotein [Ananas comosus]
16735	GM_M19_B2_G04_MF	g507910	BLASTN	380	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16736	GM_M19_B2_G04_MR	g507910	BLASTN	360	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16737	GM_M19_B2_G11_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16738	GM_M19_B2_H01_MR	g1755162	BLASTX	323	2e-28	57	(U75192) germin-like protein [Arabidopsis thaliana]
16739	GM_M19_B2_H02_MF	g507910	BLASTN	379	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16740	GM_M19_B2_H02_MR	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16741	GM_M19_B2_H03_MR	g4063760	BLASTX	263	1e-20	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16742	GM_M19_B2_H06_MF	g3695395	BLASTX	235	5e-18	41	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
16743	GM_M19_B2_H10_MR	g3337395	BLASTN	420	6e-12	60	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
16744	GM_M19_B2_H11_MR	g3449334	BLASTN	318	3e-11	73	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]
16745	GM_M19_B2_H12_MF	g4063760	BLASTX	229	6e-17	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16746	GM_M20_A1_A02_MF	g507910	BLASTN	633	5e-22	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16747	GM_M20_A1_A02_MR	g507910	BLASTN	597	2e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
16748	GM_M20_A1_A06_MF	g2804155	BLASTN	399	6e-11	66	Human DNA sequence from PAC 426I6 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat
16749	GM_M20_A1_A10_MF	g4063760	BLASTX	264	9e-21	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16750	GM_M20_A1_B04_MF	g1666236	BLASTX	187	1e-13	30	(U76261) unknown [Hordeum vulgare]
16751	GM_M20_A1_B05_MF	g2522228	BLASTX	488	8e-46	72	(AB007466) reverse transcriptase-like protein [Vicia faba]
16752	GM_M20_A1_B11_MF	g3142328	BLASTN	472	2e-14	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16753	GM_M20_A1_B11_MR	g3777527	BLASTX	483	2e-44	94	(AF053008) gag-pol polyprotein [Glycine max]
16754	GM_M20_A1_C05_MF	g507910	BLASTN	414	4e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16755	GM_M20_A1_C06_MF	g3319351	BLASTX	308	3e-25	57	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
16756	GM_M20_A1_C08_MF	g2842493	BLASTX	167	7e-16	86	(AL021749) predicted protein [Arabidopsis thaliana]
16757	GM_M20_A1_C08_MR	g2522228	BLASTX	423	6e-39	55	(AB007466) reverse transcriptase-like protein [Vicia faba]
16758	GM_M20_A1_D04_MF	g13096	BLASTN	394	7e-11	61	Leishmania tarentolae maxicircle DNA fragment
16759	GM_M20_A1_D06_MF	g507910	BLASTN	451	9e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16760	GM_M20_A1_D07_MR	g505129	BLASTN	351	7e-09	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
16761	GM_M20_A1_D08_MF	g2673914	BLASTX	186	6e-13	46	(AC002561) hypothetical protein [Arabidopsis thaliana]
16762	GM_M20_A1_D09_MF	g3142328	BLASTN	803	2e-29	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16763	GM_M20_A1_D11_MF	g3033389	BLASTX	189	8e-13	36	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
16764	GM_M20_A1_D11_MR	g3894387	BLASTX	206	1e-14	40	(AF053995) Hcr2-0B [Lycopersicon esculentum]
16765	GM_M20_A1_E06_MF	g1171583	BLASTN	243	6e-09	68	P.falciparum complete gene map of plastid-like DNA (IR-A)

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16766	GM_M20_A1_E10_MR	g18559	BLASTN	361	3e-09	67	G.max gene for catalase
16767	GM_M20_A1_E11_MR	g124226	BLASTX	171	9e-15	100	INITIATION FACTOR 5A-2 (EIF-5A) (EIF-4D) gi 100278 pir S21059 translation initiation factor eIF-5A.2 - curled-leaved tobacco gi 19702 (X63542) eukaryotic initiation factor 5A (2) [Nicotiana plumbaginifolia]
16768	GM_M20_A1_E12_MR	g4063760	BLASTX	437	4e-39	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16769	GM_M20_A1_F07_MR	g3097320	BLASTN	560	3e-18	74	Glycine max gene for Bd 30K, complete cds
16770	GM_M20_A1_F09_MF	g1769897	BLASTX	219	2e-16	40	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16771	GM_M20_A1_F10_MF	g3097320	BLASTN	975	4e-37	79	Glycine max gene for Bd 30K, complete cds
16772	GM_M20_A1_G05_MF	g507910	BLASTN	397	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16773	GM_M20_A1_G07_MR	g1709919	BLASTX	564	5e-54	78	AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) (GPAT) gi 439105 (L23834) glutamine phosphoribosylpyrophosphate amidotransferase [Vigna aconitifolia]
16774	GM_M20_A1_G08_MR	g2133292	BLASTX	167	3e-10	29	pol polyprotein homolog - fungus (Fusarium oxysporum) retrotransposon skippy gi 510697 (L34658) pol polyprotein [Fusarium oxysporum]
16775	GM_M20_A1_H04_MR	g3822225	BLASTX	131	1e-16	61	(AF079183) RING-H2 finger protein RHG1a [Arabidopsis thaliana]
16776	GM_M20_A1_H05_MR	g3645899	BLASTX	195	2e-13	43	(U68408) 5' end not determined experimentally [Zea mays]
16777	GM_M20_A1_H07_MF	g100484	BLASTX	313	3e-26	51	hypothetical protein - garden snapdragon
16778	GM_M20_A1_H09_MF	g18559	BLASTN	954	3e-36	77	G.max gene for catalase
16779	GM_M20_A1_H09_MR	g3777527	BLASTX	698	8e-67	94	(AF053008) gag-pol polyprotein [Glycine max]
16780	GM_M20_A1_H10_MR	g3142328	BLASTN	577	4e-19	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16781	GM_M20_A1_H11_MR	g3924609	BLASTX	175	4e-11	47	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
16782	GM_M20_A2_A01_MR	g2129618	BLASTX	250	2e-19	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16783	GM_M20_A2_A02_MF	g3810596	BLASTX	151	8e-09	29	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
16784	GM_M20_A2_A03_MR	g3142379	BLASTX	228	1e-17	58	(AF053008) envelope-like [Glycine max]
16785	GM_M20_A2_A06_MF	g3142328	BLASTN	984	4e-62	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16786	GM_M20_A2_A09_MF	g3097320	BLASTN	1008	1e-38	81	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16787	GM_M20_A2_A10_MF	g2462134	BLASTX	170	2e-13	37	(Y13368) reverse transcriptase [Beta vulgaris]
16788	GM_M20_A2_A12_MF	g3892061	BLASTX	150	5e-09	27	(AC002330) putative reverse transcriptase [Arabidopsis thaliana]
16789	GM_M20_A2_B01_MR	g3687234	BLASTX	185	3e-12	52	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
16790	GM_M20_A2_B04_MF	g4038056	BLASTX	254	1e-29	49	(AC005897) putative transposon [Arabidopsis thaliana]
16791	GM_M20_A2_B06_MR	g3777527	BLASTX	191	4e-17	42	(AF053008) gag-pol polyprotein [Glycine max]
16792	GM_M20_A2_B07_MF	g3142328	BLASTN	359	3e-09	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16793	GM_M20_A2_B10_MF	g2129618	BLASTX	216	1e-15	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16794	GM_M20_A2_B12_MF	g2245104	BLASTX	234	2e-17	37	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
16795	GM_M20_A2_C08_MF	g2253569	BLASTN	379	6e-11	67	Plasmodium falciparum microsatellite TA99 sequence
16796	GM_M20_A2_C09_MF	g18559	BLASTN	330	2e-11	71	G.max gene for catalase
16797	GM_M20_A2_C10_MR	g3063456	BLASTX	152	3e-09	41	(AC003981) F22O13.18 [Arabidopsis thaliana]
16798	GM_M20_A2_C12_MF	g3250687	BLASTX	264	4e-22	46	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
16799	GM_M20_A2_C12_MR	g2979540	BLASTN	564	2e-18	67	Arabidopsis thaliana chromosome II BAC F17K2 genomic sequence, complete sequence [Arabidopsis thaliana]
16800	GM_M20_A2_D01_MR	g155854	BLASTN	447	1e-13	61	Babesia bigemina antigen (Bbg 1.1) mRNA, 3' end.
16801	GM_M20_A2_D04_MR	g2996647	BLASTN	476	2e-14	65	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
16802	GM_M20_A2_D05_MF	g3063438	BLASTN	367	1e-09	69	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]
16803	GM_M20_A2_D07_MR	g2996647	BLASTN	462	8e-14	63	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
16804	GM_M20_A2_E02_MF	g3097320	BLASTN	648	3e-22	74	Glycine max gene for Bd 30K, complete cds
16805	GM_M20_A2_E02_MR	g3777527	BLASTX	151	5e-11	47	(AF053008) gag-pol polyprotein [Glycine max]
16806	GM_M20_A2_E03_MF	g18559	BLASTN	428	1e-17	69	G.max gene for catalase
16807	GM_M20_A2_F02_MF	g496384	BLASTN	483	5e-15	75	Tobacco mRNA for protein kinase NPK5, complete cds
16808	GM_M20_A2_F06_MR	g3915613	BLASTX	106	9e-09	38	PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B)
16809	GM_M20_A2_F11_MF	g2995405	BLASTX	416	3e-37	60	(Y12432) polyprotein [Ananas comosus]
16810	GM_M20_A2_F11_MR	g2995405	BLASTX	242	1e-18	45	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16811	GM_M20_A2_G01_MF	g478809	BLASTX	270	3e-22	40	protein kinase 6 (EC 2.7.1.-) - soybean gi 170047 (M67449) protein kinase [Glycine max] gi 444789 prf 1908223A protein kinase [Glycine max]
16812	GM_M20_A2_G01_MR	g3779024	BLASTX	223	9e-29	61	(AC005171) unknown protein [Arabidopsis thaliana]
16813	GM_M20_A2_G02_MR	g3426334	BLASTN	517	2e-16	64	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
16814	GM_M20_A2_G09_MR	g3540206	BLASTX	405	1e-35	52	(AC004260) Hypothetical protein [Arabidopsis thaliana]
16815	GM_M20_A2_G10_MR	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16816	GM_M20_A2_H03_MR	g1771194	BLASTN	417	8e-12	77	L.japonicus gene encoding RING finger protein
16817	GM_M20_A2_H04_MF	g3142328	BLASTN	1853	3e-77	97	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16818	GM_M20_A2_H04_MR	g3845281	BLASTN	405	3e-11	64	Plasmodium falciparum chromosome 2, section 56 of 73 of the complete sequence
16819	GM_M20_A2_H09_MR	g3702323	BLASTX	604	4e-58	86	(AC005397) unknown protein [Arabidopsis thaliana]
16820	GM_M20_A2_H10_MF	g1769898	BLASTX	231	1e-17	39	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16821	GM_M20_A2_H11_MR	g1666236	BLASTX	177	7e-16	28	(U76261) unknown [Hordeum vulgare]
16822	GM_M20_A2_H12_MF	g3249105	BLASTX	237	1e-18	62	(AC003114) Contains similarity to protein phosphatase 2C (ABI1) gb X78886 from A. thaliana. [Arabidopsis thaliana]
16823	GM_M20_B1_A02_MR	g3097320	BLASTN	1275	1e-50	79	Glycine max gene for Bd 30K, complete cds
16824	GM_M20_B1_A11_MF	g507910	BLASTN	386	8e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
16825	GM_M20_B1_A11_MR	g507910	BLASTN	406	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16826	GM_M20_B1_A12_MR	g1129068	BLASTX	176	2e-24	91	malate dehydrogenase; EC 1.1.1.40; malic enzyme
16827	GM_M20_B1_B04_MF	g3063438	BLASTN	367	1e-09	69	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]
16828	GM_M20_B1_B07_MF	g507910	BLASTN	405	1e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
16829	GM_M20_B1_B07_MR	g507910	BLASTN	362	9e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
16830	GM_M20_B1_C03_MF	g3319362	BLASTX	235	1e-17	40	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
16831	GM_M20_B1_C05_MF	g1769899	BLASTX	153	3e-10	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16832	GM_M20_B1_C06_MR	g13773	BLASTN	415	2e-12	64	Torulopsis glabrata mitochondrial genes for tRNAs -Tyr, -Asn, -Ala, -Ile -Trp (from Var1-LrRNA intergenic region) >gi 343959 gb M11906 YSLMTIG09 Yeast (T.glabrata) mitochondrial DNA between var1 and L rRNA genes.
16833	GM_M20_B1_C07_MR	g3935164	BLASTX	94	5e-09	36	(AC004557) F17L21.7 [Arabidopsis thaliana]
16834	GM_M20_B1_C08_MF	g507910	BLASTN	427	1e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16835	GM_M20_B1_C08_MR	g4063760	BLASTX	142	3e-10	33	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16836	GM_M20_B1_C10_MF	g1769899	BLASTX	192	2e-14	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16837	GM_M20_B1_C10_MR	g2462134	BLASTX	270	4e-22	38	(Y13368) reverse transcriptase [Beta vulgaris]
16838	GM_M20_B1_D03_MR	g1514643	BLASTX	145	8e-16	58	(Z70524) PDR5-like ABC transporter [Spirodela polyrrhiza]
16839	GM_M20_B1_D04_MF	g12212	BLASTN	1209	2e-52	93	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
16840	GM_M20_B1_D04_MR	g2734643	BLASTX	369	4e-52	66	(U48738) ribosomal protein subunit 2 [Agalinis sp.]
16841	GM_M20_B1_D10_MF	g1167523	BLASTX	157	3e-09	33	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
16842	GM_M20_B1_D10_MR	g2443320	BLASTX	211	5e-15	38	(D85597) polyprotein [Oryza australiensis]
16843	GM_M20_B1_E03_MR	g3142328	BLASTN	1293	1e-51	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16844	GM_M20_B1_E04_MR	g3142328	BLASTN	1268	2e-50	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16845	GM_M20_B1_E07_MF	g992916	BLASTN	427	1e-20	76	Glycine max (clones 513 and 1221) acetyl coA carboxylase (ACCase-A) gene, complete cds.
16846	GM_M20_B1_E08_MF	g3097320	BLASTN	732	4e-26	81	Glycine max gene for Bd 30K, complete cds
16847	GM_M20_B1_E09_MF	g2760325	BLASTX	220	9e-17	66	(AC002130) F1N21.10 [Arabidopsis thaliana]
16848	GM_M20_B1_E10_MF	g18559	BLASTN	381	3e-10	80	G.max gene for catalase
16849	GM_M20_B1_E11_MR	g2995405	BLASTX	226	8e-17	52	(Y12432) polyprotein [Ananas comosus]
16850	GM_M20_B1_E12_MF	g2281101	BLASTX	233	8e-18	51	(AC002333) LecRK1 protein kinase isolog [Arabidopsis thaliana]
16851	GM_M20_B1_F01_MR	g18559	BLASTN	951	4e-36	73	G.max gene for catalase
16852	GM_M20_B1_F02_MF	g3097320	BLASTN	430	2e-12	71	Glycine max gene for Bd 30K, complete cds
16853	GM_M20_B1_F02_MR	g4038056	BLASTX	310	8e-26	50	(AC005897) putative transposon [Arabidopsis thaliana]
16854	GM_M20_B1_F03_MF	g3063438	BLASTN	364	2e-09	72	Complete sequence of Arabidopsis F22O13, complete sequence [Arabidopsis thaliana]
16855	GM_M20_B1_F04_MF	g18559	BLASTN	623	2e-31	81	G.max gene for catalase
16856	GM_M20_B1_F07_MR	g3142328	BLASTN	580	3e-19	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16857	GM_M20_B1_F10_MF	g603890	BLASTX	183	1e-13	57	(Z46949) pathogenesis-related protein PR-6 type [Sambucus nigra]
16858	GM_M20_B1_F12_MF	g81857	BLASTX	111	4e-17	64	IgE-dependent histamine-releasing factor homolog - alfalfa (fragment) gi 19658 (X63872) translationally controlled tumor protein [Medicago sativa]
16859	GM_M20_B1_G03_MR	g160698	BLASTN	363	3e-10	58	P.berghei telomeric repeat region subfragment a DNA.
16860	GM_M20_B1_G05_MR	g3097320	BLASTN	386	2e-10	61	Glycine max gene for Bd 30K, complete cds
16861	GM_M20_B1_H03_MF	g3287695	BLASTX	191	5e-13	45	(AC003979) Similar to hypothetical protein C34B7.2 gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis thaliana]

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16862	GM_M20_B1_H04_MF	g3377834	BLASTX	150	7e-09	30	(AF075598) No definition line found [Arabidopsis thaliana]
16863	GM_M20_B1_H07_MR	g100484	BLASTX	171	4e-11	40	hypothetical protein - garden snapdragon
16864	GM_M20_B1_H11_MR	g3645899	BLASTX	199	8e-18	42	(U68408) 5' end not determined experimentally [Zea mays]
16865	GM_M20_B2_A04_MF	g2522228	BLASTX	419	2e-38	74	(AB007466) reverse transcriptase-like protein [Vicia faba]
16866	GM_M20_B2_A08_MR	g3075392	BLASTX	227	9e-18	69	(AC004484) putative steroid dehydrogenase [Arabidopsis thaliana]
16867	GM_M20_B2_A11_MR	g2098713	BLASTX	336	2e-29	67	(U82977) pectinesterase [Citrus sinensis]
16868	GM_M20_B2_A12_MF	g2879886	BLASTN	346	9e-09	67	Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes
16869	GM_M20_B2_B02_MF	g313723	BLASTN	372	6e-10	79	P.sativum hemC mRNA for hydroxymethylbilane synthase
16870	GM_M20_B2_B02_MR	g2970554	BLASTN	613	1e-20	71	Glycine max aspartokinase-homoserine dehydrogenase (AK-HSDH) gene, partial cds
16871	GM_M20_B2_B03_MF	g3056587	BLASTX	147	8e-10	70	(AC004255) T1F9.8 [Arabidopsis thaliana]
16872	GM_M20_B2_B05_MR	g2995405	BLASTX	387	4e-34	53	(Y12432) polyprotein [Ananas comosus]
16873	GM_M20_B2_B06_MR	g2995405	BLASTX	235	1e-24	45	(Y12432) polyprotein [Ananas comosus]
16874	GM_M20_B2_B09_MR	g18559	BLASTN	352	6e-09	67	G.max gene for catalase
16875	GM_M20_B2_B10_MF	g1666096	BLASTX	284	3e-24	70	(Y09113) dioxygenase [Marah macrocarpa]
16876	GM_M20_B2_B12_MF	g22490	BLASTX	189	4e-14	39	(X01380) ORF1 [Zea mays]
16877	GM_M20_B2_C05_MF	g3142328	BLASTN	370	1e-09	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16878	GM_M20_B2_C10_MR	g2462134	BLASTX	130	3e-14	53	(Y13368) reverse transcriptase [Beta vulgaris]
16879	GM_M20_B2_C12_MR	g505129	BLASTN	395	7e-11	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
16880	GM_M20_B2_D01_MF	g2760325	BLASTX	210	7e-18	78	(AC002130) F1N21.10 [Arabidopsis thaliana]
16881	GM_M20_B2_D02_MF	g1142703	BLASTN	276	2e-14	76	Glycine max satellite STR120-B.1.
16882	GM_M20_B2_D02_MR	g2522230	BLASTX	285	3e-24	43	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
16883	GM_M20_B2_D03_MF	g4092470	BLASTN	365	2e-09	60	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
16884	GM_M20_B2_D04_MR	g1360613	BLASTX	161	5e-10	34	(X97304) ORF V gene product [Strawberry vein banding virus]
16885	GM_M20_B2_D06_MF	g99755	BLASTX	300	3e-27	50	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
16886	GM_M20_B2_D11_MR	g2264313	BLASTN	417	8e-12	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence [Arabidopsis thaliana]
16887	GM_M20_B2_E09_MR	g4063760	BLASTX	488	1e-44	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16888	GM_M20_B2_E10_MR	g100484	BLASTX	330	4e-28	50	hypothetical protein - garden snapdragon
16889	GM_M20_B2_E12_MR	g3461840	BLASTX	184	5e-12	36	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
16890	GM_M20_B2_F03_MF	g507910	BLASTN	607	8e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16891	GM_M20_B2_F03_MR	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
16892	GM_M20_B2_F04_MR	g559262	BLASTN	253	8e-09	62	Saccharomyces cerevisiae mitochondrion transfer RNA-Thr2 (tRNA-Thr2); transfer RNA-Cys (tRNA-Cys); transfer RNA-His (tRNA-His) genes.
16893	GM_M20_B2_F06_MF	g3820757	BLASTN	417	4e-12	64	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
16894	GM_M20_B2_F07_MR	g2129618	BLASTX	259	3e-20	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16895	GM_M20_B2_F09_MR	g4063760	BLASTX	513	3e-47	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16896	GM_M20_B2_G01_MF	g3097320	BLASTN	801	2e-37	76	Glycine max gene for Bd 30K, complete cds
16897	GM_M20_B2_G02_MR	g4038056	BLASTX	397	4e-35	49	(AC005897) putative transposon [Arabidopsis thaliana]
16898	GM_M20_B2_G08_MR	g3805846	BLASTX	314	9e-26	79	(AL031986) DNA-directed RNA polymerase (EC 2.7.7.6) II largest chain [Arabidopsis thaliana]
16899	GM_M20_B2_G12_MF	g1944188	BLASTN	475	9e-15	75	Soybean DNA for nodulin 35, partial cds
16900	GM_M20_B2_H04_MR	g3176680	BLASTX	337	3e-29	44	(AC003671) Identical to polygalacuronase isoenzyme 1 beta subunit homolog mRNA gb U63373. EST gb AA404878 comes from this gene. [Arabidopsis thaliana]
16901	GM_M20_B2_H09_MF	g2129618	BLASTX	203	2e-14	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16902	GM_M20_B2_H10_MR	g3334667	BLASTX	204	6e-15	38	(Y10493) putative cytochrome P450 [Glycine max]
16903	GM_M20_B2_H12_MR	g3777527	BLASTX	322	1e-26	72	(AF053008) gag-pol polyprotein [Glycine max]
16904	GM_M21_A1_A03_MF	g4063756	BLASTN	440	8e-13	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
16905	GM_M21_A1_A03_MR	g507910	BLASTN	424	2e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16906	GM_M21_A1_A08_MF	g4063770	BLASTX	191	4e-13	36	(AB004906) transposase [Ipomoea purpurea]
16907	GM_M21_A1_A10_MF	g2811226	BLASTX	266	2e-21	92	(AF042669) fimbrin 2 [Arabidopsis thaliana] gi 2811232 (AF042671) fimbrin 2 [Arabidopsis thaliana]
16908	GM_M21_A1_A10_MR	g20044	BLASTN	375	6e-10	61	Tobacco DNA for retroviral-like transposon Tnt 1-94
16909	GM_M21_A1_B01_MR	g2443320	BLASTX	389	6e-34	52	(D85597) polyprotein [Oryza australiensis]
16910	GM_M21_A1_B05_MF	g4038056	BLASTX	179	2e-26	53	(AC005897) putative transposon [Arabidopsis thaliana]
16911	GM_M21_A1_B05_MR	g3695395	BLASTX	208	9e-17	43	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16912	GM_M21_A1_B08_MF	g507910	BLASTN	380	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16913	GM_M21_A1_B08_MR	g507910	BLASTN	401	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
16914	GM_M21_A1_B09_MR	g2979597	BLASTN	376	6e-10	64	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
16915	GM_M21_A1_B10_MF	g4063760	BLASTX	496	2e-45	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16916	GM_M21_A1_B10_MR	g2522230	BLASTX	262	7e-22	42	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
16917	GM_M21_A1_B12_MR	g18559	BLASTN	554	4e-18	68	G.max gene for catalase
16918	GM_M21_A1_C01_MR	g2501460	BLASTX	155	2e-18	66	PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE HAUSP (UBIQUITIN THIOLESTERASE HAUSP) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE HAUSP) (DEUBIQUITINATING ENZYME HAUSP) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE) gi 1545952 gnl PID e244584 (Z72499) herpesvirus associated ubiquitin-specific protease (HAUSP) [Homo sapiens]
16919	GM_M21_A1_C02_MF	g4038594	BLASTX	329	1e-28	79	(AJ222798) DET1 protein [Lycopersicon esculentum]
16920	GM_M21_A1_C03_MR	g3834451	BLASTX	319	6e-28	59	(AF072732) polygalacturonase 7 [Lycopersicon esculentum]
16921	GM_M21_A1_C10_MR	g130405	BLASTX	295	4e-24	45	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 17.6) gi 74642 pir GNFF17 retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) transposon 17.6 gi 1335613 gnl PID e1849 (X01472) ORF 2, pot. reverse transcriptase [Drosophila melanogaster] gi 224319 prf 1101404B ORF 2 [Drosophila melanogaster]
16922	GM_M21_A1_C11_MR	g3695385	BLASTX	265	4e-22	45	(AF096370) similar to Medicago truncatula MtN21 (GB:Y15293) [Arabidopsis thaliana]
16923	GM_M21_A1_C12_MF	g3033389	BLASTX	154	4e-09	32	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
16924	GM_M21_A1_C12_MR	g3033389	BLASTX	276	3e-22	45	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
16925	GM_M21_A1_D03_MF	g3021343	BLASTN	742	1e-27	74	Cicer arietinum mRNA for hypothetical protein homologous to EST B23019
16926	GM_M21_A1_D03_MR	g2085783	BLASTN	391	1e-10	62	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
16927	GM_M21_A1_D06_MF	g2245087	BLASTX	167	1e-11	40	(Z97343) hypothetical protein [Arabidopsis thaliana]
16928	GM_M21_A1_D08_MF	g18559	BLASTN	382	3e-10	71	G.max gene for catalase
16929	GM_M21_A1_D08_MR	g2443320	BLASTX	381	4e-33	51	(D85597) polyprotein [Oryza australiensis]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16930	GM_M21_A1_D09_MR	g1167523	BLASTX	348	1e-29	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
16931	GM_M21_A1_D11_MF	g3650039	BLASTX	227	4e-17	42	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
16932	GM_M21_A1_E08_MF	g3738114	BLASTN	406	3e-11	64	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
16933	GM_M21_A1_E10_MR	g3650039	BLASTX	179	6e-12	38	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
16934	GM_M21_A1_F04_MF	g4092471	BLASTN	367	1e-09	60	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
16935	GM_M21_A1_F06_MF	g478148	BLASTX	423	6e-39	91	reverse transcriptase (copia-like retrotransposon) - soybean (fragment) >gi 169949 (M94493) reverse transcriptase [Glycine max]
16936	GM_M21_A1_F07_MF	g2443320	BLASTX	123	9e-16	49	(D85597) polyprotein [Oryza australiensis]
16937	GM_M21_A1_F08_MR	g3687234	BLASTX	167	2e-10	49	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
16938	GM_M21_A1_F09_MR	g4050011	BLASTN	399	5e-11	70	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
16939	GM_M21_A1_F11_MF	g3650039	BLASTX	203	1e-14	39	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
16940	GM_M21_A1_G05_MR	g2642431	BLASTX	224	2e-16	58	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
16941	GM_M21_A1_G06_MF	g4063760	BLASTX	267	5e-21	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16942	GM_M21_A1_G12_MR	g4063760	BLASTX	443	8e-40	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16943	GM_M21_A1_H03_MR	g170080	BLASTN	1058	5e-41	86	Soybean seed lectin gene transposable element tgm1.
16944	GM_M21_A2_A02_MF	g3142328	BLASTN	538	3e-24	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16945	GM_M21_A2_A02_MR	g1621467	BLASTX	625	2e-60	86	(U73106) laccase [Liriodendron tulipifera]
16946	GM_M21_A2_A03_MF	g507910	BLASTN	346	5e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
16947	GM_M21_A2_A03_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
16948	GM_M21_A2_A07_MF	g1769898	BLASTX	237	2e-25	72	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16949	GM_M21_A2_A08_MR	g507910	BLASTN	579	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
16950	GM_M21_A2_B01_MF	g2443878	BLASTX	150	5e-10	62	(AC002294) Unknown protein [Arabidopsis thaliana]
16951	GM_M21_A2_B03_MF	g3777527	BLASTX	269	4e-28	54	(AF053008) gag-pol polyprotein [Glycine max]
16952	GM_M21_A2_B03_MR	g968986	BLASTN	365	1e-09	73	Glycine max ferritin gene, nuclear gene encoding chloroplast protein, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16953	GM_M21_A2_B04_MF	g2522228	BLASTX	376	6e-34	56	(AB007466) reverse transcriptase-like protein [Vicia faba]
16954	GM_M21_A2_B09_MF	g905361	BLASTX	418	4e-38	92	(U22103) gag-protease polyprotein [Glycine max]
16955	GM_M21_A2_C02_MR	g226407	BLASTX	343	5e-29	50	retrotransposon del1-46 [Lilium henryi]
16956	GM_M21_A2_C03_MF	g2129618	BLASTX	162	6e-10	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
16957	GM_M21_A2_C03_MR	g905361	BLASTX	200	3e-14	37	(U22103) gag-protease polyprotein [Glycine max]
16958	GM_M21_A2_D02_MR	g3777527	BLASTX	236	1e-17	37	(AF053008) gag-pol polyprotein [Glycine max]
16959	GM_M21_A2_D04_MF	g2244803	BLASTX	232	1e-18	38	(Z97336) reverse transcriptase-like protein [Arabidopsis thaliana]
16960	GM_M21_A2_D10_MR	g3142328	BLASTN	1202	2e-47	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16961	GM_M21_A2_E07_MF	g1173187	BLASTX	209	2e-27	93	40S RIBOSOMAL PROTEIN S23 (S12) gi 1362041 pir S56673 ribosomal protein S23.e, cytosolic (clone RJ3) - garden strawberry gi 643074 (U19940) putative 40S ribosomal protein s12 [Fragaria x ananassa]
16962	GM_M21_A2_F01_MR	g3097320	BLASTN	1159	2e-45	79	Glycine max gene for Bd 30K, complete cds
16963	GM_M21_A2_F02_MR	g3510344	BLASTN	357	4e-09	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJG14, complete sequence [Arabidopsis thaliana]
16964	GM_M21_A2_F07_MR	g1167523	BLASTX	358	1e-30	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
16965	GM_M21_A2_F08_MR	g507910	BLASTN	579	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
16966	GM_M21_A2_F10_MR	g2088662	BLASTX	255	3e-21	61	(AF002109) unknown protein [Arabidopsis thaliana]
16967	GM_M21_A2_G02_MF	g3549672	BLASTX	154	1e-09	93	(AL031394) putative protein [Arabidopsis thaliana]
16968	GM_M21_A2_G02_MR	g1346261	BLASTX	335	3e-29	50	GLUTAMYL-TRNA REDUCTASE 2 PRECURSOR (GLUTR) gi 1015319 gnl PID d1011751 (D67088) glutamyl-tRNA reductase [Cucumis sativus]
16969	GM_M21_A2_G03_MR	g3386611	BLASTX	136	5e-13	50	(AC004665) unknown protein [Arabidopsis thaliana]
16970	GM_M21_A2_G04_MF	g3142328	BLASTN	944	8e-36	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16971	GM_M21_A2_G06_MR	g3097320	BLASTN	1163	1e-45	81	Glycine max gene for Bd 30K, complete cds
16972	GM_M21_A2_G07_MR	g3426334	BLASTN	514	3e-16	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
16973	GM_M21_A2_G10_MR	g3549664	BLASTX	156	2e-09	50	(AL031394) putative protein [Arabidopsis thaliana]
16974	GM_M21_A2_G11_MR	g3142328	BLASTN	1974	7e-83	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16975	GM_M21_A2_H02_MF	g840618	BLASTN	349	6e-09	66	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16976	GM_M21_A2_H03_MR	g3142328	BLASTN	1328	3e-53	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16977	GM_M21_A2_H06_MR	g2979567	BLASTN	422	5e-12	66	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-328A3, complete sequence [Homo sapiens]
16978	GM_M21_A2_H09_MF	g100484	BLASTX	270	1e-31	59	hypothetical protein - garden snapdragon
16979	GM_M21_A2_H09_MR	g1769898	BLASTX	218	3e-28	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16980	GM_M21_B1_A05_MR	g1769897	BLASTX	229	1e-21	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
16981	GM_M21_B1_A09_MF	g14227	BLASTN	356	1e-09	68	Yeast cytochrome c oxidase transcription initiation region subunit 1 (COX1) from mitochondrial DNA
16982	GM_M21_B1_A10_MF	g130582	BLASTX	420	3e-37	65	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
16983	GM_M21_B1_A11_MR	g3097320	BLASTN	1003	2e-38	82	Glycine max gene for Bd 30K, complete cds
16984	GM_M21_B1_A12_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
16985	GM_M21_B1_B02_MR	g2618683	BLASTN	553	6e-18	67	Arabidopsis thaliana chromosome II BAC T32G6 genomic sequence, complete sequence [Arabidopsis thaliana]
16986	GM_M21_B1_B04_MF	g2656030	BLASTN	705	8e-25	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUL8
16987	GM_M21_B1_B05_MF	g100484	BLASTX	312	3e-26	49	hypothetical protein - garden snapdragon
16988	GM_M21_B1_B06_MF	g1703380	BLASTX	146	7e-15	100	ADP-RIBOSYLATION FACTOR gi 1132483 gnl PID d1005135 (D17760) ADP-ribosylation factor [Oryza sativa]
16989	GM_M21_B1_B06_MR	g3702341	BLASTX	166	6e-12	56	(AC005397) hypothetical protein [Arabidopsis thaliana]
16990	GM_M21_B1_B10_MR	g18559	BLASTN	1071	2e-41	77	G.max gene for catalase
16991	GM_M21_B1_B12_MR	g2500354	BLASTX	330	4e-29	64	60S RIBOSOMAL PROTEIN L10 (EQM) gi 1902894 gnl PID d1020219 (AB001891) QM family protein [Solanum melongena]
16992	GM_M21_B1_C01_MF	g3777527	BLASTX	197	2e-13	33	(AF053008) gag-pol polyprotein [Glycine max]
16993	GM_M21_B1_C01_MR	g3142328	BLASTN	1703	2e-70	86	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
16994	GM_M21_B1_C05_MF	g3193221	BLASTN	392	1e-10	79	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
16995	GM_M21_B1_C09_MF	g4063760	BLASTX	178	1e-11	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
16996	GM_M21_B1_C09_MR	g507910	BLASTN	613	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
16997	GM_M21_B1_C12_MF	g1769899	BLASTX	116	1e-16	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
16998	GM_M21_B1_D02_MR	g3273387	BLASTN	375	7e-10	62	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
16999	GM_M21_B1_D06_MF	g1762436	BLASTX	172	1e-11	64	(U60277) acyl-acyl carrier protein desaturase [Asclepias syriaca]
17000	GM_M21_B1_D06_MR	g100484	BLASTX	361	2e-33	61	hypothetical protein - garden snapdragon
17001	GM_M21_B1_D08_MF	g2541876	BLASTX	253	3e-20	49	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
17002	GM_M21_B1_D12_MF	g3193221	BLASTN	383	3e-10	78	Glycine max malate dehydrogenase (Mdh-2) gene, nuclear gene encoding mitochondrial protein, partial cds
17003	GM_M21_B1_E02_MR	g18559	BLASTN	988	9e-38	76	G.max gene for catalase
17004	GM_M21_B1_E11_MF	g2522228	BLASTX	191	1e-16	61	(AB007466) reverse transcriptase-like protein [Vicia faba]
17005	GM_M21_B1_F03_MF	g3777527	BLASTX	556	1e-51	93	(AF053008) gag-pol polyprotein [Glycine max]
17006	GM_M21_B1_F11_MR	g2347190	BLASTX	163	4e-10	37	(AC002338) Na/H antiporter isolog [Arabidopsis thaliana] gi 3150398 (AC004165) putative Na/H antiporter [Arabidopsis thaliana]
17007	GM_M21_B1_F12_MR	g170029	BLASTN	420	5e-12	83	Glycine max cv. Dare nodulin 26 gene fragment.
17008	GM_M21_B1_G04_MR	g905361	BLASTX	196	8e-14	33	(U22103) gag-protease polyprotein [Glycine max]
17009	GM_M21_B1_G05_MF	g4050011	BLASTN	500	1e-15	65	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
17010	GM_M21_B1_G07_MF	g3021552	BLASTN	435	1e-12	77	Pisum sativum gdcT gene
17011	GM_M21_B1_G08_MF	g629693	BLASTX	346	9e-31	49	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
17012	GM_M21_B1_G08_MR	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17013	GM_M21_B1_G09_MF	g1769897	BLASTX	133	9e-09	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17014	GM_M21_B1_H03_MR	g507910	BLASTN	581	1e-19	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17015	GM_M21_B1_H04_MF	g507910	BLASTN	341	8e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17016	GM_M21_B1_H04_MR	g507910	BLASTN	399	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17017	GM_M21_B1_H09_MR	g2760165	BLASTN	356	5e-09	66	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC9, complete sequence [Arabidopsis thaliana]
17018	GM_M21_B2_A02_MF	g507910	BLASTN	343	7e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17019	GM_M21_B2_A02_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17020	GM_M21_B2_A07_MF	g507910	BLASTN	418	3e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17021	GM_M21_B2_A07_MR	g905361	BLASTX	291	4e-24	70	(U22103) gag-protease polyprotein [Glycine max]
17022	GM_M21_B2_A08_MF	g3097320	BLASTN	448	3e-13	72	Glycine max gene for Bd 30K, complete cds
17023	GM_M21_B2_B01_MR	g2995405	BLASTX	297	4e-33	66	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17024	GM_M21_B2_B02_MF	g541967	BLASTX	166	6e-11	77	glycine cleavage system protein T precursor - garden pea >gi 407475 (X74793) T-protein of the glycine decarboxylase complex [Pisum sativum]
17025	GM_M21_B2_B09_MF	g421955	BLASTX	398	3e-36	56	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
17026	GM_M21_B2_B11_MF	g3096920	BLASTX	307	2e-26	45	(AL023094) putative ketoacyl-CoA synthase [Arabidopsis thaliana]
17027	GM_M21_B2_C07_MF	g2245115	BLASTX	156	2e-09	69	(Z97343) unnamed protein product [Arabidopsis thaliana]
17028	GM_M21_B2_C11_MF	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17029	GM_M21_B2_C11_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17030	GM_M21_B2_D02_MR	g3219151	BLASTX	123	1e-11	71	(AB015181) cdc2 related [Mesembryanthemum crystallinum]
17031	GM_M21_B2_D10_MR	g2443320	BLASTX	119	4e-13	38	(D85597) polyprotein [Oryza australiensis]
17032	GM_M21_B2_D11_MF	g2129709	BLASTX	237	9e-18	44	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
17033	GM_M21_B2_E01_MF	g3142328	BLASTN	709	4e-25	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17034	GM_M21_B2_E02_MF	g3746069	BLASTX	152	1e-08	28	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
17035	GM_M21_B2_E08_MF	g3810596	BLASTX	319	1e-26	50	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
17036	GM_M21_B2_E10_MF	g99922	BLASTX	350	3e-31	78	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17037	GM_M21_B2_F01_MF	g507910	BLASTN	545	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
17038	GM_M21_B2_F04_MF	g2522227	BLASTX	198	4e-15	51	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
17039	GM_M21_B2_F11_MF	g3645899	BLASTX	220	2e-25	52	(U68408) 5' end not determined experimentally [Zea mays]
17040	GM_M21_B2_G01_MR	g2895613	BLASTN	348	5e-09	62	Colias alexandra alexandra large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
17041	GM_M21_B2_G02_MR	g3171159	BLASTN	599	5e-20	67	Homo sapiens chromosome 21q22.3 PAC 21L13, complete sequence [Homo sapiens]
17042	GM_M21_B2_G03_MF	g1480927	BLASTN	1392	2e-57	91	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
17043	GM_M21_B2_G03_MR	g2129618	BLASTX	112	3e-13	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17044	GM_M21_B2_G08_MF	g3242717	BLASTX	207	1e-15	92	(AC003040) putative APG protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17045	GM_M21_B2_G09_MF	g136251	BLASTX	287	4e-24	76	TRYPTOPHAN SYNTHASE BETA CHAIN 1 PRECURSOR gi 99767 pir A31393 tryptophan synthase (EC 4.2.1.20) beta chain - Arabidopsis thaliana gi 166892 (M23872) tryptophan synthase beta subunit [Arabidopsis thaliana]
17046	GM_M21_B2_G10_MR	g2979597	BLASTN	378	5e-10	64	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]
17047	GM_M21_B2_G11_MR	g3142328	BLASTN	1229	9e-49	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17048	GM_M21_B2_H02_MR	g3097320	BLASTN	1207	1e-47	82	Glycine max gene for Bd 30K, complete cds
17049	GM_M21_B2_H07_MF	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17050	GM_M21_B2_H07_MR	g507910	BLASTN	382	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17051	GM_M22_A1_A09_MF	g2626751	BLASTN	445	4e-13	63	Triticum aestivum retrotransposon Tar1, partial sequence.
17052	GM_M22_A1_A12_MF	g507910	BLASTN	362	9e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17053	GM_M22_A1_B08_MF	g3319362	BLASTX	180	3e-16	41	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17054	GM_M22_A1_B09_MF	g12212	BLASTN	1146	1e-50	91	S.alba chloroplast rp123 and rp12 genes for ribosomal proteins L23 and L2
17055	GM_M22_A1_B10_MF	g3510347	BLASTN	504	1e-15	70	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MSJ11, complete sequence [Arabidopsis thaliana]
17056	GM_M22_A1_B11_MF	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17057	GM_M22_A1_C02_MF	g3645899	BLASTX	369	5e-32	54	(U68408) 5' end not determined experimentally [Zea mays]
17058	GM_M22_A1_C03_MF	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17059	GM_M22_A1_C04_MF	g3142328	BLASTN	772	5e-28	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17060	GM_M22_A1_C06_MF	g3810596	BLASTX	292	7e-24	39	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
17061	GM_M22_A1_C08_MF	g3142328	BLASTN	975	3e-37	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17062	GM_M22_A1_C09_MF	g3142328	BLASTN	816	5e-30	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17063	GM_M22_A1_C11_MF	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17064	GM_M22_A1_D09_MF	g3548797	BLASTN	425	4e-12	66	Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence, complete sequence [Arabidopsis thaliana]
17065	GM_M22_A1_D10_MF	g531389	BLASTX	283	1e-22	44	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17066	GM_M22_A1_E01_MF	g3445238	BLASTX	227	3e-18	62	(AL022347) putative protein [Arabidopsis thaliana] gi 3451059 gnl PID e1316746 (AL031326) putative protein [Arabidopsis thaliana]
17067	GM_M22_A1_E02_MF	g507910	BLASTN	549	3e-18	84	Glycine max BSR-101 satellite SB92 genomic sequence.
17068	GM_M22_A1_E07_MF	g4063770	BLASTX	193	5e-20	39	(AB004906) transposase [Ipomoea purpurea]
17069	GM_M22_A1_E12_MF	g20999	BLASTN	296	1e-11	63	P.vulgaris gln-delta gene for plastid-located glutamine synthetase (promotor region)
17070	GM_M22_A1_F02_MF	g507910	BLASTN	376	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17071	GM_M22_A1_F04_MF	g1769898	BLASTX	444	4e-41	59	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17072	GM_M22_A1_F08_MF	g3687234	BLASTX	193	3e-13	52	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
17073	GM_M22_A1_G04_MF	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17074	GM_M22_A1_H07_MF	g3097320	BLASTN	1210	9e-48	81	Glycine max gene for Bd 30K, complete cds
17075	GM_M22_A1_H11_MF	g3097320	BLASTN	955	3e-36	78	Glycine max gene for Bd 30K, complete cds
17076	GM_M22_A2_A01_MF	g507910	BLASTN	588	6e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
17077	GM_M22_A2_A04_MF	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17078	GM_M22_A2_A11_MF	g255578	BLASTN	637	1e-22	86	small auxin up RNA gene cluster: orf X10A [Glycine max=soybeans, cv. Wayne, Genomic, 666 nt]
17079	GM_M22_A2_B02_MF	g3142379	BLASTX	243	2e-19	57	(AF053008) envelope-like [Glycine max]
17080	GM_M22_A2_C06_MF	g3097320	BLASTN	621	4e-21	82	Glycine max gene for Bd 30K, complete cds
17081	GM_M22_A2_C10_MF	g1431738	BLASTN	670	2e-23	78	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
17082	GM_M22_A2_F01_MF	g3212863	BLASTX	285	3e-24	80	(AC004005) putative translation initiation factor [Arabidopsis thaliana]
17083	GM_M22_A2_F03_MF	g18559	BLASTN	841	4e-31	73	G.max gene for catalase
17084	GM_M22_A2_F06_MF	g2764526	BLASTN	398	6e-11	65	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
17085	GM_M22_A2_F07_MF	g507910	BLASTN	345	6e-09	67	Glycine max BSR-101 satellite SB92 genomic sequence.
17086	GM_M22_A2_F11_MF	g2522227	BLASTX	218	3e-17	44	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
17087	GM_M22_A2_F12_MF	g1769897	BLASTX	183	1e-12	34	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17088	GM_M22_A2_G06_MF	g2264320	BLASTN	497	2e-15	61	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
17089	GM_M22_A2_G08_MF	g3777527	BLASTX	168	1e-12	35	(AF053008) gag-pol polyprotein [Glycine max]
17090	GM_M22_A2_G11_MF	g1167523	BLASTX	190	9e-13	33	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
17091	GM_M22_A2_H02_MF	g1167523	BLASTX	299	6e-26	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17092	GM_M22_A2_H07_MF	g507910	BLASTN	358	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17093	GM_M22_A2_H08_MF	g3645899	BLASTX	334	3e-28	48	(U68408) 5' end not determined experimentally [Zea mays]
17094	GM_M22_B1_A03_MR	g99922	BLASTX	173	9e-21	68	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17095	GM_M22_B1_A04_MF	g18559	BLASTN	483	7e-15	72	G.max gene for catalase
17096	GM_M22_B1_A08_MR	g4038056	BLASTX	389	3e-34	52	(AC005897) putative transposon [Arabidopsis thaliana]
17097	GM_M22_B1_B05_MR	g3645899	BLASTX	441	1e-39	61	(U68408) 5' end not determined experimentally [Zea mays]
17098	GM_M22_B1_B06_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17099	GM_M22_B1_B07_MR	g3142328	BLASTN	791	7e-29	68	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17100	GM_M22_B1_B12_MR	g3645899	BLASTX	298	2e-24	49	(U68408) 5' end not determined experimentally [Zea mays]
17101	GM_M22_B1_C01_MR	g2522228	BLASTX	433	5e-40	74	(AB007466) reverse transcriptase-like protein [Vicia faba]
17102	GM_M22_B1_C02_MF	g170603	BLASTN	550	6e-19	74	Broad bean (V.faba) BamHI repetitive element, 990 bp family.
17103	GM_M22_B1_C02_MR	g4063760	BLASTX	608	2e-57	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17104	GM_M22_B1_C03_MR	g3513745	BLASTX	164	7e-10	31	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
17105	GM_M22_B1_C04_MR	g1769898	BLASTX	272	4e-22	38	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17106	GM_M22_B1_C07_MR	g3176776	BLASTN	338	5e-09	67	Homo sapiens allele 4 fragile site locus (FRA10B) minisatellite, 5' sequence
17107	GM_M22_B1_C08_MR	g226407	BLASTX	498	2e-45	62	retrotransposon del1-46 [Lilium henryi]
17108	GM_M22_B1_C11_MR	g3777527	BLASTX	728	5e-70	97	(AF053008) gag-pol polyprotein [Glycine max]
17109	GM_M22_B1_C12_MR	g422418	BLASTX	260	2e-20	41	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
17110	GM_M22_B1_D02_MF	g507910	BLASTN	574	3e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
17111	GM_M22_B1_D05_MF	g3777527	BLASTX	673	4e-64	94	(AF053008) gag-pol polyprotein [Glycine max]
17112	GM_M22_B1_D06_MF	g4063769	BLASTN	503	9e-16	70	Ipomoea purpurea transposable element Tip100 gene for transposase, complete cds
17113	GM_M22_B1_D08_MR	g4063760	BLASTX	443	8e-40	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17114	GM_M22_B1_D09_MR	g1769897	BLASTX	251	6e-20	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17115	GM_M22_B1_D10_MR	g905361	BLASTX	184	2e-12	33	(U22103) gag-protease polyprotein [Glycine max]
17116	GM_M22_B1_E07_MF	g507910	BLASTN	366	6e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17117	GM_M22_B1_E07_MR	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17118	GM_M22_B1_E08_MF	g322661	BLASTX	182	2e-13	71	S-receptor kinase-related protein - Chinese kale gi 17919 (Z18862) S-receptor kinase related protein [Brassica oleracea]
17119	GM_M22_B1_E10_MR	g1171591	BLASTN	405	3e-11	64	P.falciparum complete gene map of plastid-like DNA (IR-B)

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17120	GM_M22_B1_E12_MF	g4063760	BLASTX	167	8e-21	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17121	GM_M22_B1_F01_MR	g13507	BLASTN	243	2e-10	67	Yeast mitochondrial gene for ATPase (genes oli-2 and oli-4).
17122	GM_M22_B1_F03_MF	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17123	GM_M22_B1_F05_MF	g2129618	BLASTX	221	3e-16	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17124	GM_M22_B1_F09_MF	g13619	BLASTN	412	1e-12	63	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
17125	GM_M22_B1_F10_MF	g3777527	BLASTX	635	4e-60	97	(AF053008) gag-pol polyprotein [Glycine max]
17126	GM_M22_B1_F11_MR	g3097320	BLASTN	745	1e-26	78	Glycine max gene for Bd 30K, complete cds
17127	GM_M22_B1_F12_MF	g4150933	BLASTN	350	9e-09	63	Homo sapiens BAC clone NH0520M18 from 7q31.1-q31.2, complete sequence [Homo sapiens]
17128	GM_M22_B1_G02_MF	g2129618	BLASTX	161	7e-10	32	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17129	GM_M22_B1_G03_MF	g2522228	BLASTX	193	1e-31	55	(AB007466) reverse transcriptase-like protein [Vicia faba]
17130	GM_M22_B1_G04_MF	g1617270	BLASTX	193	2e-13	74	(X94624) acyl-CoA synthetase [Brassica napus]
17131	GM_M22_B1_G06_MR	g3377855	BLASTX	227	2e-33	77	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
17132	GM_M22_B1_G07_MF	g18559	BLASTN	925	6e-35	75	G.max gene for catalase
17133	GM_M22_B1_G08_MF	g905361	BLASTX	435	4e-40	96	(U22103) gag-protease polyprotein [Glycine max]
17134	GM_M22_B1_G09_MF	g4115365	BLASTX	312	1e-25	53	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
17135	GM_M22_B1_G11_MF	g3097320	BLASTN	937	2e-35	81	Glycine max gene for Bd 30K, complete cds
17136	GM_M22_B1_H01_MF	g3777527	BLASTX	182	8e-12	33	(AF053008) gag-pol polyprotein [Glycine max]
17137	GM_M22_B1_H01_MR	g505129	BLASTN	397	5e-11	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17138	GM_M22_B1_H04_MR	g4063760	BLASTX	106	5e-10	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17139	GM_M22_B1_H06_MR	g3377834	BLASTX	149	9e-09	34	(AF075598) No definition line found [Arabidopsis thaliana]
17140	GM_M22_B1_H08_MF	g4063760	BLASTX	265	9e-21	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17141	GM_M22_B2_A01_MR	g3789709	BLASTN	496	2e-15	68	Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence [Homo sapiens]
17142	GM_M22_B2_A02_MR	g505129	BLASTN	374	6e-10	67	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17143	GM_M22_B2_A03_MF	g507910	BLASTN	590	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17144	GM_M22_B2_A03_MR	g905361	BLASTX	335	7e-29	84	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17145	GM_M22_B2_A04_MF	g2129618	BLASTX	196	1e-13	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17146	GM_M22_B2_A06_MR	g3097320	BLASTN	484	7e-15	70	Glycine max gene for Bd 30K, complete cds
17147	GM_M22_B2_A10_MF	g3097320	BLASTN	685	6e-24	84	Glycine max gene for Bd 30K, complete cds
17148	GM_M22_B2_A11_MF	g507910	BLASTN	591	4e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
17149	GM_M22_B2_A11_MR	g507910	BLASTN	601	1e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17150	GM_M22_B2_B01_MF	g4063760	BLASTX	274	8e-22	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17151	GM_M22_B2_B01_MR	g507910	BLASTN	615	4e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17152	GM_M22_B2_B06_MF	g2708743	BLASTX	93	9e-09	43	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
17153	GM_M22_B2_B06_MR	g1262280	BLASTN	366	1e-09	62	Mesembryanthemum crystallinum Atpv5 gene, promoter region.
17154	GM_M22_B2_B07_MR	g13610	BLASTN	387	9e-11	59	Yeast mitochondrial var1 gene (allele 40.0) a ribosomal protein >gi 343948 gb J01525 YSCMTVAR1 Yeast (S.cerevisiae) mitochondrial var1 gene, 40.0 allele.
17155	GM_M22_B2_B08_MF	g3176768	BLASTN	442	6e-14	64	Homo sapiens allele 1 fragile site locus (FRA10B) minisatellite, 3' sequence
17156	GM_M22_B2_B08_MR	g1515105	BLASTX	214	2e-24	65	(Y07613) heat shock protein 90A [Arabidopsis thaliana]
17157	GM_M22_B2_B09_MF	g340796	BLASTN	402	4e-12	60	Figure 6. DNA sequence of three 3' apoB VNTR alleles.
17158	GM_M22_B2_B09_MR	g2160150	BLASTX	166	1e-12	50	(AC000375) EST gb T43829 comes from this gene. [Arabidopsis thaliana]
17159	GM_M22_B2_B10_MF	g3645899	BLASTX	165	4e-17	43	(U68408) 5' end not determined experimentally [Zea mays]
17160	GM_M22_B2_B12_MR	g1236920	BLASTN	352	6e-09	62	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
17161	GM_M22_B2_C05_MF	g507910	BLASTN	588	6e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17162	GM_M22_B2_C10_MF	g505129	BLASTN	338	7e-11	69	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17163	GM_M22_B2_C12_MR	g2121303	BLASTN	378	5e-10	61	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
17164	GM_M22_B2_D03_MF	g2522228	BLASTX	193	1e-31	55	(AB007466) reverse transcriptase-like protein [Vicia faba]
17165	GM_M22_B2_D04_MF	g3821288	BLASTN	381	1e-10	70	Pisum sativum repeated element highly similar to the BamHI repeated sequence families of Vicia faba
17166	GM_M22_B2_D09_MR	g3176795	BLASTN	381	1e-10	63	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
17167	GM_M22_B2_D11_MR	g4038056	BLASTX	327	1e-27	51	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17168	GM_M22_B2_E01_MR	g4063756	BLASTN	463	7e-14	61	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17169	GM_M22_B2_E02_MF	g3142328	BLASTN	725	7e-26	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17170	GM_M22_B2_E02_MR	g1785736	BLASTX	151	4e-10	55	(Y08502) orf119 [Arabidopsis thaliana]
17171	GM_M22_B2_E03_MF	g4063760	BLASTX	326	3e-27	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17172	GM_M22_B2_E07_MR	g3777527	BLASTX	233	3e-17	43	(AF053008) gag-pol polyprotein [Glycine max]
17173	GM_M22_B2_E08_MF	g3513747	BLASTX	310	2e-25	45	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
17174	GM_M22_B2_E09_MR	g4165194	BLASTX	306	3e-25	41	(AJ009736) Pol protein [Drosophila melanogaster]
17175	GM_M22_B2_E10_MF	g3142328	BLASTN	668	3e-23	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17176	GM_M22_B2_E12_MF	g2462058	BLASTX	321	4e-28	53	(Y13389) reverse transcriptase [Antirrhinum majus]
17177	GM_M22_B2_F01_MF	g170603	BLASTN	559	2e-19	74	Broad bean (V.faba) BamHI repetitive element, 990 bp family.
17178	GM_M22_B2_F01_MR	g4063760	BLASTX	575	1e-56	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17179	GM_M22_B2_F04_MF	g2995179	BLASTN	445	5e-13	64	Homo sapiens DNA sequence from PAC 262D12 on chromosome q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIK...
17180	GM_M22_B2_F04_MR	g4063760	BLASTX	202	4e-14	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17181	GM_M22_B2_F05_MF	g2879886	BLASTN	399	4e-11	66	Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes
17182	GM_M22_B2_F12_MF	g3777526	BLASTN	745	1e-26	93	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
17183	GM_M22_B2_F12_MR	g3777527	BLASTX	206	1e-18	42	(AF053008) gag-pol polyprotein [Glycine max]
17184	GM_M22_B2_G03_MF	g2129618	BLASTX	252	1e-19	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17185	GM_M22_B2_G04_MR	g505129	BLASTN	358	3e-09	62	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17186	GM_M22_B2_G08_MR	g18559	BLASTN	379	4e-10	63	G.max gene for catalase
17187	GM_M22_B2_G09_MR	g1076286	BLASTX	527	4e-50	80	amidophosphoribosyltransferase - Arabidopsis thaliana gi 469193 gnl PID d1006574 (D28868) amidophosphoribosyltransferase [Arabidopsis thaliana]
17188	GM_M22_B2_G11_MF	g4140712	BLASTX	383	1e-34	60	(AF110183) putative integrase [Oryza sativa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17189	GM_M22_B2_G12_MR	g3645899	BLASTX	287	3e-23	51	(U68408) 5' end not determined experimentally [Zea mays]
17190	GM_M22_B2_H05_MF	g2244915	BLASTX	170	8e-11	39	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
17191	GM_M22_B2_H06_MR	g2244915	BLASTX	202	3e-14	34	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
17192	GM_M22_B2_H09_MF	g1666236	BLASTX	178	1e-12	29	(U76261) unknown [Hordeum vulgare]
17193	GM_M22_B2_H12_MR	g3985952	BLASTN	544	2e-17	65	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]
17194	GM_M23_A1_A01_MF	g2522230	BLASTX	183	2e-13	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
17195	GM_M23_A1_A02_MF	g99922	BLASTX	567	3e-54	85	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17196	GM_M23_A1_A04_MR	g2879886	BLASTN	431	1e-12	60	Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes
17197	GM_M23_A1_A08_MF	g3688328	BLASTX	281	7e-24	54	(AJ228325) reverse transcriptase [Ginkgo biloba]
17198	GM_M23_A1_A08_MR	g2213607	BLASTX	140	2e-22	59	(AC000103) F21J9.1 [Arabidopsis thaliana]
17199	GM_M23_A1_A09_MF	g2522227	BLASTX	172	4e-12	53	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
17200	GM_M23_A1_A09_MR	g18695	BLASTN	702	4e-25	87	Soybean nodulin 22 gene
17201	GM_M23_A1_A10_MF	g2827705	BLASTX	193	1e-13	38	(AL021684) predicted protein [Arabidopsis thaliana]
17202	GM_M23_A1_A11_MF	g18559	BLASTN	830	1e-30	77	G.max gene for catalase
17203	GM_M23_A1_A11_MR	g2443320	BLASTX	281	2e-22	46	(D85597) polyprotein [Oryza australiensis]
17204	GM_M23_A1_B04_MF	g2879886	BLASTN	379	3e-10	62	Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes
17205	GM_M23_A1_B04_MR	g1762933	BLASTX	160	4e-11	49	(U66263) tumor-related protein [Nicotiana tabacum]
17206	GM_M23_A1_B06_MF	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17207	GM_M23_A1_B06_MR	g507910	BLASTN	489	2e-15	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17208	GM_M23_A1_B08_MF	g507910	BLASTN	375	2e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17209	GM_M23_A1_B08_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17210	GM_M23_A1_B11_MR	g4063760	BLASTX	372	3e-32	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17211	GM_M23_A1_C02_MF	g343742	BLASTN	227	6e-09	64	Yeast (S.cerevisiae) mitochondrial ATPase complex subunit 9 proteolipid, 3' flank.
17212	GM_M23_A1_C04_MF	g3097320	BLASTN	872	2e-32	85	Glycine max gene for Bd 30K, complete cds
17213	GM_M23_A1_C04_MR	g2979597	BLASTN	405	3e-11	62	Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17214	GM_M23_A1_C05_MR	g3426048	BLASTX	353	2e-31	84	(AC005168) putative hydroxymethylglutaryl-CoA lyase precursor [Arabidopsis thaliana]
17215	GM_M23_A1_C10_MR	g100484	BLASTX	227	1e-31	59	hypothetical protein - garden snapdragon
17216	GM_M23_A1_D01_MR	g3776466	BLASTN	375	5e-10	64	Homo sapiens immunoglobulin-like transcript 10 protein gene, exons 7 and 8 and complete cds
17217	GM_M23_A1_D02_MR	g130582	BLASTX	223	3e-16	38	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
17218	GM_M23_A1_D03_MR	g1142701	BLASTN	1225	5e-49	82	Glycine max satellite STR120-A.3.
17219	GM_M23_A1_D04_MR	g3097320	BLASTN	480	1e-14	68	Glycine max gene for Bd 30K, complete cds
17220	GM_M23_A1_D09_MF	g4038056	BLASTX	224	1e-16	50	(AC005897) putative transposon [Arabidopsis thaliana]
17221	GM_M23_A1_D10_MF	g2462058	BLASTX	333	2e-29	55	(Y13389) reverse transcriptase [Antirrhinum majus]
17222	GM_M23_A1_D11_MF	g1769897	BLASTX	160	4e-14	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17223	GM_M23_A1_D12_MR	g3777527	BLASTX	711	3e-68	94	(AF053008) gag-pol polyprotein [Glycine max]
17224	GM_M23_A1_E01_MF	g20999	BLASTN	303	5e-12	64	P.vulgaris gln-delta gene for plastid-located glutamine synthetase (promotor region)
17225	GM_M23_A1_F03_MF	g2586082	BLASTX	283	1e-22	43	(U72725) retrofit [Oryza longistaminata]
17226	GM_M23_A1_F03_MR	g3337361	BLASTX	240	1e-21	40	(AC004481) ankyrin-like protein [Arabidopsis thaliana]
17227	GM_M23_A1_F04_MR	g4063760	BLASTX	134	1e-09	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17228	GM_M23_A1_F06_MF	g4063760	BLASTX	244	3e-38	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17229	GM_M23_A1_F10_MR	g3142328	BLASTN	1909	7e-80	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17230	GM_M23_A1_F11_MR	g905361	BLASTX	644	4e-66	98	(U22103) gag-protease polyprotein [Glycine max]
17231	GM_M23_A1_G02_MR	g505129	BLASTN	351	7e-09	61	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17232	GM_M23_A1_G03_MR	g100484	BLASTX	378	2e-33	52	hypothetical protein - garden snapdragon
17233	GM_M23_A1_G04_MF	g3687234	BLASTX	210	5e-15	39	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
17234	GM_M23_A1_G11_MR	g905361	BLASTX	232	1e-17	40	(U22103) gag-protease polyprotein [Glycine max]
17235	GM_M23_A1_G12_MR	g3341678	BLASTX	354	5e-31	52	(AC003672) putative zinc finger protein [Arabidopsis thaliana]
17236	GM_M23_A1_H05_MF	g507910	BLASTN	368	5e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17237	GM_M23_A1_H05_MR	g507910	BLASTN	393	4e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17238	GM_M23_A1_H07_MR	g2384696	BLASTX	156	7e-10	48	(AF013216) acyl-CoA oxidase [Myxococcus xanthus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17239	GM_M23_A1_H08_MF	g4063760	BLASTX	253	1e-19	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17240	GM_M23_A2_A01_MR	g3097320	BLASTN	353	6e-09	68	Glycine max gene for Bd 30K, complete cds
17241	GM_M23_A2_A02_MF	g3810596	BLASTX	161	7e-10	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
17242	GM_M23_A2_A08_MF	g18559	BLASTN	901	8e-34	76	G.max gene for catalase
17243	GM_M23_A2_A11_MR	g3319366	BLASTX	143	5e-09	56	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
17244	GM_M23_A2_B04_MR	g1167523	BLASTX	340	5e-32	53	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
17245	GM_M23_A2_C01_MR	g1666236	BLASTX	218	4e-17	32	(U76261) unknown [Hordeum vulgare]
17246	GM_M23_A2_C06_MF	g4063756	BLASTN	443	6e-13	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17247	GM_M23_A2_C08_MF	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17248	GM_M23_A2_C08_MR	g507910	BLASTN	383	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17249	GM_M23_A2_C10_MR	g18559	BLASTN	973	4e-37	77	G.max gene for catalase
17250	GM_M23_A2_C12_MR	g3510505	BLASTX	182	4e-21	41	(AF030881) pol polyprotein [Fugu rubripes]
17251	GM_M23_A2_D01_MF	g507910	BLASTN	562	9e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
17252	GM_M23_A2_D01_MR	g4063756	BLASTN	429	2e-12	73	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17253	GM_M23_A2_D02_MR	g3046847	BLASTN	442	6e-13	67	Arabidopsis thaliana genomic DNA, chromosome5, TAC clone: K11J9, complete sequence [Arabidopsis thaliana]
17254	GM_M23_A2_D03_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17255	GM_M23_A2_D11_MR	g476936	BLASTX	150	7e-09	90	NADPH--ferrihemoprotein reductase (EC 1.6.2.4) - mung bean
17256	GM_M23_A2_E02_MF	g2129618	BLASTX	192	4e-13	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17257	GM_M23_A2_F03_MF	g3930515	BLASTX	121	4e-11	47	(AF059674) putative gag protein [Nicotiana tabacum]
17258	GM_M23_A2_F05_MF	g3901012	BLASTX	269	3e-27	82	(AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]
17259	GM_M23_A2_F06_MF	g349606	BLASTN	361	4e-10	67	Buchnera aphidicola Arginyl tRNA synthetase (argS) gene, 5' end of cds and 16S ribosomal RNA promoter region.
17260	GM_M23_A2_F06_MR	g2129618	BLASTX	260	2e-20	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17261	GM_M23_A2_F07_MR	g3142328	BLASTN	1970	1e-82	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17262	GM_M23_A2_F11_MR	g905361	BLASTX	610	3e-61	97	(U22103) gag-protease polyprotein [Glycine max]
17263	GM_M23_A2_G01_MR	g3777526	BLASTN	418	7e-12	84	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17264	GM_M23_A2_G06_MR	g133421	BLASTX	616	2e-58	85	DNA-DIRECTED RNA POLYMERASE BETA CHAIN gi 81502 pir C29959 DNA-directed RNA polymerase (EC 2.7.7.6) beta chain - spinach chloroplast gi 295121 (M55297) RNA polymerase [Spinacia oleracea]
17265	GM_M23_A2_G08_MF	g4063760	BLASTX	221	4e-16	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17266	GM_M23_A2_H01_MF	g3758836	BLASTN	248	8e-09	69	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
17267	GM_M23_A2_H07_MR	g905361	BLASTX	192	3e-16	41	(U22103) gag-protease polyprotein [Glycine max]
17268	GM_M23_A2_H10_MF	g507910	BLASTN	366	6e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17269	GM_M23_A2_H10_MR	g507910	BLASTN	444	2e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
17270	GM_M23_A2_H12_MR	g3777527	BLASTX	693	3e-66	96	(AF053008) gag-pol polyprotein [Glycine max]
17271	GM_M23_B1_A03_MF	g342961	BLASTN	338	4e-09	63	paramecium species 4.172 mt dna dimer: replication init. region, clone 1.
17272	GM_M23_B1_A05_MF	g2129618	BLASTX	209	6e-15	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17273	GM_M23_B1_A07_MR	g4038056	BLASTX	274	6e-22	47	(AC005897) putative transposon [Arabidopsis thaliana]
17274	GM_M23_B1_A11_MR	g4151068	BLASTX	241	2e-18	83	(Y10862) ribonucleotide reductase [Nicotiana tabacum]
17275	GM_M23_B1_B02_MF	g1944188	BLASTN	697	4e-25	73	Soybean DNA for nodulin 35, partial cds
17276	GM_M23_B1_B08_MR	g3859610	BLASTN	561	3e-18	65	Arabidopsis thaliana BAC T9E19
17277	GM_M23_B1_B11_MF	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17278	GM_M23_B1_C03_MF	g1666236	BLASTX	207	8e-16	30	(U76261) unknown [Hordeum vulgare]
17279	GM_M23_B1_C10_MF	g2098709	BLASTX	385	7e-35	68	(U82975) pectinesterase [Citrus sinensis]
17280	GM_M23_B1_C12_MR	g2462134	BLASTX	226	3e-17	35	(Y13368) reverse transcriptase [Beta vulgaris]
17281	GM_M23_B1_D07_MR	g2801680	BLASTN	468	9e-15	77	Glycine max telomere-associated sequence STAS9
17282	GM_M23_B1_D10_MR	g1708424	BLASTX	235	1e-27	65	ISOFLAVONE REDUCTASE HOMOLOG gi 1230614 (U48590) isoflavone reductase-like protein [Lupinus albus]
17283	GM_M23_B1_D11_MR	g3695395	BLASTX	157	1e-09	37	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
17284	GM_M23_B1_D12_MF	g421955	BLASTX	103	2e-10	36	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
17285	GM_M23_B1_D12_MR	g3810596	BLASTX	193	3e-13	40	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
17286	GM_M23_B1_E02_MR	g2104945	BLASTN	482	8e-15	76	Glycine max copia-like retrotransposon Tgmr, complete sequence
17287	GM_M23_B1_E03_MR	g3287695	BLASTX	199	6e-29	82	(AC003979) Similar to hypothetical protein C34B7.2 gb 1729503 from C. elegans cosmid gb Z83220. [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17288	GM_M23_B1_E04_MF	g3582333	BLASTX	148	7e-09	77	(AC005496) hypothetical protein [Arabidopsis thaliana]
17289	GM_M23_B1_E06_MR	g3250676	BLASTX	292	2e-24	44	(AL024486) putative protein [Arabidopsis thaliana]
17290	GM_M23_B1_F01_MF	g1144548	BLASTN	349	1e-09	62	Anopheles bwambae 12S ribosomal RNA, D-loop, and tRNA-Ile mitochondrial genes, partial sequence.
17291	GM_M23_B1_F04_MF	g1167523	BLASTX	222	4e-16	36	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
17292	GM_M23_B1_F04_MR	g3319362	BLASTX	280	1e-22	46	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17293	GM_M23_B1_F08_MF	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17294	GM_M23_B1_F08_MR	g507910	BLASTN	374	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17295	GM_M23_B1_G01_MR	g3142328	BLASTN	800	3e-29	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17296	GM_M23_B1_G03_MF	g1146165	BLASTX	167	4e-11	74	(L47479) urophorphyrin III methylase [Arabidopsis thaliana]
17297	GM_M23_B1_G07_MF	g3047100	BLASTN	359	3e-09	65	Arabidopsis thaliana BAC F6N23
17298	GM_M23_B1_G08_MR	g3319366	BLASTX	155	2e-10	53	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
17299	GM_M23_B1_G12_MF	g100484	BLASTX	351	2e-30	59	hypothetical protein - garden snapdragon
17300	GM_M23_B1_H02_MR	g3777527	BLASTX	716	9e-69	94	(AF053008) gag-pol polyprotein [Glycine max]
17301	GM_M23_B1_H06_MF	g18695	BLASTN	449	2e-13	76	Soybean nodulin 22 gene
17302	GM_M23_B1_H07_MF	g1931647	BLASTX	162	3e-10	61	(U95973) endomembrane protein EMP70 precusor isolog [Arabidopsis thaliana]
17303	GM_M23_B1_H07_MR	g3135962	BLASTN	384	3e-10	65	Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence [Homo sapiens]
17304	GM_M23_B1_H12_MR	g1946355	BLASTX	402	6e-36	52	(U93215) maize transposon MuDR mudrA protein isolog [Arabidopsis thaliana] gi 2880040 (AC002340) maize transposon MuDR mudrA-like protein [Arabidopsis thaliana]
17305	GM_M24_A1_A03_MF	g3097320	BLASTN	689	4e-24	74	Glycine max gene for Bd 30K, complete cds
17306	GM_M24_A1_A04_MF	g3645899	BLASTX	387	6e-34	59	(U68408) 5' end not determined experimentally [Zea mays]
17307	GM_M24_A1_A08_MF	g3097320	BLASTN	363	2e-09	67	Glycine max gene for Bd 30K, complete cds
17308	GM_M24_A1_A11_MR	g18559	BLASTN	966	9e-37	79	G.max gene for catalase
17309	GM_M24_A1_B07_MF	g507910	BLASTN	571	3e-19	79	Glycine max BSR-101 satellite SB92 genomic sequence.
17310	GM_M24_A1_C07_MR	g2129618	BLASTX	178	1e-11	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17311	GM_M24_A1_C09_MF	g4063760	BLASTX	118	1e-10	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17312	GM_M24_A1_C09_MR	g507910	BLASTN	695	8e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17313	GM_M24_A1_C10_MR	g2760830	BLASTX	470	7e-44	73	(AC003105) putative beta-ketoacyl-CoA synthase [Arabidopsis thaliana]
17314	GM_M24_A1_D04_MF	g626007	BLASTX	314	2e-26	57	phospholipase D (EC 3.1.4.4) - castor bean
17315	GM_M24_A1_D04_MR	g1711512	BLASTX	194	8e-14	86	SIGNAL RECOGNITION PARTICLE 54 KD PROTEIN 2 (SRP54) gi 1076577 pir S51598 signal recognition particle 54K protein - tomato (cv. UC82-B) gi 556902 (Z34527) 54-kD signal recognition particle (SRP) specific protein [Lycopersicon esculentum]
17316	GM_M24_A1_E02_MR	g587603	BLASTN	358	3e-09	62	P.falciparum gene for beta subunit RNA polymerase
17317	GM_M24_A1_E09_MR	g13767	BLASTN	337	4e-09	62	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
17318	GM_M24_A1_E10_MR	g1142699	BLASTN	494	5e-16	85	Glycine max satellite STR120-A.1.
17319	GM_M24_A1_F04_MR	g3550435	BLASTN	510	5e-16	62	Hordeum vulgare Hotr1 gene
17320	GM_M24_A1_F06_MR	g4063760	BLASTX	141	4e-10	33	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17321	GM_M24_A1_F11_MF	g1769898	BLASTX	116	2e-13	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17322	GM_M24_A1_F12_MR	g2262105	BLASTX	189	5e-13	57	(AC002343) unknown protein [Arabidopsis thaliana]
17323	GM_M24_A1_G04_MF	g4159702	BLASTN	497	2e-15	68	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K2N11, complete sequence [Arabidopsis thaliana]
17324	GM_M24_A1_G05_MF	g3142328	BLASTN	872	2e-32	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17325	GM_M24_A1_H02_MF	g3097320	BLASTN	575	5e-19	86	Glycine max gene for Bd 30K, complete cds
17326	GM_M24_A1_H02_MR	g629693	BLASTX	301	5e-26	46	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
17327	GM_M24_A1_H04_MR	g3319345	BLASTX	106	5e-09	34	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
17328	GM_M24_A1_H07_MF	g4063760	BLASTX	407	6e-36	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17329	GM_M24_A1_H08_MF	g1168408	BLASTX	277	2e-23	93	FRUCTOSE-BISPHOSPHATE ALDOLASE, CYTOPLASMIC ISOZYME 1 gi 2118268 pir S58168 fructose-bisphosphate aldolase (EC 4.1.2.13) - garden pea gi 927507 (X89828) fructose-1,6-bisphosphate aldolase [Pisum sativum]
17330	GM_M24_A2_A02_MF	g3097320	BLASTN	733	4e-26	77	Glycine max gene for Bd 30K, complete cds
17331	GM_M24_A2_A11_MR	g4160362	BLASTN	402	4e-11	64	Saccharomyces cerevisiae complete mitochondrial genome
17332	GM_M24_A2_B03_MF	g2586082	BLASTX	167	3e-10	58	(U72725) retrofit [Oryza longistaminata]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17333	GM_M24_A2_B07_MR	g2121303	BLASTN	360	3e-09	64	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
17334	GM_M24_A2_B08_MR	g130582	BLASTX	374	2e-32	52	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
17335	GM_M24_A2_C02_MF	g2760837	BLASTX	382	1e-34	61	(AC003105) putative cytochrome P450 [Arabidopsis thaliana]
17336	GM_M24_A2_C02_MR	g1946279	BLASTX	283	2e-29	50	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
17337	GM_M24_A2_C05_MR	g18695	BLASTN	371	7e-10	66	Soybean nodulin 22 gene
17338	GM_M24_A2_C07_MF	g4063760	BLASTX	197	1e-13	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17339	GM_M24_A2_C09_MR	g130582	BLASTX	226	1e-16	38	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
17340	GM_M24_A2_C10_MF	g3176795	BLASTN	396	2e-11	63	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
17341	GM_M24_A2_C12_MF	g899342	BLASTX	251	1e-20	39	(X77110) chitinase, class V [Nicotiana tabacum]
17342	GM_M24_A2_D01_MR	g505129	BLASTN	349	8e-09	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17343	GM_M24_A2_D02_MR	g4063760	BLASTX	336	5e-34	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17344	GM_M24_A2_D05_MR	g18559	BLASTN	361	3e-09	79	G.max gene for catalase
17345	GM_M24_A2_D07_MR	g1666236	BLASTX	144	9e-09	30	(U76261) unknown [Hordeum vulgare]
17346	GM_M24_A2_D09_MF	g3645899	BLASTX	389	4e-34	71	(U68408) 5' end not determined experimentally [Zea mays]
17347	GM_M24_A2_D10_MF	g2443320	BLASTX	226	2e-29	53	(D85597) polyprotein [Oryza australiensis]
17348	GM_M24_A2_E01_MF	g4038471	BLASTX	183	1e-18	76	(AF111029) 40S ribosomal protein S27 homolog [Zea mays]
17349	GM_M24_A2_E09_MR	g3097320	BLASTN	469	3e-14	68	Glycine max gene for Bd 30K, complete cds
17350	GM_M24_A2_E11_MF	g4063760	BLASTX	221	4e-16	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17351	GM_M24_A2_E12_MR	g3805964	BLASTX	560	2e-53	71	(Y13773) laccase [Populus balsamifera subsp. trichocarpa]
17352	GM_M24_A2_F04_MR	g18559	BLASTN	370	1e-09	70	G.max gene for catalase
17353	GM_M24_A2_F05_MF	g3142379	BLASTX	267	7e-29	68	(AF053008) envelope-like [Glycine max]
17354	GM_M24_A2_F07_MF	g2626753	BLASTX	195	2e-22	74	(AB008782) sulfate transporter [Arabidopsis thaliana]
17355	GM_M24_A2_F08_MF	g4033838	BLASTX	287	5e-24	63	(Y18550) sigma-like factor [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17356	GM_M24_A2_F08_MR	g3641780	BLASTN	354	6e-09	62	Homo sapiens PAC clone DJ1159C10 from 7q34-q36, complete sequence [Homo sapiens]
17357	GM_M24_A2_G03_MF	g3097320	BLASTN	451	2e-13	72	Glycine max gene for Bd 30K, complete cds
17358	GM_M24_A2_G06_MR	g3080423	BLASTX	320	9e-27	50	(AL022604) putative protein [Arabidopsis thaliana]
17359	GM_M24_A2_G08_MR	g3097320	BLASTN	418	7e-12	72	Glycine max gene for Bd 30K, complete cds
17360	GM_M24_A2_G10_MF	g2443320	BLASTX	216	2e-28	56	(D85597) polyprotein [Oryza australiensis]
17361	GM_M24_A2_H05_MF	g507910	BLASTN	524	5e-17	81	Glycine max BSR-101 satellite SB92 genomic sequence.
17362	GM_M24_A2_H05_MR	g507910	BLASTN	579	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17363	GM_M24_B1_A01_MF	g4063760	BLASTX	468	2e-42	68	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17364	GM_M24_B1_A08_MR	g4063756	BLASTN	485	7e-15	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17365	GM_M24_B1_A12_MR	g3426334	BLASTN	424	4e-12	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
17366	GM_M24_B1_B01_MR	g507910	BLASTN	591	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17367	GM_M24_B1_B02_MF	g1769897	BLASTX	305	7e-26	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17368	GM_M24_B1_B05_MR	g1480927	BLASTN	626	2e-21	83	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
17369	GM_M24_B1_B06_MF	g3482916	BLASTX	234	7e-18	39	(AC003970) Hypothetical protein [Arabidopsis thaliana]
17370	GM_M24_B1_B09_MR	g3810596	BLASTX	139	2e-13	46	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
17371	GM_M24_B1_B11_MR	g3142328	BLASTN	472	2e-14	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17372	GM_M24_B1_C03_MR	g1769897	BLASTX	308	4e-26	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17373	GM_M24_B1_C04_MF	g2827992	BLASTX	103	7e-12	64	(AF034743) UDP-glucuronosyltransferase [Pisum sativum]
17374	GM_M24_B1_C05_MF	g3355473	BLASTX	183	2e-12	53	(AC004218) hypothetical protein [Arabidopsis thaliana]
17375	GM_M24_B1_C05_MR	g3513747	BLASTX	227	1e-16	33	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
17376	GM_M24_B1_C06_MF	g3915873	BLASTX	658	6e-64	98	SUCROSE SYNTHASE (SUCROSE-UDP GLUCOSYLTRANSFERASE) (NODULIN-100) >gi 2606081 (AF030231) sucrose synthase [Glycine max]
17377	GM_M24_B1_C06_MR	g2052508	BLASTX	153	9e-20	70	(U95759) lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme [Arabidopsis thaliana]
17378	GM_M24_B1_C11_MF	g4092470	BLASTN	829	2e-30	70	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
17379	GM_M24_B1_D03_MR	g4038056	BLASTX	116	1e-11	50	(AC005897) putative transposon [Arabidopsis thaliana]
17380	GM_M24_B1_D04_MF	g3377834	BLASTX	149	1e-08	27	(AF075598) No definition line found [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17381	GM_M24_B1_D05_MF	g4063760	BLASTX	448	2e-40	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17382	GM_M24_B1_D05_MR	g507910	BLASTN	434	5e-13	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17383	GM_M24_B1_D07_MF	g3777527	BLASTX	238	8e-18	41	(AF053008) gag-pol polyprotein [Glycine max]
17384	GM_M24_B1_D07_MR	g3142328	BLASTN	652	1e-22	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17385	GM_M24_B1_D11_MF	g3810595	BLASTX	222	4e-16	45	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
17386	GM_M24_B1_E01_MR	g18559	BLASTN	710	4e-25	72	G.max gene for catalase
17387	GM_M24_B1_E03_MR	g2398523	BLASTX	159	1e-10	72	(Y13721) Transcription factor [Arabidopsis thaliana]
17388	GM_M24_B1_E07_MF	g66619	BLASTX	250	8e-25	74	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19) precursor - tomato
17389	GM_M24_B1_E10_MR	g1931641	BLASTX	157	1e-09	43	(U95973) unknown protein [Arabidopsis thaliana]
17390	GM_M24_B1_E11_MR	g13556	BLASTN	244	4e-12	61	Yeast mitochondrial DNA with tRNA-Asp gene
17391	GM_M24_B1_E12_MR	g905361	BLASTX	205	8e-15	37	(U22103) gag-protease polyprotein [Glycine max]
17392	GM_M24_B1_F01_MR	g3779030	BLASTX	195	9e-15	28	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
17393	GM_M24_B1_F03_MR	g3777527	BLASTX	288	4e-23	43	(AF053008) gag-pol polyprotein [Glycine max]
17394	GM_M24_B1_F04_MR	g629693	BLASTX	173	9e-12	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
17395	GM_M24_B1_F06_MF	g1666236	BLASTX	97	6e-09	28	(U76261) unknown [Hordeum vulgare]
17396	GM_M24_B1_G07_MF	g18559	BLASTN	377	5e-10	75	G.max gene for catalase
17397	GM_M24_B1_G09_MR	g3845213	BLASTN	357	4e-09	62	Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence
17398	GM_M24_B1_G11_MF	g4063760	BLASTX	227	9e-17	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17399	GM_M24_B1_H06_MR	g2522228	BLASTX	249	3e-20	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
17400	GM_M24_B2_A03_MF	g130188	BLASTX	307	3e-31	71	PHYTOCHROME A gi 81937 pir S06856 phytochrome - garden pea gi 169132 (M37217) phytochrome [Pisum sativum] gi 295830 (X14077) phytochrome apoprotein [Pisum sativum] gi 226757 prf 1604466A phytochrome [Pisum sativum]
17401	GM_M24_B2_B02_MF	g3142328	BLASTN	1901	2e-79	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17402	GM_M24_B2_B04_MF	g4063756	BLASTN	450	3e-13	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17403	GM_M24_B2_B05_MR	g505129	BLASTN	422	4e-12	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17404	GM_M24_B2_C03_MR	g2462936	BLASTX	187	6e-14	49	(Y12321) open reading frame 2 [Brassica oleracea]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17405	GM_M24_B2_C09_MF	g2245073	BLASTN	377	5e-10	69	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 8
17406	GM_M24_B2_C12_MF	g3142328	BLASTN	482	1e-29	83	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17407	GM_M24_B2_D04_MF	g3820976	BLASTN	374	7e-10	63	Human DNA sequence from clone 101G11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complet...
17408	GM_M24_B2_D05_MR	g2982431	BLASTX	239	5e-18	40	(AL022224) leucine rich repeat-like protein [Arabidopsis thaliana]
17409	GM_M24_B2_D06_MR	g2961349	BLASTX	189	3e-14	41	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
17410	GM_M24_B2_D08_MF	g3097320	BLASTN	496	2e-15	70	Glycine max gene for Bd 30K, complete cds
17411	GM_M24_B2_E04_MF	g18559	BLASTN	927	5e-35	77	G.max gene for catalase
17412	GM_M24_B2_E10_MF	g3645899	BLASTX	177	9e-16	41	(U68408) 5' end not determined experimentally [Zea mays]
17413	GM_M24_B2_E11_MF	g2522228	BLASTX	348	5e-31	77	(AB007466) reverse transcriptase-like protein [Vicia faba]
17414	GM_M24_B2_E11_MR	g3319362	BLASTX	178	1e-11	31	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17415	GM_M24_B2_F02_MR	g99755	BLASTX	318	5e-29	52	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
17416	GM_M24_B2_F03_MF	g2586082	BLASTX	321	1e-26	55	(U72725) retrofit [Oryza longistaminata]
17417	GM_M24_B2_F05_MR	g2459417	BLASTX	154	6e-11	75	(AC002332) putative pre-mRNA splicing factor PRP19 [Arabidopsis thaliana]
17418	GM_M24_B2_F06_MF	g4063760	BLASTX	223	2e-16	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17419	GM_M24_B2_F09_MF	g2129618	BLASTX	196	1e-13	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17420	GM_M24_B2_G02_MF	g2764526	BLASTN	365	2e-09	60	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
17421	GM_M24_B2_G04_MR	g507910	BLASTN	395	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17422	GM_M24_B2_G07_MR	g4063760	BLASTX	218	1e-19	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17423	GM_M24_B2_G09_MR	g1769899	BLASTX	315	2e-27	78	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17424	GM_M24_B2_G12_MF	g1769897	BLASTX	163	2e-10	33	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17425	GM_M24_B2_H01_MF	g4038056	BLASTX	251	2e-19	42	(AC005897) putative transposon [Arabidopsis thaliana]
17426	GM_M24_B2_H01_MR	g4150933	BLASTN	395	8e-11	63	Homo sapiens BAC clone NH0520M18 from 7q31.1-q31.2, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17427	GM_M24_B2_H03_MF	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17428	GM_M24_B2_H03_MR	g507910	BLASTN	377	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17429	GM_M24_B2_H04_MF	g2995405	BLASTX	172	4e-11	37	(Y12432) polyprotein [Ananas comosus]
17430	GM_M24_B2_H04_MR	g505129	BLASTN	423	4e-12	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17431	GM_M24_B2_H06_MF	g2522228	BLASTX	389	3e-35	70	(AB007466) reverse transcriptase-like protein [Vicia faba]
17432	GM_M24_B2_H07_MR	g3777527	BLASTX	653	5e-62	93	(AF053008) gag-pol polyprotein [Glycine max]
17433	GM_M24_B2_H10_MR	g4063760	BLASTX	504	3e-46	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17434	GM_M24_B2_H11_MR	g3142328	BLASTN	862	4e-32	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17435	GM_M24_B2_H12_MF	g3036807	BLASTX	261	6e-26	67	(AL022373) putative protein [Arabidopsis thaliana]
17436	GM_M25_A1_A03_MF	g905361	BLASTX	618	1e-59	97	(U22103) gag-protease polyprotein [Glycine max]
17437	GM_M25_A1_A05_MR	g3142328	BLASTN	999	3e-38	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17438	GM_M25_A1_B01_MR	g3777527	BLASTX	196	3e-25	80	(AF053008) gag-pol polyprotein [Glycine max]
17439	GM_M25_A1_B04_MR	g2656026	BLASTN	354	6e-09	64	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MDF20
17440	GM_M25_A1_B10_MR	g507910	BLASTN	350	3e-09	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17441	GM_M25_A1_C01_MF	g3142330	BLASTX	610	9e-59	93	(U96295) envelope-like [Glycine max]
17442	GM_M25_A1_C06_MF	g3645899	BLASTX	215	2e-22	48	(U68408) 5' end not determined experimentally [Zea mays]
17443	GM_M25_A1_D05_MR	g905361	BLASTX	714	9e-70	99	(U22103) gag-protease polyprotein [Glycine max]
17444	GM_M25_A1_D08_MR	g4160362	BLASTN	392	1e-10	63	Saccharomyces cerevisiae complete mitochondrial genome
17445	GM_M25_A1_D09_MF	g4160362	BLASTN	352	7e-09	64	Saccharomyces cerevisiae complete mitochondrial genome
17446	GM_M25_A1_E03_MR	g3845197	BLASTN	422	5e-12	63	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
17447	GM_M25_A1_E07_MF	g20612	BLASTN	376	2e-24	75	Phaseolus vulgaris tRNA-Pro(UGG1) gene cluster
17448	GM_M25_A1_E07_MR	g2244866	BLASTX	539	9e-50	73	(Z97337) hypothetical protein [Arabidopsis thaliana]
17449	GM_M25_A1_F02_MF	g507910	BLASTN	547	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
17450	GM_M25_A1_F02_MR	g507910	BLASTN	556	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
17451	GM_M25_A1_F05_MR	g3645899	BLASTX	286	4e-23	48	(U68408) 5' end not determined experimentally [Zea mays]
17452	GM_M25_A1_F06_MR	g100484	BLASTX	193	2e-13	37	hypothetical protein - garden snapdragon
17453	GM_M25_A1_F08_MR	g2586082	BLASTX	224	3e-22	48	(U72725) retrofit [Oryza longistaminata]
17454	GM_M25_A1_F09_MF	g4038056	BLASTX	344	2e-29	54	(AC005897) putative transposon [Arabidopsis thaliana]
17455	GM_M25_A1_F11_MR	g3142328	BLASTN	733	3e-26	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17456	GM_M25_A1_G02_MF	g3097320	BLASTN	1208	1e-47	82	Glycine max gene for Bd 30K, complete cds
17457	GM_M25_A1_G03_MF	g1707020	BLASTX	407	3e-37	65	(U78721) hypothetical protein [Arabidopsis thaliana]
17458	GM_M25_A1_G05_MF	g505129	BLASTN	355	4e-09	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17459	GM_M25_A1_G11_MR	g507910	BLASTN	552	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
17460	GM_M25_A1_G12_MR	g3845197	BLASTN	524	1e-16	70	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
17461	GM_M25_A1_H01_MF	g3142328	BLASTN	710	4e-25	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17462	GM_M25_A1_H05_MF	g1399271	BLASTX	326	6e-28	79	(U31833) calmodulin-domain protein kinase CDPK isoform 2 [Arabidopsis thaliana]
17463	GM_M25_A1_H12_MR	g2828327	BLASTN	510	7e-17	67	Lycopersicon esculentum cv Red River unknown sequence PCR random amplified RAPD band 10
17464	GM_M25_A2_A05_MF	g1916643	BLASTX	281	7e-24	60	(U71604) desacetoxyvindoline 4-hydroxylase [Catharanthus roseus]
17465	GM_M25_A2_A08_MR	g3033389	BLASTX	194	2e-13	37	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
17466	GM_M25_A2_A10_MR	g3549672	BLASTX	154	1e-09	93	(AL031394) putative protein [Arabidopsis thaliana]
17467	GM_M25_A2_B02_MF	g170080	BLASTN	490	3e-15	78	Soybean seed lectin gene transposable element tgm1.
17468	GM_M25_A2_B08_MF	g3650039	BLASTX	269	1e-21	49	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
17469	GM_M25_A2_B09_MF	g3142328	BLASTN	806	2e-29	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17470	GM_M25_A2_B11_MR	g2129618	BLASTX	201	4e-14	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17471	GM_M25_A2_C02_MR	g409571	BLASTN	333	6e-09	66	Helicoverpa armigera mitochondrion D-loop, partial 12S rRNA gene, and partial tRNA-Met gene.
17472	GM_M25_A2_C03_MR	g507910	BLASTN	389	6e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17473	GM_M25_A2_C10_MF	g130582	BLASTX	171	3e-17	56	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
17474	GM_M25_A2_D01_MR	g18588	BLASTN	370	1e-09	75	Soybean gene 3 for chalcone synthetase protein
17475	GM_M25_A2_D03_MF	g2997694	BLASTX	148	1e-09	37	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
17476	GM_M25_A2_D04_MF	g1171583	BLASTN	377	5e-10	61	P.falciparum complete gene map of plastid-like DNA (IR-A)

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17477	GM_M25_A2_D04_MR	g2244752	BLASTX	146	1e-08	38	(Z97335) hypothetical protein [Arabidopsis thaliana]
17478	GM_M25_A2_D08_MF	g85105	BLASTX	183	4e-12	36	pol polyprotein - fruit fly (Drosophila melanogaster) transposon 1731 gi 8702 (X07656) pol polypeptide (AA 1-982) [Drosophila melanogaster]
17479	GM_M25_A2_D12_MR	g3367534	BLASTX	660	5e-63	90	(AC004392) Strong similarity to coatamer alpha subunit (HEPCOP) homolog gb U24105 from Homo sapiens. [Arabidopsis thaliana]
17480	GM_M25_A2_E07_MF	g2129618	BLASTX	196	1e-13	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17481	GM_M25_A2_F03_MR	g116162	BLASTX	212	1e-16	56	G2/MITOTIC-SPECIFIC CYCLIN S13-7 (B-LIKE CYCLIN) gi 2146780 pir S74672 mitotic-specific cyclin S13-7 - soybean (fragment) gi 829266 (X62303) mitotic cyclin [Glycine max]
17482	GM_M25_A2_F04_MF	g2323254	BLASTN	392	1e-10	64	Human Chromosome X, complete sequence [Homo sapiens]
17483	GM_M25_A2_F09_MR	g3097320	BLASTN	603	3e-20	69	Glycine max gene for Bd 30K, complete cds
17484	GM_M25_A2_F10_MR	g130582	BLASTX	281	2e-22	42	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
17485	GM_M25_A2_F11_MR	g3097320	BLASTN	460	8e-14	69	Glycine max gene for Bd 30K, complete cds
17486	GM_M25_A2_F12_MF	g421955	BLASTX	206	2e-15	40	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
17487	GM_M25_A2_G04_MF	g1171591	BLASTN	363	2e-09	63	P.falciparum complete gene map of plastid-like DNA (IR-B)
17488	GM_M25_A2_G05_MR	g2341025	BLASTX	143	5e-16	74	(AC000104) F19P19.2 [Arabidopsis thaliana]
17489	GM_M25_A2_G09_MF	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17490	GM_M25_A2_G09_MR	g3777527	BLASTX	698	8e-67	97	(AF053008) gag-pol polyprotein [Glycine max]
17491	GM_M25_A2_H01_MR	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17492	GM_M25_A2_H02_MR	g1666236	BLASTX	198	8e-15	33	(U76261) unknown [Hordeum vulgare]
17493	GM_M25_A2_H05_MF	g4038056	BLASTX	251	2e-19	42	(AC005897) putative transposon [Arabidopsis thaliana]
17494	GM_M25_A2_H07_MR	g3845197	BLASTN	431	2e-12	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
17495	GM_M25_A2_H10_MR	g99922	BLASTX	455	2e-42	65	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17496	GM_M25_A2_H12_MF	g114610	BLASTX	248	5e-23	80	ATP SYNTHASE EPSILON CHAIN gi 67866 pir PWNTE H+-transporting ATP synthase (EC 3.6.1.34) epsilon chain - common tobacco chloroplast gi 11839 (Z00044) ATPase epsilon subunit [Nicotiana tabacum] gi 552955 (K00507) ATPase epsilon subunit [Nicotiana tabacum] gi 225207 prf 1211235AM ATPase epsilon [Nicotiana tabacum]
17497	GM_M25_B1_A01_MR	g2842490	BLASTX	301	5e-26	51	(AL021749) heat-shock protein [Arabidopsis thaliana]
17498	GM_M25_B1_A05_MR	g2760331	BLASTX	232	2e-17	35	(AC002130) F1N21.16 [Arabidopsis thaliana]
17499	GM_M25_B1_A06_MF	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17500	GM_M25_B1_A11_MR	g4126312	BLASTN	489	5e-15	64	Homo sapiens 8q21.3: Nibrin (NBS1), 2,4-dienoyl-CoA reductase (DECR), and calbindin 1 (CALB1) genes, complete sequence [Homo sapiens]
17501	GM_M25_B1_B02_MF	g130582	BLASTX	415	9e-37	63	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
17502	GM_M25_B1_B09_MF	g4063760	BLASTX	174	1e-14	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17503	GM_M25_B1_B09_MR	g1769898	BLASTX	266	2e-21	53	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17504	GM_M25_B1_B11_MR	g285741	BLASTX	226	2e-17	49	(D14550) EDGP precursor [Daucus carota]
17505	GM_M25_B1_B12_MF	g729092	BLASTX	563	8e-54	81	CALCIUM-DEPENDENT PROTEIN KINASE, ISOFORM AK1 (CDPK) gi 477484 pir A49082 calcium-dependent protein kinase isoform AK1 - Arabidopsis thaliana gi 304105 (L14771) calcium-dependent protein kinase [Arabidopsis thaliana]
17506	GM_M25_B1_B12_MR	g531389	BLASTX	255	1e-19	41	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
17507	GM_M25_B1_C05_MR	g505129	BLASTN	358	3e-09	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17508	GM_M25_B1_C10_MR	g4063760	BLASTX	566	6e-53	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17509	GM_M25_B1_C12_MF	g2149808	BLASTX	167	2e-24	73	(U92853) maturase [Betula papyrifera]
17510	GM_M25_B1_D01_MR	g507910	BLASTN	602	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17511	GM_M25_B1_D05_MF	g4063760	BLASTX	123	6e-14	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17512	GM_M25_B1_D05_MR	g507910	BLASTN	589	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17513	GM_M25_B1_D06_MR	g13534	BLASTN	366	1e-09	61	Yeast (S. cerevisiae) mitochondrial gene for cytochrome B extending from map position 71.3 to 80.2. (Strain D273-10B.)

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17514	GM_M25_B1_D09_MF	g507910	BLASTN	422	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17515	GM_M25_B1_D10_MF	g421955	BLASTX	196	2e-27	41	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
17516	GM_M25_B1_E03_MR	g3184283	BLASTX	278	3e-22	69	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]
17517	GM_M25_B1_E05_MF	g507910	BLASTN	386	8e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17518	GM_M25_B1_E07_MR	g2708743	BLASTX	116	2e-11	48	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
17519	GM_M25_B1_F03_MF	g4063760	BLASTX	494	3e-45	69	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17520	GM_M25_B1_F06_MF	g905361	BLASTX	192	2e-13	36	(U22103) gag-protease polyprotein [Glycine max]
17521	GM_M25_B1_G04_MF	g4063756	BLASTN	480	1e-14	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17522	GM_M25_B1_G04_MR	g507910	BLASTN	415	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17523	GM_M25_B1_G07_MR	g3650039	BLASTX	247	3e-19	39	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
17524	GM_M25_B1_G10_MR	g905361	BLASTX	237	3e-18	42	(U22103) gag-protease polyprotein [Glycine max]
17525	GM_M25_B1_G12_MF	g2764526	BLASTN	428	3e-12	62	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
17526	GM_M25_B2_A01_MF	g2522228	BLASTX	182	1e-12	70	(AB007466) reverse transcriptase-like protein [Vicia faba]
17527	GM_M25_B2_A01_MR	g3777527	BLASTX	463	9e-47	94	(AF053008) gag-pol polyprotein [Glycine max]
17528	GM_M25_B2_A06_MF	g2522228	BLASTX	171	2e-11	38	(AB007466) reverse transcriptase-like protein [Vicia faba]
17529	GM_M25_B2_A07_MF	g1769897	BLASTX	183	1e-12	33	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17530	GM_M25_B2_A08_MF	g4063760	BLASTX	178	2e-11	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17531	GM_M25_B2_A10_MF	g3452140	BLASTX	180	3e-13	64	(AJ004901) resistance protein [Glycine max]
17532	GM_M25_B2_A11_MF	g3395435	BLASTX	256	1e-20	44	(AC004683) myosin heavy chain-like protein [Arabidopsis thaliana]
17533	GM_M25_B2_B02_MF	g3377855	BLASTX	161	1e-10	37	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
17534	GM_M25_B2_B03_MF	g1000971	BLASTN	293	5e-10	70	Hansenula wingei mitochondrial DNA, complete sequence
17535	GM_M25_B2_B04_MF	g3777527	BLASTX	177	3e-11	31	(AF053008) gag-pol polyprotein [Glycine max]
17536	GM_M25_B2_B05_MF	g3097320	BLASTN	489	4e-15	65	Glycine max gene for Bd 30K, complete cds
17537	GM_M25_B2_B08_MF	g3777527	BLASTX	572	2e-53	92	(AF053008) gag-pol polyprotein [Glycine max]
17538	GM_M25_B2_B09_MF	g292994	BLASTN	366	2e-10	64	Jalmenus evagoras evagoras mitochondrial D-loop DNA, transfer RNA-Met gene, and 12S ribosomal RNA gene, 5' end.
17539	GM_M25_B2_B09_MR	g2462058	BLASTX	153	3e-10	50	(Y13389) reverse transcriptase [Antirrhinum majus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17540	GM_M25_B2_C03_MR	g3758836	BLASTN	373	5e-11	64	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
17541	GM_M25_B2_C04_MR	g2501353	BLASTX	216	1e-22	89	TRANSKETOLASE, CHLOROPLAST (TK) gi 1084440 pir S54300 transketolase (EC 2.2.1.1) 3 - Craterostigma plantagineum (fragment) gi 664901 (Z46646) transketolase [Craterostigma plantagineum]
17542	GM_M25_B2_C05_MF	g3033389	BLASTX	167	2e-10	37	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
17543	GM_M25_B2_C11_MF	g3142328	BLASTN	894	2e-33	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17544	GM_M25_B2_D01_MR	g3873182	BLASTN	548	1e-17	68	Homo sapiens chromosome 17, clone hRPK.235_I_10, complete sequence [Homo sapiens]
17545	GM_M25_B2_D03_MR	g905361	BLASTX	680	4e-66	97	(U22103) gag-protease polyprotein [Glycine max]
17546	GM_M25_B2_D06_MR	g99922	BLASTX	692	2e-67	86	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17547	GM_M25_B2_D07_MF	g4150930	BLASTN	371	1e-09	71	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
17548	GM_M25_B2_D08_MF	g507910	BLASTN	740	8e-27	89	Glycine max BSR-101 satellite SB92 genomic sequence.
17549	GM_M25_B2_D08_MR	g4063756	BLASTN	464	6e-14	71	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17550	GM_M25_B2_D09_MR	g2764525	BLASTN	736	2e-26	68	Pisum sativum genomic DNA encoding truncated Ty3/Gypsy-like retroelement Cyclops-1
17551	GM_M25_B2_D10_MF	g2462826	BLASTX	248	5e-19	54	(AF000657) unknown protein [Arabidopsis thaliana]
17552	GM_M25_B2_D10_MR	g2632254	BLASTX	167	5e-11	54	(Y12465) serine/threonine kinase [Sorghum bicolor]
17553	GM_M25_B2_D12_MF	g2522227	BLASTX	217	4e-17	55	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
17554	GM_M25_B2_E05_MF	g4063760	BLASTX	335	3e-28	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17555	GM_M25_B2_E06_MF	g3047116	BLASTX	184	4e-13	68	(AF058919) No definition line found [Arabidopsis thaliana]
17556	GM_M25_B2_E08_MF	g1684913	BLASTX	265	7e-21	46	(U77888) receptor-like protein kinase [Ipomoea nil]
17557	GM_M25_B2_F02_MF	g507910	BLASTN	369	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17558	GM_M25_B2_F02_MR	g507910	BLASTN	354	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17559	GM_M25_B2_F03_MF	g342964	BLASTN	349	1e-09	61	paramecium species 5,311 mt dna dimer: replication init. region.
17560	GM_M25_B2_F03_MR	g99730	BLASTX	164	5e-23	53	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17561	GM_M25_B2_F05_MF	g99922	BLASTX	309	7e-27	54	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17562	GM_M25_B2_F05_MR	g99922	BLASTX	176	3e-12	64	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17563	GM_M25_B2_G04_MF	g4063756	BLASTN	485	7e-15	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17564	GM_M25_B2_G05_MF	g4038056	BLASTX	340	5e-29	50	(AC005897) putative transposon [Arabidopsis thaliana]
17565	GM_M25_B2_G05_MR	g3142328	BLASTN	1318	8e-53	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17566	GM_M25_B2_G06_MF	g1769897	BLASTX	167	6e-11	42	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17567	GM_M25_B2_G07_MR	g226407	BLASTX	286	6e-30	68	retrotransposon del1-46 [Lilium henryi]
17568	GM_M25_B2_G10_MF	g3176693	BLASTN	341	3e-15	78	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]
17569	GM_M25_B2_G11_MF	g3738302	BLASTX	91	6e-09	61	(AC005309) tubby-like protein [Arabidopsis thaliana]
17570	GM_M25_B2_G11_MR	g3337361	BLASTX	215	9e-16	62	(AC004481) ankyrin-like protein [Arabidopsis thaliana]
17571	GM_M25_B2_G12_MR	g3319366	BLASTX	186	8e-14	40	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
17572	GM_M25_B2_H04_MR	g3319362	BLASTX	134	2e-25	50	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17573	GM_M25_B2_H05_MR	g1167523	BLASTX	156	3e-09	29	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
17574	GM_M25_B2_H06_MR	g3426334	BLASTN	350	8e-09	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
17575	GM_M25_B2_H09_MF	g507910	BLASTN	393	4e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
17576	GM_M25_B2_H09_MR	g507910	BLASTN	387	7e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17577	GM_M25_B2_H10_MF	g4063756	BLASTN	450	3e-13	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17578	GM_M25_B2_H12_MF	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17579	GM_M25_B2_H12_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17580	GM_M26_A1_A04_MR	g3930515	BLASTX	107	1e-10	47	(AF059674) putative gag protein [Nicotiana tabacum]
17581	GM_M26_A1_A07_MF	g3287696	BLASTX	292	5e-24	55	(AC003979) Strong similarity to phosphoribosylanthranilate transferase gb D86180 from Pisum sativum. This ORF may be part of a larger gene that lies in the overlapping region. [Arabidopsis thaliana]
17582	GM_M26_A1_A11_MF	g3859610	BLASTN	395	8e-11	65	Arabidopsis thaliana BAC T9E19
17583	GM_M26_A1_A12_MF	g3941522	BLASTX	175	1e-12	74	(AF062915) putative transcription factor [Arabidopsis thaliana]
17584	GM_M26_A1_B03_MF	g3142379	BLASTX	316	1e-27	56	(AF053008) envelope-like [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17585	GM_M26_A1_B05_MR	g3063690	BLASTN	353	7e-09	63	Arabidopsis thaliana DNA chromosome 4, BAC clone F4D11 (ESSAII project)
17586	GM_M26_A1_B06_MR	g3695399	BLASTX	214	2e-15	40	(AF096372) contains similarity to Arabidopsis thaliana retrotransposon Athila (GB:X81801) [Arabidopsis thaliana]
17587	GM_M26_A1_B09_MF	g2522228	BLASTX	343	2e-30	55	(AB007466) reverse transcriptase-like protein [Vicia faba]
17588	GM_M26_A1_C09_MF	g3142328	BLASTN	545	1e-17	73	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17589	GM_M26_A1_D02_MR	g4063760	BLASTX	300	1e-24	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17590	GM_M26_A1_D03_MF	g3176689	BLASTX	156	6e-09	29	(AC003671) Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gb Z35927 from S. cerevisiae. [Arabidopsis thaliana]
17591	GM_M26_A1_D03_MR	g3461840	BLASTX	313	9e-26	44	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
17592	GM_M26_A1_D09_MF	g2342686	BLASTX	159	1e-10	46	(AC000106) Similar to Saccharomyces hypothetical protein YDR051c (gb Z49209). ESTs gb T44436,gb 42252 come from this gene. [Arabidopsis thaliana]
17593	GM_M26_A1_E01_MR	g3645899	BLASTX	374	2e-32	59	(U68408) 5' end not determined experimentally [Zea mays]
17594	GM_M26_A1_E04_MF	g3650039	BLASTX	209	3e-15	39	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
17595	GM_M26_A1_E11_MR	g3645899	BLASTX	241	3e-19	48	(U68408) 5' end not determined experimentally [Zea mays]
17596	GM_M26_A1_F09_MF	g218268	BLASTN	389	4e-11	76	Glycine max pol gene for reverse transcriptase, partial sequence
17597	GM_M26_A1_G01_MF	g3777527	BLASTX	594	9e-56	85	(AF053008) gag-pol polyprotein [Glycine max]
17598	GM_M26_A1_G03_MR	g3645899	BLASTX	366	1e-31	50	(U68408) 5' end not determined experimentally [Zea mays]
17599	GM_M26_A1_G05_MF	g3157933	BLASTX	224	1e-16	45	(AC002131) Contains similarity to box helicases gb U29097 from C. elegans and to the ENBP1 gene product gb X95995 from Vicia sativa. [Arabidopsis thaliana]
17600	GM_M26_A1_G08_MR	g461812	BLASTX	184	3e-26	47	CYTOCHROME P450 LXXII (PROBABLE GERANIOL-10-HYDROXYLASE) (GE10H) gi 167484 (L10081) Cytochrome P-450 protein [Catharanthus roseus] gi 445604 prf 1909351A cytochrome P450 [Catharanthus roseus]
17601	GM_M26_A1_G09_MR	g2642431	BLASTX	338	2e-28	53	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
17602	GM_M26_A1_G10_MF	g507910	BLASTN	354	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17603	GM_M26_A1_G10_MR	g507910	BLASTN	371	4e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17604	GM_M26_A1_H06_MF	g2335089	BLASTN	847	3e-31	73	Arabidopsis thaliana chromosome II BAC T11A7 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17605	GM_M26_A2_A05_MR	g2129618	BLASTX	139	4e-09	32	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17606	GM_M26_A2_B03_MF	g322701	BLASTX	436	3e-40	88	Tubulin beta-2 chain - soybean
17607	GM_M26_A2_B04_MF	g507910	BLASTN	346	5e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
17608	GM_M26_A2_B04_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17609	GM_M26_A2_B11_MF	g3142379	BLASTX	289	1e-24	63	(AF053008) envelope-like [Glycine max]
17610	GM_M26_A2_C02_MF	g4006827	BLASTX	277	2e-22	48	(AC005970) subtilisin-like protease [Arabidopsis thaliana]
17611	GM_M26_A2_C02_MR	g1944188	BLASTN	529	3e-17	70	Soybean DNA for nodulin 35, partial cds
17612	GM_M26_A2_C06_MF	g507910	BLASTN	380	1e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17613	GM_M26_A2_C07_MR	g4063760	BLASTX	158	2e-09	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17614	GM_M26_A2_C12_MR	g505129	BLASTN	304	4e-10	69	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17615	GM_M26_A2_D02_MF	g3097320	BLASTN	444	5e-13	72	Glycine max gene for Bd 30K, complete cds
17616	GM_M26_A2_D02_MR	g2522230	BLASTX	301	5e-26	41	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
17617	GM_M26_A2_D03_MR	g3097320	BLASTN	1182	2e-46	81	Glycine max gene for Bd 30K, complete cds
17618	GM_M26_A2_D06_MF	g3142328	BLASTN	976	3e-37	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17619	GM_M26_A2_D07_MR	g2522230	BLASTX	184	1e-13	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
17620	GM_M26_A2_D10_MF	g99922	BLASTX	603	5e-58	88	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17621	GM_M26_A2_D12_MR	g18559	BLASTN	928	5e-35	77	G.max gene for catalase
17622	GM_M26_A2_E03_MR	g1666236	BLASTX	98	2e-09	38	(U76261) unknown [Hordeum vulgare]
17623	GM_M26_A2_F02_MF	g2462134	BLASTX	166	8e-11	33	(Y13368) reverse transcriptase [Beta vulgaris]
17624	GM_M26_A2_F03_MR	g1142699	BLASTN	1163	3e-46	83	Glycine max satellite STR120-A.1.
17625	GM_M26_A2_F04_MR	g507910	BLASTN	360	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17626	GM_M26_A2_F05_MF	g1813704	BLASTX	227	9e-17	40	(U82559) aldehyde oxidase 1 homolog [Lycopersicon esculentum]
17627	GM_M26_A2_F08_MF	g4063760	BLASTX	368	9e-32	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17628	GM_M26_A2_F09_MR	g2598589	BLASTX	317	1e-27	46	(Y15367) MtN19 [Medicago truncatula]
17629	GM_M26_A2_G01_MR	g905361	BLASTX	385	2e-34	100	(U22103) gag-protease polyprotein [Glycine max]
17630	GM_M26_A2_G04_MF	g1230613	BLASTN	353	3e-09	75	Lupinus albus isoflavone reductase-like protein mRNA, complete cds.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17631	GM_M26_A2_G06_MR	g130582	BLASTX	170	1e-10	44	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
17632	GM_M26_A2_H02_MR	g3059060	BLASTN	416	9e-12	61	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
17633	GM_M26_A2_H05_MR	g2129581	BLASTX	496	9e-46	75	envelope Ca2+-ATPase precursor - Arabidopsis thaliana gi 471089 gnl PID d1003597 (D13984) chloroplast envelope Ca2+-ATPase precursor [Arabidopsis thaliana]
17634	GM_M26_A2_H08_MF	g507910	BLASTN	602	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17635	GM_M26_A2_H08_MR	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17636	GM_M26_B2_A07_MR	g507910	BLASTN	396	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17637	GM_M26_B2_C10_MR	g507910	BLASTN	397	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17638	GM_M26_B2_C11_MR	g1769898	BLASTX	148	4e-10	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17639	GM_M26_B2_D06_MR	g421955	BLASTX	134	2e-27	61	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
17640	GM_M26_B2_D10_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17641	GM_M26_B2_E07_MR	g507910	BLASTN	389	6e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17642	GM_M26_B2_F03_MR	g507910	BLASTN	550	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
17643	GM_M26_B2_F05_MR	g2351073	BLASTN	761	2e-27	69	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYJ24
17644	GM_M26_B2_F08_MR	g507910	BLASTN	599	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17645	GM_M26_B2_F10_MR	g3269288	BLASTX	142	4e-09	58	(AL030978) putative protein [Arabidopsis thaliana]
17646	GM_M26_B2_G02_MR	g905361	BLASTX	289	6e-24	96	(U22103) gag-protease polyprotein [Glycine max]
17647	GM_M26_B2_G03_MR	g13774	BLASTN	353	3e-09	60	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
17648	GM_M26_B2_G05_MR	g3097320	BLASTN	456	1e-13	70	Glycine max gene for Bd 30K, complete cds
17649	GM_M26_B2_G07_MR	g18559	BLASTN	997	3e-38	76	G.max gene for catalase
17650	GM_M26_B2_G08_MR	g1480927	BLASTN	1064	9e-42	94	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17651	GM_M26_B2_H01_MR	g3142328	BLASTN	1091	2e-42	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17652	GM_M26_B2_H03_MR	g1142702	BLASTN	343	5e-09	68	Glycine max satellite STR120-A.4.
17653	GM_M26_B2_H05_MR	g2808683	BLASTX	182	4e-12	35	(AJ002235) Cf-4 [Lycopersicon hirsutum]
17654	GM_M26_B2_H09_MR	g116054	BLASTX	158	6e-10	82	CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK) gi 280393 pir A43713 calcium-dependent protein kinase (EC 2.7.1.-) - soybean gi 169931 (M64987) Glycine max calcium dependent protein kinase mRNA. [Glycine max]
17655	GM_M26_B2_H10_MR	g3128201	BLASTX	126	3e-09	33	(AC004521) unknown protein [Arabidopsis thaliana]
17656	GM_M27_A1_B01_MR	g1769898	BLASTX	367	5e-41	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17657	GM_M27_A1_B03_MF	g507910	BLASTN	589	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17658	GM_M27_A1_B03_MR	g507910	BLASTN	638	3e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
17659	GM_M27_A1_B07_MF	g507910	BLASTN	488	2e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
17660	GM_M27_A1_B09_MF	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17661	GM_M27_A1_B09_MR	g507910	BLASTN	370	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17662	GM_M27_A1_B11_MF	g2129709	BLASTX	160	1e-09	32	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
17663	GM_M27_A1_C02_MF	g4038056	BLASTX	328	9e-28	52	(AC005897) putative transposon [Arabidopsis thaliana]
17664	GM_M27_A1_C03_MF	g3097320	BLASTN	543	2e-17	84	Glycine max gene for Bd 30K, complete cds
17665	GM_M27_A1_C04_MF	g4115916	BLASTX	188	1e-13	40	(AF118222) F3H7.9 gene product [Arabidopsis thaliana]
17666	GM_M27_A1_C08_MR	g1769897	BLASTX	233	6e-18	36	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17667	GM_M27_A1_C10_MR	g4063760	BLASTX	403	2e-35	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17668	GM_M27_A1_C12_MF	g18559	BLASTN	498	1e-15	67	G.max gene for catalase
17669	GM_M27_A1_C12_MR	g2995405	BLASTX	497	5e-46	67	(Y12432) polyprotein [Ananas comosus]
17670	GM_M27_A1_D01_MR	g2829915	BLASTX	286	2e-23	45	(AC002291) Hypothetical protein [Arabidopsis thaliana]
17671	GM_M27_A1_D02_MF	g3777527	BLASTX	132	3e-10	32	(AF053008) gag-pol polyprotein [Glycine max]
17672	GM_M27_A1_D07_MF	g3930515	BLASTX	121	7e-09	47	(AF059674) putative gag protein [Nicotiana tabacum]
17673	GM_M27_A1_D07_MR	g1142699	BLASTN	1166	2e-46	83	Glycine max satellite STR120-A.1.
17674	GM_M27_A1_D10_MF	g2129618	BLASTX	202	3e-14	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17675	GM_M27_A1_D11_MF	g2129618	BLASTX	203	2e-14	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17676	GM_M27_A1_E04_MF	g3550435	BLASTN	469	4e-14	63	Hordeum vulgare Hotr1 gene
17677	GM_M27_A1_E10_MR	g3097320	BLASTN	433	1e-12	75	Glycine max gene for Bd 30K, complete cds
17678	GM_M27_A1_F03_MF	g3927831	BLASTX	193	7e-14	81	(AC005727) similar to mouse ankyrin 3 [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17679	GM_M27_A1_F06_MF	g2129618	BLASTX	175	2e-11	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17680	GM_M27_A1_F12_MR	g3097836	BLASTN	438	9e-13	64	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
17681	GM_M27_A1_G01_MF	g4063760	BLASTX	262	2e-20	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17682	GM_M27_A1_G09_MF	g3142328	BLASTN	963	1e-36	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17683	GM_M27_A1_G09_MR	g3645899	BLASTX	396	4e-37	61	(U68408) 5' end not determined experimentally [Zea mays]
17684	GM_M27_A1_H01_MR	g18559	BLASTN	975	3e-37	77	G.max gene for catalase
17685	GM_M27_A1_H05_MR	g18559	BLASTN	1026	2e-39	78	G.max gene for catalase
17686	GM_M27_A1_H06_MF	g99922	BLASTX	487	1e-47	80	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17687	GM_M27_A1_H08_MF	g2708743	BLASTX	170	1e-10	36	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
17688	GM_M27_A1_H10_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17689	GM_M27_A2_A02_MR	g3582328	BLASTX	145	3e-11	40	(AC005496) hypothetical protein [Arabidopsis thaliana]
17690	GM_M27_A2_A05_MR	g507910	BLASTN	620	2e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17691	GM_M27_A2_B05_MR	g2129709	BLASTX	311	1e-25	40	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
17692	GM_M27_A2_B07_MR	g2213632	BLASTX	194	5e-14	52	(AC000103) F21J9.24 [Arabidopsis thaliana]
17693	GM_M27_A2_C04_MR	g3142328	BLASTN	688	4e-24	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17694	GM_M27_A2_D08_MR	g18559	BLASTN	666	4e-23	76	G.max gene for catalase
17695	GM_M27_A2_E04_MR	g507910	BLASTN	385	9e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17696	GM_M27_A2_E12_MR	g3142328	BLASTN	838	5e-31	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17697	GM_M27_A2_F02_MR	g2252634	BLASTX	428	4e-39	48	(U95973) hypothetical protein [Arabidopsis thaliana]
17698	GM_M27_A2_F06_MR	g3510262	BLASTX	153	1e-09	66	(AC005310) NAM like protein [Arabidopsis thaliana]
17699	GM_M27_A2_F10_MR	g1769898	BLASTX	135	9e-13	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17700	GM_M27_A2_G01_MR	g3059060	BLASTN	402	4e-11	65	Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideraemia protein, T...
17701	GM_M27_A2_G02_MR	g2864626	BLASTX	237	2e-18	43	(AL021811) cytochrome p450 - like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17702	GM_M27_A2_G06_MR	g1769897	BLASTX	287	7e-24	72	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17703	GM_M27_A2_G10_MR	g3645899	BLASTX	197	1e-13	49	(U68408) 5' end not determined experimentally [Zea mays]
17704	GM_M27_A2_H02_MR	g1769897	BLASTX	157	9e-10	29	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17705	GM_M27_A2_H08_MR	g3097320	BLASTN	559	3e-18	79	Glycine max gene for Bd 30K, complete cds
17706	GM_M27_A2_H11_MR	g4063760	BLASTX	414	1e-36	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17707	GM_M27_B2_A02_MF	g3097320	BLASTN	526	9e-17	73	Glycine max gene for Bd 30K, complete cds
17708	GM_M27_B2_B01_MF	g2465923	BLASTX	265	2e-25	64	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]
17709	GM_M27_B2_B05_MF	g4033532	BLASTX	197	2e-23	61	(X78274) polygalacturonase-inhibiting protein [Glycine max]
17710	GM_M27_B2_B06_MF	g9908	BLASTN	358	3e-09	66	P. falciparum SD17 gene for knob-associated histidine-rich protein
17711	GM_M27_B2_B07_MF	g2495179	BLASTX	162	1e-10	85	PORPHOBILINOGEN DEAMINASE PRECURSOR (PBG) (HYDROXYMETHYLBILANE SYNTHASE) (HMBS) (PRE-UROPORPHYRINOGEN SYNTHASE) gi 1084340 pir S50762 hydroxymethylbilane synthase (EC 4.3.1.8) precursor - Arabidopsis thaliana gi 313150 (X73535) hydroxymethylbilane synthase [Arabidopsis thaliana] gi 313838 (X73839) hydroxymethylbilane synthase [Arabidopsis thaliana]
17712	GM_M27_B2_C01_MF	g2465923	BLASTX	268	1e-25	65	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]
17713	GM_M27_B2_C03_MF	g3810835	BLASTX	146	8e-09	34	(AL032684) putative RNA-binding protein [Schizosaccharomyces pombe]
17714	GM_M27_B2_C06_MF	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
17715	GM_M27_B2_C08_MF	g4063756	BLASTN	480	1e-14	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17716	GM_M27_B2_D06_MF	g3097320	BLASTN	570	9e-19	76	Glycine max gene for Bd 30K, complete cds
17717	GM_M27_B2_D12_MF	g3777527	BLASTX	571	3e-53	97	(AF053008) gag-pol polyprotein [Glycine max]
17718	GM_M27_B2_E01_MF	g18559	BLASTN	518	2e-16	71	G.max gene for catalase
17719	GM_M27_B2_E03_MF	g3319362	BLASTX	171	6e-11	36	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17720	GM_M27_B2_F03_MF	g2129709	BLASTX	190	1e-12	34	reverse transcriptase - Arabidopsis thaliana retrotransposon Ta11-1 gi 976278 (L47193) reverse transcriptase [Arabidopsis thaliana]
17721	GM_M27_B2_F08_MF	g3777526	BLASTN	526	9e-17	80	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
17722	GM_M27_B2_F11_MF	g170605	BLASTN	526	4e-17	67	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17723	GM_M27_B2_G03_MF	g3738114	BLASTN	439	9e-13	69	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
17724	GM_M27_B2_G05_MF	g3702731	BLASTN	475	2e-14	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MFC19, complete sequence [Arabidopsis thaliana]
17725	GM_M27_B2_G09_MF	g1418331	BLASTX	377	2e-33	54	(X95909) receptor like protein kinase [Arabidopsis thaliana]
17726	GM_M27_B2_G12_MF	g3033389	BLASTX	185	2e-12	41	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
17727	GM_M27_B2_H03_MF	g1666236	BLASTX	152	2e-15	34	(U76261) unknown [Hordeum vulgare]
17728	GM_M27_B2_H08_MF	g3513301	BLASTN	352	7e-09	63	Homo sapiens chromosome 19, cosmid R26894, complete sequence [Homo sapiens]
17729	GM_M28_A1_A01_MF	g3097320	BLASTN	1207	1e-47	82	Glycine max gene for Bd 30K, complete cds
17730	GM_M28_A1_A02_MR	g3319362	BLASTX	378	5e-33	56	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17731	GM_M28_A1_A08_MF	g1438878	BLASTN	367	8e-10	80	Glycine max choline kinase GmCK1p mRNA, complete cds
17732	GM_M28_A1_B02_MF	g505129	BLASTN	376	5e-10	65	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
17733	GM_M28_A1_B08_MF	g2586082	BLASTX	256	9e-20	48	(U72725) retrofit [Oryza longistaminata]
17734	GM_M28_A1_C04_MR	g3142328	BLASTN	1148	4e-45	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17735	GM_M28_A1_C10_MF	g4063760	BLASTX	202	4e-14	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17736	GM_M28_A1_C10_MR	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
17737	GM_M28_A1_C12_MR	g4063760	BLASTX	277	4e-22	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17738	GM_M28_A1_D01_MF	g3142328	BLASTN	989	7e-38	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17739	GM_M28_A1_D01_MR	g3777527	BLASTX	663	4e-63	95	(AF053008) gag-pol polyprotein [Glycine max]
17740	GM_M28_A1_D02_MR	g1666236	BLASTX	213	1e-16	33	(U76261) unknown [Hordeum vulgare]
17741	GM_M28_A1_D09_MF	g2995405	BLASTX	186	2e-12	48	(Y12432) polyprotein [Ananas comosus]
17742	GM_M28_A1_E01_MF	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
17743	GM_M28_A1_E12_MR	g507910	BLASTN	380	1e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17744	GM_M28_A1_F05_MR	g421955	BLASTX	421	1e-38	58	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
17745	GM_M28_A1_F07_MR	g18559	BLASTN	667	3e-23	73	G.max gene for catalase
17746	GM_M28_A1_F10_MR	g1769898	BLASTX	344	6e-30	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17747	GM_M28_A1_G01_MR	g2522228	BLASTX	310	6e-27	56	(AB007466) reverse transcriptase-like protein [Vicia faba]
17748	GM_M28_A1_G02_MF	g100484	BLASTX	223	2e-19	53	hypothetical protein - garden snapdragon
17749	GM_M28_A1_G02_MR	g226407	BLASTX	269	4e-21	42	retrotransposon del1-46 [Lilium henryi]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17750	GM_M28_A1_G06_MR	g3810595	BLASTX	104	2e-10	55	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
17751	GM_M28_A1_H01_MF	g3860271	BLASTX	150	1e-08	36	(AC005824) putative selenium-binding protein [Arabidopsis thaliana]
17752	GM_M28_A1_H03_MF	g4038056	BLASTX	150	3e-14	41	(AC005897) putative transposon [Arabidopsis thaliana]
17753	GM_M28_A1_H06_MF	g536873	BLASTX	247	7e-19	42	(M34549) POL3 gene product [Saccharomyces cerevisiae]
17754	GM_M28_A1_H07_MF	g2462134	BLASTX	289	3e-24	50	(Y13368) reverse transcriptase [Beta vulgaris]
17755	GM_M28_A1_H09_MR	g507910	BLASTN	375	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17756	GM_M28_A1_H10_MF	g1769899	BLASTX	235	3e-22	70	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17757	GM_M28_A1_H10_MR	g3097320	BLASTN	478	1e-14	70	Glycine max gene for Bd 30K, complete cds
17758	GM_M28_A2_A02_MR	g3426334	BLASTN	446	4e-13	63	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
17759	GM_M28_A2_A11_MR	g4140712	BLASTX	314	2e-27	47	(AF110183) putative integrase [Oryza sativa]
17760	GM_M28_A2_B05_MF	g2618603	BLASTN	436	1e-12	62	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSL3, complete sequence [Arabidopsis thaliana]
17761	GM_M28_A2_B07_MF	g4138265	BLASTX	239	4e-19	81	(AJ006228) Avr9 elicitor response protein [Nicotiana tabacum]
17762	GM_M28_A2_B12_MR	g18559	BLASTN	382	3e-10	64	G.max gene for catalase
17763	GM_M28_A2_C01_MR	g3337395	BLASTN	427	3e-12	63	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
17764	GM_M28_A2_C02_MR	g4160362	BLASTN	353	7e-09	62	Saccharomyces cerevisiae complete mitochondrial genome
17765	GM_M28_A2_C03_MF	g4063760	BLASTX	479	1e-43	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17766	GM_M28_A2_C03_MR	g3695395	BLASTX	235	5e-18	37	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
17767	GM_M28_A2_D03_MF	g2764526	BLASTN	701	1e-24	70	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
17768	GM_M28_A2_D03_MR	g18559	BLASTN	857	8e-32	78	G.max gene for catalase
17769	GM_M28_A2_D05_MR	g3021268	BLASTX	177	2e-11	36	(AL022347) putative protein [Arabidopsis thaliana]
17770	GM_M28_A2_D09_MF	g3142328	BLASTN	1558	9e-64	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17771	GM_M28_A2_D10_MR	g2895633	BLASTN	360	1e-09	61	Zerene cesonia large subunit ribosomal RNA gene, partial sequence; tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs
17772	GM_M28_A2_D12_MF	g3241935	BLASTN	513	4e-16	64	Arabidopsis thaliana chromosome IV from 19 cM, complete sequence [Arabidopsis thaliana]
17773	GM_M28_A2_E05_MF	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17774	GM_M28_A2_E05_MR	g507910	BLASTN	380	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17775	GM_M28_A2_E09_MF	g2764526	BLASTN	414	1e-11	62	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
17776	GM_M28_A2_F01_MF	g905361	BLASTX	399	6e-36	91	(U22103) gag-protease polyprotein [Glycine max]
17777	GM_M28_A2_F02_MF	g99729	BLASTX	129	5e-20	54	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
17778	GM_M28_A2_F03_MF	g3097320	BLASTN	580	3e-19	80	Glycine max gene for Bd 30K, complete cds
17779	GM_M28_A2_F10_MR	g2522230	BLASTX	293	4e-25	45	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
17780	GM_M28_A2_F11_MF	g4092471	BLASTN	401	4e-11	64	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
17781	GM_M28_A2_G05_MR	g166949	BLASTX	430	1e-39	58	(M32885) cytochrome P-450LXXIA1 (cyp71A1) [Persea americana]
17782	GM_M28_A2_G08_MR	g2264315	BLASTN	683	8e-24	76	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MRN17, complete sequence [Arabidopsis thaliana]
17783	GM_M28_A2_H05_MF	g4063760	BLASTX	360	2e-33	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17784	GM_M28_A2_H05_MR	g507910	BLASTN	587	6e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17785	GM_M28_A2_H06_MR	g3599418	BLASTN	400	4e-11	65	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
17786	GM_M28_A2_H07_MF	g2191149	BLASTX	229	4e-24	85	(AF007269) Similar to protein kinase [Arabidopsis thaliana]
17787	GM_M28_A2_H10_MF	g226407	BLASTX	366	2e-31	57	retrotransposon del1-46 [Lilium henryi]
17788	GM_M28_A2_H12_MF	g99922	BLASTX	596	3e-57	90	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
17789	GM_M28_B1_A05_MR	g1785739	BLASTX	157	9e-22	38	(Y08502) orf240b [Arabidopsis thaliana]
17790	GM_M28_B1_A06_MR	g1142701	BLASTN	1215	1e-48	81	Glycine max satellite STR120-A.3.
17791	GM_M28_B1_A11_MR	g3033375	BLASTX	361	3e-32	58	(AC004238) putative berberine bridge enzyme [Arabidopsis thaliana]
17792	GM_M28_B1_A12_MR	g3046693	BLASTX	343	3e-35	87	(AL022140) receptor like protein (fragment) [Arabidopsis thaliana]
17793	GM_M28_B1_B03_MR	g1666236	BLASTX	121	9e-11	32	(U76261) unknown [Hordeum vulgare]
17794	GM_M28_B1_B04_MR	g2522228	BLASTX	416	3e-38	80	(AB007466) reverse transcriptase-like protein [Vicia faba]
17795	GM_M28_B1_B06_MF	g3142328	BLASTN	531	9e-29	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17796	GM_M28_B1_B07_MR	g505129	BLASTN	360	3e-09	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17797	GM_M28_B1_B09_MR	g2642431	BLASTX	283	1e-22	44	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
17798	GM_M28_B1_B10_MF	g2129618	BLASTX	168	1e-10	38	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17799	GM_M28_B1_B12_MR	g2781364	BLASTX	153	6e-10	29	(AC003113) F24O1.20 [Arabidopsis thaliana]
17800	GM_M28_B1_C06_MF	g1666236	BLASTX	148	3e-09	30	(U76261) unknown [Hordeum vulgare]
17801	GM_M28_B1_C06_MR	g18559	BLASTN	1076	9e-42	76	G.max gene for catalase
17802	GM_M28_B1_C10_MF	g2995405	BLASTX	389	2e-34	57	(Y12432) polyprotein [Ananas comosus]
17803	GM_M28_B1_D02_MR	g1633043	BLASTN	817	4e-30	82	Lupinus angustifolius conglutin gamma gene, complete cds
17804	GM_M28_B1_D04_MF	g2443320	BLASTX	291	2e-23	46	(D85597) polyprotein [Oryza australiensis]
17805	GM_M28_B1_D10_MF	g2462134	BLASTX	354	1e-31	50	(Y13368) reverse transcriptase [Beta vulgaris]
17806	GM_M28_B1_E01_MR	g4156188	BLASTN	426	3e-12	65	Homo sapiens clone DJ0784G16, complete sequence [Homo sapiens]
17807	GM_M28_B1_E03_MF	g3510505	BLASTX	244	1e-18	45	(AF030881) pol polyprotein [Fugu rubripes]
17808	GM_M28_B1_E06_MR	g3319362	BLASTX	276	4e-22	48	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17809	GM_M28_B1_E07_MF	g1769898	BLASTX	278	1e-22	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17810	GM_M28_B1_E08_MR	g3097320	BLASTN	705	7e-25	81	Glycine max gene for Bd 30K, complete cds
17811	GM_M28_B1_E11_MF	g2829910	BLASTX	249	4e-19	48	(AC002291) Unknown protein, contains regulator of chromosome condensation motifs [Arabidopsis thaliana]
17812	GM_M28_B1_F02_MR	g3021268	BLASTX	145	1e-13	71	(AL022347) putative protein [Arabidopsis thaliana]
17813	GM_M28_B1_F03_MF	g3176806	BLASTN	423	6e-13	65	Homo sapiens allele 17 fragile site locus (FRA10B) minisatellite, 5' sequence
17814	GM_M28_B1_F03_MR	g18695	BLASTN	475	1e-14	66	Soybean nodulin 22 gene
17815	GM_M28_B1_F05_MF	g421954	BLASTX	142	1e-16	42	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
17816	GM_M28_B1_F07_MR	g2995405	BLASTX	183	3e-12	67	(Y12432) polyprotein [Ananas comosus]
17817	GM_M28_B1_F08_MF	g2129618	BLASTX	158	2e-09	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17818	GM_M28_B1_F10_MR	g100484	BLASTX	282	5e-23	48	hypothetical protein - garden snapdragon
17819	GM_M28_B1_F11_MF	g3097320	BLASTN	406	2e-11	68	Glycine max gene for Bd 30K, complete cds
17820	GM_M28_B1_G01_MF	g1865677	BLASTX	153	5e-09	91	(Y08568) trehalose-6-phosphate synthase [Arabidopsis thaliana]
17821	GM_M28_B1_G07_MR	g4104931	BLASTX	164	8e-14	80	(AF042196) auxin response factor 8 [Arabidopsis thaliana]
17822	GM_M28_B1_G08_MF	g1769899	BLASTX	267	2e-22	76	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17823	GM_M28_B1_H02_MR	g3894211	BLASTN	441	7e-13	65	Homo sapiens PAC clone DJ0888A21 from 7q31, complete sequence [Homo sapiens]
17824	GM_M28_B1_H03_MF	g2995405	BLASTX	153	4e-24	54	(Y12432) polyprotein [Ananas comosus]
17825	GM_M28_B1_H03_MR	g3650039	BLASTX	204	3e-16	42	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
17826	GM_M28_B1_H08_MF	g2924772	BLASTX	197	5e-15	84	(AC002334) unknown protein [Arabidopsis thaliana]
17827	GM_M28_B1_H09_MR	g507910	BLASTN	403	1e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
17828	GM_M28_B1_H12_MR	g507910	BLASTN	374	3e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17829	GM_M28_B2_A05_MF	g4038056	BLASTX	161	6e-21	49	(AC005897) putative transposon [Arabidopsis thaliana]
17830	GM_M28_B2_A06_MR	g2462056	BLASTX	144	1e-11	50	(Y13388) reverse transcriptase [Antirrhinum majus]
17831	GM_M28_B2_A07_MF	g507910	BLASTN	356	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
17832	GM_M28_B2_A08_MR	g3033400	BLASTX	237	9e-18	41	(AC004238) putative Ser/Thr protein kinase [Arabidopsis thaliana]
17833	GM_M28_B2_A09_MF	g3047060	BLASTN	365	2e-09	63	Arabidopsis thaliana BAC F7N22
17834	GM_M28_B2_B05_MR	g1236920	BLASTN	358	3e-09	63	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
17835	GM_M28_B2_B10_MR	g1840106	BLASTN	353	2e-09	63	Human fragile site locus (FRA16B) minisatellite repeat
17836	GM_M28_B2_C04_MF	g130398	BLASTX	210	5e-15	41	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 297) gi 85089 pir B24872 retrovirus-related pol polyprotein homolog - fruit fly (Drosophila melanogaster) transposon 297
17837	GM_M28_B2_C04_MR	g2462058	BLASTX	296	2e-25	49	(Y13389) reverse transcriptase [Antirrhinum majus]
17838	GM_M28_B2_C08_MR	g1431738	BLASTN	511	3e-16	81	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
17839	GM_M28_B2_C09_MF	g1171591	BLASTN	389	1e-10	65	P.falciparum complete gene map of plastid-like DNA (IR-B)
17840	GM_M28_B2_C12_MF	g507910	BLASTN	401	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
17841	GM_M28_B2_C12_MR	g507910	BLASTN	407	9e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
17842	GM_M28_B2_D02_MF	g2213608	BLASTX	174	4e-11	43	(AC000103) F21J9.2 [Arabidopsis thaliana]
17843	GM_M28_B2_D03_MR	g4063760	BLASTX	269	3e-21	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17844	GM_M28_B2_D05_MF	g3402722	BLASTX	217	3e-16	93	(AC004261) CPDK-related protein [Arabidopsis thaliana]
17845	GM_M28_B2_D05_MR	g1174718	BLASTX	174	3e-11	48	PUTATIVE RECEPTOR PROTEIN KINASE TMK1 PRECURSOR gi 322579 pir JQ1674 receptor protein kinase TMK1 (EC 2.7.1.-) precursor - Arabidopsis thaliana gi 166888 (L00670) protein kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17846	GM_M28_B2_D07_MR	g3402693	BLASTX	164	1e-18	88	(AC004697) unknown protein [Arabidopsis thaliana]
17847	GM_M28_B2_D08_MR	g3513747	BLASTX	288	5e-23	50	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
17848	GM_M28_B2_D09_MR	g18768	BLASTN	432	4e-13	77	Soybean Tgm6 transposable element 3' end
17849	GM_M28_B2_D10_MR	g3184285	BLASTX	203	1e-17	62	(AC004136) hypothetical protein [Arabidopsis thaliana]
17850	GM_M28_B2_D12_MF	g1666236	BLASTX	160	2e-10	32	(U76261) unknown [Hordeum vulgare]
17851	GM_M28_B2_E02_MR	g3142328	BLASTN	1159	1e-45	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17852	GM_M28_B2_E03_MF	g1169782	BLASTX	387	4e-35	72	FUSCA PROTEIN FUS6 gi 432446 (L26498) FUS6 [Arabidopsis thaliana]
17853	GM_M28_B2_E03_MR	g1769898	BLASTX	289	6e-24	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17854	GM_M28_B2_E04_MR	g1184075	BLASTX	178	9e-18	39	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
17855	GM_M28_B2_E12_MF	g18559	BLASTN	386	2e-10	71	G.max gene for catalase
17856	GM_M28_B2_F01_MR	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
17857	GM_M28_B2_F03_MR	g1143321	BLASTN	853	7e-32	90	Glycine max alfa-carboxyltransferase (accA-2) precursor mRNA, complete cds.
17858	GM_M28_B2_F04_MR	g2367675	BLASTX	176	2e-11	33	(AF017040) Pol [Dictyostelium discoideum]
17859	GM_M28_B2_F05_MR	g507910	BLASTN	574	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
17860	GM_M28_B2_F06_MR	g4063760	BLASTX	299	2e-24	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17861	GM_M28_B2_F07_MR	g100484	BLASTX	251	1e-19	49	hypothetical protein - garden snapdragon
17862	GM_M28_B2_F12_MF	g1785744	BLASTX	197	5e-15	58	(Y08502) orf158 [Arabidopsis thaliana]
17863	GM_M28_B2_G01_MF	g4063760	BLASTX	443	8e-40	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17864	GM_M28_B2_G04_MF	g3319362	BLASTX	170	8e-11	38	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17865	GM_M28_B2_G05_MR	g4063760	BLASTX	380	4e-33	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17866	GM_M28_B2_G09_MR	g2995405	BLASTX	316	2e-26	56	(Y12432) polyprotein [Ananas comosus]
17867	GM_M28_B2_G10_MR	g4063760	BLASTX	555	9e-52	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17868	GM_M28_B2_H04_MR	g3033389	BLASTX	210	4e-15	40	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
17869	GM_M28_B2_H05_MF	g2213582	BLASTX	175	4e-11	33	(AC000348) T7N9.2 [Arabidopsis thaliana]
17870	GM_M28_B2_H05_MR	g3319362	BLASTX	117	1e-13	43	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
17871	GM_M28_B2_H09_MR	g2576361	BLASTX	170	3e-24	58	(U39782) lysine and histidine specific transporter [Arabidopsis thaliana]
17872	GM_M29_A1_A03_MR	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17873	GM_M29_A1_A05_MR	g3859610	BLASTN	585	2e-19	66	Arabidopsis thaliana BAC T9E19
17874	GM_M29_A1_A09_MR	g3482933	BLASTX	249	4e-27	74	(AC003970) Similar to cdc2 protein kinases [Arabidopsis thaliana]
17875	GM_M29_A1_B04_MR	g2213594	BLASTX	311	3e-26	69	(AC000348) T7N9.14 [Arabidopsis thaliana]
17876	GM_M29_A1_C01_MR	g905361	BLASTX	624	3e-60	96	(U22103) gag-protease polyprotein [Glycine max]
17877	GM_M29_A1_C04_MR	g1769898	BLASTX	138	8e-11	44	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17878	GM_M29_A1_C06_MR	g1769898	BLASTX	427	3e-39	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17879	GM_M29_A1_D01_MR	g1769898	BLASTX	449	1e-41	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17880	GM_M29_A1_D02_MR	g4063770	BLASTX	218	5e-16	39	(AB004906) transposase [Ipomoea purpurea]
17881	GM_M29_A1_D06_MR	g4063760	BLASTX	477	2e-43	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17882	GM_M29_A1_D08_MR	g1169533	BLASTX	124	6e-11	78	ENOLASE (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) gi 515827 (X80474) enolase [Neocallimastix frontalis]
17883	GM_M29_A1_D09_MR	g3097320	BLASTN	603	3e-20	69	Glycine max gene for Bd 30K, complete cds
17884	GM_M29_A1_E07_MR	g511658	BLASTN	245	2e-09	66	Hansenula wingei mitochondrial gene for NADH dehydrogenase subunit 4L, complete cds
17885	GM_M29_A1_F02_MR	g4092471	BLASTN	531	6e-17	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
17886	GM_M29_A1_F04_MR	g3777527	BLASTX	594	1e-55	98	(AF053008) gag-pol polyprotein [Glycine max]
17887	GM_M29_A1_F06_MR	g4063760	BLASTX	186	2e-12	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17888	GM_M29_A1_H04_MR	g4160362	BLASTN	385	2e-10	66	Saccharomyces cerevisiae complete mitochondrial genome
17889	GM_M29_A1_H11_MR	g4063756	BLASTN	456	1e-13	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17890	GM_M29_A2_A01_MF	g100484	BLASTX	178	5e-19	53	hypothetical protein - garden snapdragon
17891	GM_M29_A2_A12_MR	g3297806	BLASTN	489	5e-15	68	Arabidopsis thaliana DNA chromosome 4, BAC clone F17I5 (ESSAII project)
17892	GM_M29_A2_B01_MF	g1360090	BLASTX	289	1e-23	47	(X95576) C1C-Nt1 gene product [Nicotiana tabacum]
17893	GM_M29_A2_B02_MR	g3319345	BLASTX	213	2e-15	37	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
17894	GM_M29_A2_B04_MF	g4063760	BLASTX	280	2e-22	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17895	GM_M29_A2_B04_MR	g507910	BLASTN	589	5e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17896	GM_M29_A2_B07_MR	g3894389	BLASTX	210	3e-15	37	(AF053996) Hcr2-2A [Lycopersicon pimpinellifolium]
17897	GM_M29_A2_B08_MR	g18767	BLASTN	413	2e-12	70	Soybean Tgm6 transposable element 5' end
17898	GM_M29_A2_B11_MF	g3142328	BLASTN	944	8e-36	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17899	GM_M29_A2_C04_MR	g2642431	BLASTX	242	3e-18	56	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
17900	GM_M29_A2_C05_MR	g3176773	BLASTN	364	4e-10	62	Homo sapiens allele 3 fragile site locus (FRA10B) minisatellite, 5' sequence
17901	GM_M29_A2_C06_MF	g4063760	BLASTX	222	3e-16	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17902	GM_M29_A2_C06_MR	g1785739	BLASTX	240	2e-25	47	(Y08502) orf240b [Arabidopsis thaliana]
17903	GM_M29_A2_C07_MR	g2209031	BLASTX	300	2e-25	42	(AB001569) ORF of 1.56 kb [Daucus carota]
17904	GM_M29_A2_C11_MR	g1669680	BLASTN	363	2e-09	63	Human DNA sequence from PAC 293E14 contains ESTs, STS
17905	GM_M29_A2_D01_MF	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17906	GM_M29_A2_D01_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17907	GM_M29_A2_D02_MR	g2462134	BLASTX	266	1e-27	48	(Y13368) reverse transcriptase [Beta vulgaris]
17908	GM_M29_A2_D04_MR	g3128195	BLASTX	177	3e-12	79	(AC004521) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana] gi 3341673 (AC003672) putative phosphoribosyl pyrophosphate synthetase [Arabidopsis thaliana]
17909	GM_M29_A2_D05_MF	g3810596	BLASTX	262	1e-20	43	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
17910	GM_M29_A2_D05_MR	g1167523	BLASTX	316	4e-26	46	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
17911	GM_M29_A2_D08_MR	g1769898	BLASTX	162	3e-17	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17912	GM_M29_A2_E01_MF	g2995405	BLASTX	416	3e-37	55	(Y12432) polyprotein [Ananas comosus]
17913	GM_M29_A2_E04_MR	g3461840	BLASTX	333	6e-29	43	(AC005315) putative reverse transcriptase [Arabidopsis thaliana]
17914	GM_M29_A2_F03_MF	g2316016	BLASTX	201	7e-14	51	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
17915	GM_M29_A2_F07_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17916	GM_M29_A2_F08_MF	g2316016	BLASTX	202	6e-14	50	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
17917	GM_M29_A2_F09_MF	g905361	BLASTX	614	4e-59	91	(U22103) gag-protease polyprotein [Glycine max]
17918	GM_M29_A2_F09_MR	g4063760	BLASTX	323	6e-27	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17919	GM_M29_A2_G01_MF	g507910	BLASTN	565	6e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
17920	GM_M29_A2_G01_MR	g507910	BLASTN	574	3e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17921	GM_M29_A2_G08_MR	g4063760	BLASTX	594	6e-56	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17922	GM_M29_A2_G09_MR	g1705678	BLASTX	335	1e-28	87	CELL DIVISION CYCLE PROTEIN 48 HOMOLOG (VALOSIN CONTAINING PROTEIN HOMOLOG) (VCP) gi 862480 (U20213) valosin-containing protein [Glycine max]
17923	GM_M29_A2_H01_MR	g3482913	BLASTX	216	4e-30	57	(AC003970) Similar to MtN21, gi 2598575, Megicago truncatula nodulation induced gene [Arabidopsis thaliana]
17924	GM_M29_A2_H02_MF	g507910	BLASTN	399	2e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17925	GM_M29_A2_H02_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17926	GM_M29_A2_H06_MF	g3142328	BLASTN	1903	1e-79	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17927	GM_M29_A2_H07_MF	g3142328	BLASTN	939	1e-35	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17928	GM_M29_A2_H08_MR	g3859610	BLASTN	435	1e-12	60	Arabidopsis thaliana BAC T9E19
17929	GM_M29_A2_H09_MF	g18559	BLASTN	932	3e-35	74	G.max gene for catalase
17930	GM_M29_A2_H10_MR	g1040875	BLASTX	164	1e-14	67	(U30382) expansin S1 precursor [Cucumis sativus]
17931	GM_M29_A2_H11_MF	g2995405	BLASTX	464	2e-42	65	(Y12432) polyprotein [Ananas comosus]
17932	GM_M29_B1_A02_MF	g18559	BLASTN	853	1e-31	75	G.max gene for catalase
17933	GM_M29_B1_A08_MF	g4115377	BLASTX	144	2e-15	72	(AC005967) unknown protein [Arabidopsis thaliana]
17934	GM_M29_B1_A08_MR	g3513747	BLASTX	228	1e-16	40	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
17935	GM_M29_B1_A10_MF	g3777527	BLASTX	276	8e-22	41	(AF053008) gag-pol polyprotein [Glycine max]
17936	GM_M29_B1_B01_MF	g1666236	BLASTX	190	6e-14	31	(U76261) unknown [Hordeum vulgare]
17937	GM_M29_B1_B01_MR	g1769898	BLASTX	173	2e-22	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17938	GM_M29_B1_B02_MF	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
17939	GM_M29_B1_B02_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
17940	GM_M29_B1_B04_MF	g3283026	BLASTX	153	2e-13	48	putative transposase [Arabidopsis thaliana]
17941	GM_M29_B1_B05_MR	g2864621	BLASTX	174	8e-15	42	hypothetical protein [Arabidopsis thaliana]
17942	GM_M29_B1_B07_MF	g99729	BLASTX	315	2e-27	47	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
17943	GM_M29_B1_B09_MF	g2522228	BLASTX	253	1e-20	45	(AB007466) reverse transcriptase-like protein [Vicia faba]
17944	GM_M29_B1_C01_MF	g2252846	BLASTX	264	6e-21	80	(AF013293) Similar to phospholipase D [Arabidopsis thaliana]
17945	GM_M29_B1_C03_MF	g3236253	BLASTX	334	1e-28	52	(AC004684) receptor-like protein kinase [Arabidopsis thaliana]
17946	GM_M29_B1_C03_MR	g2443320	BLASTX	151	1e-11	40	(D85597) polyprotein [Oryza australiensis]
17947	GM_M29_B1_C06_MR	g4063756	BLASTN	413	1e-11	72	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
17948	GM_M29_B1_D01_MF	g2801681	BLASTN	1044	7e-41	86	Glycine max telomere-associated sequence STAS10
17949	GM_M29_B1_D03_MF	g507910	BLASTN	435	5e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
17950	GM_M29_B1_D06_MF	g2522227	BLASTX	162	4e-16	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
17951	GM_M29_B1_D10_MF	g4092471	BLASTN	358	4e-09	70	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
17952	GM_M29_B1_D10_MR	g3426334	BLASTN	441	6e-13	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17953	GM_M29_B1_D11_MF	g3142328	BLASTN	1489	1e-60	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17954	GM_M29_B1_D12_MF	g3068704	BLASTX	290	1e-23	90	(AF049236) unknown [Arabidopsis thaliana]
17955	GM_M29_B1_E07_MR	g507910	BLASTN	377	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17956	GM_M29_B1_E09_MR	g4063760	BLASTX	181	7e-12	44	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17957	GM_M29_B1_F02_MF	g2281100	BLASTX	165	2e-10	47	(AC002333) LecRK1 protein kinase isolog [Arabidopsis thaliana]
17958	GM_M29_B1_F03_MR	g3097320	BLASTN	1092	2e-42	81	Glycine max gene for Bd 30K, complete cds
17959	GM_M29_B1_F05_MR	g3777527	BLASTX	677	1e-64	93	(AF053008) gag-pol polyprotein [Glycine max]
17960	GM_M29_B1_F10_MF	g3650039	BLASTX	221	2e-16	37	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
17961	GM_M29_B1_F10_MR	g3868722	BLASTN	353	7e-09	76	Arabidopsis thaliana BAC T19G15, from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]
17962	GM_M29_B1_G02_MR	g4063760	BLASTX	473	5e-43	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17963	GM_M29_B1_G03_MR	g3142328	BLASTN	1229	9e-49	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17964	GM_M29_B1_G04_MF	g1184123	BLASTX	164	2e-11	52	(U20809) auxin-induced protein [Vigna radiata]
17965	GM_M29_B1_G04_MR	g3386605	BLASTX	179	3e-12	36	(AC004665) hypothetical protein [Arabidopsis thaliana]
17966	GM_M29_B1_G06_MF	g4063760	BLASTX	394	1e-34	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17967	GM_M29_B1_G06_MR	g4063760	BLASTX	211	1e-30	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17968	GM_M29_B1_G07_MF	g2443320	BLASTX	252	2e-23	49	(D85597) polyprotein [Oryza australiensis]
17969	GM_M29_B1_G12_MF	g3142328	BLASTN	681	7e-24	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
17970	GM_M29_B1_H01_MF	g3319345	BLASTX	163	2e-13	43	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
17971	GM_M29_B1_H01_MR	g2583133	BLASTX	143	2e-18	81	(AC002387) unknown protein [Arabidopsis thaliana]
17972	GM_M29_B1_H07_MR	g2129618	BLASTX	154	4e-09	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
17973	GM_M29_B1_H11_MF	g217930	BLASTN	367	2e-10	64	H.wingei mitochondrial tRNA gene
17974	GM_M29_B2_B01_MF	g3033389	BLASTX	179	9e-12	40	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
17975	GM_M29_B2_B01_MR	g3033389	BLASTX	197	1e-13	33	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
17976	GM_M29_B2_B05_MR	g2462936	BLASTX	140	1e-08	50	(Y12321) open reading frame 2 [Brassica oleracea]
17977	GM_M29_B2_B08_MF	g99755	BLASTX	342	8e-30	52	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
17978	GM_M29_B2_B09_MF	g2462134	BLASTX	159	5e-10	28	(Y13368) reverse transcriptase [Beta vulgaris]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
17979	GM_M29_B2_B10_MF	g507910	BLASTN	388	6e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17980	GM_M29_B2_B10_MR	g507910	BLASTN	390	5e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
17981	GM_M29_B2_C03_MR	g1480927	BLASTN	745	6e-27	88	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
17982	GM_M29_B2_C07_MF	g3097320	BLASTN	852	2e-31	73	Glycine max gene for Bd 30K, complete cds
17983	GM_M29_B2_C08_MF	g2462134	BLASTX	193	1e-13	43	(Y13368) reverse transcriptase [Beta vulgaris]
17984	GM_M29_B2_C10_MF	g2129473	BLASTX	268	1e-22	42	arabinogalactan-like protein - loblolly pine gi 607774 (U09556) arabinogalactan-like protein [Pinus taeda]
17985	GM_M29_B2_D03_MF	g1785740	BLASTX	240	1e-19	51	(Y08502) orf170 [Arabidopsis thaliana]
17986	GM_M29_B2_D05_MF	g3645899	BLASTX	312	7e-26	47	(U68408) 5' end not determined experimentally [Zea mays]
17987	GM_M29_B2_D08_MF	g3097320	BLASTN	390	1e-10	69	Glycine max gene for Bd 30K, complete cds
17988	GM_M29_B2_D09_MF	g905361	BLASTX	135	8e-10	29	(U22103) gag-protease polyprotein [Glycine max]
17989	GM_M29_B2_D09_MR	g905361	BLASTX	143	1e-09	27	(U22103) gag-protease polyprotein [Glycine max]
17990	GM_M29_B2_D11_MF	g1769898	BLASTX	346	7e-32	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
17991	GM_M29_B2_E03_MR	g3777527	BLASTX	427	6e-38	73	(AF053008) gag-pol polyprotein [Glycine max]
17992	GM_M29_B2_E04_MR	g1666236	BLASTX	164	3e-13	31	(U76261) unknown [Hordeum vulgare]
17993	GM_M29_B2_E05_MR	g2522227	BLASTX	228	3e-18	42	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
17994	GM_M29_B2_E12_MR	g507910	BLASTN	595	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
17995	GM_M29_B2_F03_MR	g4063760	BLASTX	226	1e-16	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17996	GM_M29_B2_G01_MR	g3176800	BLASTN	373	1e-10	66	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite, 3' sequence
17997	GM_M29_B2_G04_MF	g4063760	BLASTX	382	2e-33	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
17998	GM_M29_B2_G04_MR	g507910	BLASTN	422	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
17999	GM_M29_B2_G05_MR	g4063760	BLASTX	263	1e-20	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18000	GM_M29_B2_G10_MF	g3142328	BLASTN	550	6e-18	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18001	GM_M29_B2_G12_MF	g3269281	BLASTX	157	2e-09	44	(AL030978) putative protein [Arabidopsis thaliana]
18002	GM_M29_B2_H01_MF	g2522227	BLASTX	171	8e-23	49	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
18003	GM_M29_B2_H01_MR	g4063760	BLASTX	168	2e-11	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18004	GM_M29_B2_H02_MF	g4063760	BLASTX	194	7e-25	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18005	GM_M29_B2_H04_MF	g507910	BLASTN	638	3e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
18006	GM_M29_B2_H04_MR	g507910	BLASTN	601	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18007	GM_M29_B2_H08_MR	g3142328	BLASTN	812	8e-30	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18008	GM_M30_A1_A03_MR	g2181308	BLASTN	472	6e-15	80	H.sapiens telomeric DNA sequence, clone 12QTEL026, read 12QTELOO026.seq
18009	GM_M30_A1_A06_MF	g507910	BLASTN	359	1e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18010	GM_M30_A1_B02_MR	g399710	BLASTN	399	4e-11	77	G-protein coupled receptor type B {clone PPR1} [cattle, tongue, taste papillae, mRNA, 2059 nt]
18011	GM_M30_A1_B04_MR	g1809226	BLASTN	1489	3e-60	97	Human BAC clone RG104I04 from 7q21-7q22, complete sequence [Homo sapiens]
18012	GM_M30_A1_B07_MR	g3327414	BLASTN	679	1e-23	86	Homo sapiens chromosome 17, clone hRPK.879_D_6, complete sequence [Homo sapiens]
18013	GM_M30_A1_C01_MR	g1196433	BLASTX	128	5e-15	43	(M22334) unknown protein [Homo sapiens]
18014	GM_M30_A1_D10_MR	g3970967	BLASTN	388	2e-15	69	Homo sapiens PAC clone DJ1108A12 from 14q24.3, complete sequence [Homo sapiens]
18015	GM_M30_A1_D11_MR	g3924666	BLASTN	1212	1e-47	97	Homo sapiens BAC clone RG041D11 from 7q21, complete sequence [Homo sapiens]
18016	GM_M30_A1_E06_MF	g170002	BLASTN	403	2e-11	70	soybean leghemoglobin pseudogene, segment 2.
18017	GM_M30_A1_E10_MR	g3056604	BLASTN	658	3e-29	78	Homo sapiens chromosome 19, cosmid F9933, complete sequence [Homo sapiens]
18018	GM_M30_A1_F01_MR	g2342581	BLASTN	496	2e-15	70	Human DNA sequence from PAC 30P20 on chromosome Xq21.1-Xq21.3. Contains set pseudogene, ESTs and STS
18019	GM_M30_A1_F12_MR	g3115994	BLASTN	1327	7e-53	92	Homo sapiens DNA sequence from PAC 79C4 on chromosome 1q24. Contains the PMX1 gene, coding for two alternative forms of the Paired Mesoderm Homeobox protein 1 (PMX-1, PHOX-1). Contains ESTs, STSs and BAC end sequences (GSSs...
18020	GM_M30_A1_H01_MR	g2695566	BLASTN	322	2e-14	68	Human Chromosome 15 pac pDJ138o23, complete sequence [Homo sapiens]
18021	GM_M30_A1_H08_MF	g3608154	BLASTX	187	8e-13	49	(AC005314) unknown protein [Arabidopsis thaliana]
18022	GM_M30_A1_H12_MR	g1841914	BLASTN	712	4e-25	81	Human DNA sequence from PAC 481A17 on chromosome X contains ESTs
18023	GM_M30_A2_A04_MF	g2129618	BLASTX	197	1e-13	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18024	GM_M30_A2_A08_MF	g3097320	BLASTN	405	3e-11	71	Glycine max gene for Bd 30K, complete cds
18025	GM_M30_A2_A10_MF	g387902	BLASTX	119	3e-15	44	(L23524) ORF [Hordeum vulgare]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18026	GM_M30_A2_B09_MF	g3810596	BLASTX	340	5e-29	46	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
18027	GM_M30_A2_B12_MF	g2995405	BLASTX	440	8e-40	57	(Y12432) polyprotein [Ananas comosus]
18028	GM_M30_A2_C02_MF	g3080374	BLASTX	188	7e-13	31	(AL022580) putative protein [Arabidopsis thaliana]
18029	GM_M30_A2_C05_MF	g2995405	BLASTX	238	4e-18	55	(Y12432) polyprotein [Ananas comosus]
18030	GM_M30_A2_C11_MF	g507910	BLASTN	353	2e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18031	GM_M30_A2_D05_MF	g3097320	BLASTN	411	1e-11	67	Glycine max gene for Bd 30K, complete cds
18032	GM_M30_A2_D10_MF	g2995405	BLASTX	504	9e-47	61	(Y12432) polyprotein [Ananas comosus]
18033	GM_M30_A2_D11_MF	g294042	BLASTN	373	8e-10	60	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds
18034	GM_M30_A2_E03_MF	g2760322	BLASTX	153	6e-10	52	(AC002130) F1N21.7 [Arabidopsis thaliana]
18035	GM_M30_A2_E04_MF	g3513747	BLASTX	208	1e-28	45	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
18036	GM_M30_A2_F01_MF	g507910	BLASTN	428	1e-12	77	Glycine max BSR-101 satellite SB92 genomic sequence.
18037	GM_M30_A2_F05_MF	g2655098	BLASTX	294	2e-24	69	(AF023472) peptide transporter [Hordeum vulgare]
18038	GM_M30_A2_F06_MF	g3777527	BLASTX	161	1e-11	45	(AF053008) gag-pol polyprotein [Glycine max]
18039	GM_M30_A2_F08_MF	g3777527	BLASTX	663	4e-63	95	(AF053008) gag-pol polyprotein [Glycine max]
18040	GM_M30_A2_G02_MF	g507910	BLASTN	424	2e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18041	GM_M30_A2_G06_MF	g342963	BLASTN	374	3e-10	66	paramecium species 5,87 mt dna dimer: replication init. region.
18042	GM_M30_A2_G09_MF	g2522227	BLASTX	203	1e-15	50	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
18043	GM_M30_A2_H06_MF	g3097320	BLASTN	1079	8e-42	80	Glycine max gene for Bd 30K, complete cds
18044	GM_M30_A2_H09_MF	g2795809	BLASTX	199	3e-15	50	(AC003674) putative expansin [Arabidopsis thaliana]
18045	GM_M30_B1_A12_MF	g1236920	BLASTN	418	5e-12	65	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
18046	GM_M30_B1_B02_MF	g18559	BLASTN	404	3e-11	70	G.max gene for catalase
18047	GM_M30_B1_B05_MF	g905361	BLASTX	375	3e-33	83	(U22103) gag-protease polyprotein [Glycine max]
18048	GM_M30_B1_B07_MF	g99922	BLASTX	439	1e-40	70	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
18049	GM_M30_B1_C02_MR	g3097320	BLASTN	1092	2e-42	81	Glycine max gene for Bd 30K, complete cds
18050	GM_M30_B1_C04_MR	g1076755	BLASTX	619	1e-59	81	protein kinase - rice gi 450300 (L27821) protein kinase [Oryza sativa]
18051	GM_M30_B1_D09_MF	g507910	BLASTN	547	4e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
18052	GM_M30_B1_D11_MF	g3645899	BLASTX	169	5e-14	41	(U68408) 5' end not determined experimentally [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18053	GM_M30_B1_E12_MR	g507910	BLASTN	372	3e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18054	GM_M30_B1_F01_MF	g905361	BLASTX	407	7e-37	90	(U22103) gag-protease polyprotein [Glycine max]
18055	GM_M30_B1_F02_MR	g14293	BLASTN	338	4e-09	62	Yeast R0.54 mutant mitochondrial DNA lacking ori1 sequence recombination junction with tRNA-Pro and 15S rRNA genes
18056	GM_M30_B1_F04_MF	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18057	GM_M30_B1_F04_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18058	GM_M30_B1_F05_MF	g3021268	BLASTX	146	1e-19	44	(AL022347) putative protein [Arabidopsis thaliana]
18059	GM_M30_B1_F07_MF	g2462134	BLASTX	255	2e-20	42	(Y13368) reverse transcriptase [Beta vulgaris]
18060	GM_M30_B1_F10_MF	g507910	BLASTN	494	1e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
18061	GM_M30_B1_F11_MR	g2398527	BLASTX	170	4e-12	57	(Y13723) Transcription factor [Arabidopsis thaliana]
18062	GM_M30_B1_G01_MF	g2980777	BLASTX	176	6e-12	75	(AL022198) putative protein [Arabidopsis thaliana]
18063	GM_M30_B1_G04_MF	g1142702	BLASTN	1132	1e-44	97	Glycine max satellite STR120-A.4.
18064	GM_M30_B1_G04_MR	g3097320	BLASTN	1043	3e-40	78	Glycine max gene for Bd 30K, complete cds
18065	GM_M30_B1_G08_MF	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18066	GM_M30_B1_G08_MR	g507910	BLASTN	341	8e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18067	GM_M30_B1_G12_MF	g2995405	BLASTX	154	6e-23	62	(Y12432) polyprotein [Ananas comosus]
18068	GM_M30_B1_H04_MF	g13767	BLASTN	339	3e-09	67	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
18069	GM_M30_B1_H05_MR	g4038056	BLASTX	207	9e-15	45	(AC005897) putative transposon [Arabidopsis thaliana]
18070	GM_M30_B1_H08_MR	g728905	BLASTX	206	2e-14	43	PROBABLE CALCIUM-TRANSPORTING ATPASE 3 (ENDOPLASMIC RETICULUM CA2+-ATPASE) gi 1078206 pir S51995 probable ATPase (EC 3.6.1.-) DRS2 - yeast (Saccharomyces cerevisiae) gi 171114 (L01795) ATPase [Saccharomyces cerevisiae] gi 595560 (U12980) Drs2p: Membrane spanning Ca-ATPase(P-type), member of the cation transport(E1-E2) ATPase [Saccharomyces cerevisiae]
18071	GM_M30_B1_H10_MF	g3777527	BLASTX	307	4e-25	47	(AF053008) gag-pol polyprotein [Glycine max]
18072	GM_M30_B1_H12_MF	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
18073	GM_M30_B2_A03_MR	g3426334	BLASTN	384	2e-10	60	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
18074	GM_M30_B2_A05_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18075	GM_M30_B2_A08_MF	g2462134	BLASTX	321	8e-28	40	(Y13368) reverse transcriptase [Beta vulgaris]
18076	GM_M30_B2_A09_MF	g507910	BLASTN	552	2e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
18077	GM_M30_B2_B05_MF	g507910	BLASTN	349	4e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18078	GM_M30_B2_B11_MF	g18559	BLASTN	821	3e-30	75	G.max gene for catalase
18079	GM_M30_B2_B12_MF	g2995405	BLASTX	399	2e-35	59	(Y12432) polyprotein [Ananas comosus]
18080	GM_M30_B2_C04_MF	g2961349	BLASTX	197	1e-13	52	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
18081	GM_M30_B2_C04_MR	g1167523	BLASTX	172	1e-25	43	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18082	GM_M30_B2_C05_MR	g2832242	BLASTN	415	1e-11	61	Zea mays 22-kDa alpha zein gene cluster, complete sequence
18083	GM_M30_B2_C06_MR	g3819710	BLASTX	373	1e-33	71	(AJ224161) delta-8 sphingolipid desaturase [Arabidopsis thaliana]
18084	GM_M30_B2_E06_MF	g4063760	BLASTX	309	2e-25	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18085	GM_M30_B2_E11_MF	g3047086	BLASTX	95	5e-09	35	(AF058914) similar to reverse transcriptase (Pfam: transcript_fact.hmm, score: 72.31) [Arabidopsis thaliana]
18086	GM_M30_B2_F07_MF	g2995405	BLASTX	349	5e-30	51	(Y12432) polyprotein [Ananas comosus]
18087	GM_M30_B2_F10_MR	g905361	BLASTX	194	1e-13	37	(U22103) gag-protease polyprotein [Glycine max]
18088	GM_M30_B2_G03_MF	g18559	BLASTN	376	5e-10	68	G.max gene for catalase
18089	GM_M30_B2_G04_MR	g3763969	BLASTN	404	3e-11	62	Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE ...
18090	GM_M30_B2_G05_MF	g2443320	BLASTX	166	3e-10	41	(D85597) polyprotein [Oryza australiensis]
18091	GM_M30_B2_G06_MF	g4063760	BLASTX	182	6e-12	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18092	GM_M30_B2_H12_MR	g320565	BLASTX	211	2e-16	48	transposon TA1-1 KAS-1 - Arabidopsis thaliana (fragment)
18093	GM_M31_A1_A05_MR	g2995951	BLASTX	149	6e-10	54	(AF053564) auxin-induced protein [Mesembryanthemum crystallinum]
18094	GM_M31_A1_A09_MR	g18683	BLASTN	696	4e-30	81	G.max N-20t gene
18095	GM_M31_A1_A12_MR	g3550435	BLASTN	557	4e-18	63	Hordeum vulgare Hotr1 gene
18096	GM_M31_A1_B02_MR	g2827534	BLASTX	171	3e-11	88	(AL021633) predicted protein [Arabidopsis thaliana]
18097	GM_M31_A1_B08_MR	g629693	BLASTX	170	2e-11	29	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
18098	GM_M31_A1_B09_MR	g116054	BLASTX	672	2e-65	98	CALCIUM-DEPENDENT PROTEIN KINASE SK5 (CDPK) gi 280393 pir A43713 calcium-dependent protein kinase (EC 2.7.1.-) - soybean gi 169931 (M64987) Glycine max calcium dependent protein kinase mRNA. [Glycine max]
18099	GM_M31_A1_B11_MR	g18559	BLASTN	1058	6e-41	78	G.max gene for catalase
18100	GM_M31_A1_C05_MR	g4063760	BLASTX	281	2e-22	63	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18101	GM_M31_A1_C11_MR	g1167523	BLASTX	358	1e-30	51	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18102	GM_M31_A1_C12_MR	g3776559	BLASTX	407	3e-37	77	(AC005388) Strong similarity to gene F14J9.26 gi 3482933 cdc2 protein kinase homolog from A. thaliana BAC gb AC003970. ESTs gb Z35332 and gb F19907 come from this gene. [Arabidopsis thaliana]
18103	GM_M31_A1_D05_MR	g2642431	BLASTX	267	6e-21	50	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
18104	GM_M31_A1_D10_MR	g4038056	BLASTX	387	4e-34	52	(AC005897) putative transposon [Arabidopsis thaliana]
18105	GM_M31_A1_D12_MR	g2995405	BLASTX	331	4e-28	49	(Y12432) polyprotein [Ananas comosus]
18106	GM_M31_A1_E11_MF	g507910	BLASTN	533	2e-17	81	Glycine max BSR-101 satellite SB92 genomic sequence.
18107	GM_M31_A1_E11_MR	g507910	BLASTN	581	1e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
18108	GM_M31_A1_F03_MF	g507910	BLASTN	601	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
18109	GM_M31_A1_F03_MR	g4063760	BLASTX	279	3e-22	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18110	GM_M31_A1_F12_MF	g3212869	BLASTX	155	2e-09	72	(AC004005) unknown protein [Arabidopsis thaliana]
18111	GM_M31_A1_F12_MR	g2262116	BLASTX	163	3e-10	31	(AC002343) cellulose synthase isolog [Arabidopsis thaliana]
18112	GM_M31_A1_G10_MF	g3142328	BLASTN	690	6e-38	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18113	GM_M31_A1_G11_MF	g18559	BLASTN	870	2e-32	75	G.max gene for catalase
18114	GM_M31_A1_H03_MF	g1769898	BLASTX	404	1e-36	61	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18115	GM_M31_A1_H09_MR	g4063760	BLASTX	364	2e-31	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18116	GM_M31_A2_A02_MR	g1335862	BLASTX	234	3e-18	83	(U42608) clathrin heavy chain [Glycine max]
18117	GM_M31_A2_A03_MF	g3097320	BLASTN	451	2e-13	71	Glycine max gene for Bd 30K, complete cds
18118	GM_M31_A2_A04_MF	g99922	BLASTX	545	7e-52	80	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
18119	GM_M31_A2_A07_MF	g3869065	BLASTN	886	5e-33	72	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]
18120	GM_M31_A2_A09_MR	g114734	BLASTX	147	1e-09	83	AUXIN-INDUCED PROTEIN AUX28 gi 81759 pir A28993 aux28 protein - soybean gi 169921 (J03919) auxin-regulated protein (Aux28) [Glycine max]
18121	GM_M31_A2_A10_MF	g2911280	BLASTX	153	1e-22	68	(U73937) PK12 protein kinase [Nicotiana tabacum]
18122	GM_M31_A2_A12_MF	g3645899	BLASTX	218	4e-19	50	(U68408) 5' end not determined experimentally [Zea mays]
18123	GM_M31_A2_B04_MF	g4063760	BLASTX	266	6e-21	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18124	GM_M31_A2_B05_MR	g3426334	BLASTN	439	7e-13	60	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
18125	GM_M31_A2_B08_MR	g3777527	BLASTX	253	1e-40	90	(AF053008) gag-pol polyprotein [Glycine max]
18126	GM_M31_A2_B11_MR	g1769898	BLASTX	439	1e-40	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18127	GM_M31_A2_C01_MR	g18559	BLASTN	377	5e-10	71	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18128	GM_M31_A2_C05_MF	g4092470	BLASTN	502	1e-15	71	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
18129	GM_M31_A2_C05_MR	g126766	BLASTX	121	8e-10	67	MALATE SYNTHASE, GLYOXYSOMAL gi 68216 pir SYRPMA malate synthase (EC 4.1.3.2), glyoxysomal - rape gi 167150 (J04468) malate synthase (EC 4.1.3.2) [Brassica napus]
18130	GM_M31_A2_C09_MF	g18695	BLASTN	520	1e-16	82	Soybean nodulin 22 gene
18131	GM_M31_A2_C10_MF	g905361	BLASTX	99	5e-09	31	(U22103) gag-protease polyprotein [Glycine max]
18132	GM_M31_A2_C11_MF	g1769898	BLASTX	387	1e-34	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18133	GM_M31_A2_D01_MR	g1321941	BLASTX	119	1e-11	64	(Z48564) dihydrolipoamide dehydrogenase [Synechocystis PCC6803]
18134	GM_M31_A2_D02_MF	g1345132	BLASTX	152	7e-09	41	(U47029) ERECTA [Arabidopsis thaliana] gi 1389566 gnl PID d1012536 (D83257) receptor protein kinase [Arabidopsis thaliana] gi 3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]
18135	GM_M31_A2_D03_MR	g2244976	BLASTX	230	2e-18	64	(Z97340) hypothetical protein [Arabidopsis thaliana]
18136	GM_M31_A2_D04_MF	g3097320	BLASTN	639	7e-22	81	Glycine max gene for Bd 30K, complete cds
18137	GM_M31_A2_D05_MF	g2570102	BLASTX	250	1e-20	42	(Y12603) CCLS 65 [Silene latifolia]
18138	GM_M31_A2_D06_MF	g3777527	BLASTX	655	3e-62	97	(AF053008) gag-pol polyprotein [Glycine max]
18139	GM_M31_A2_D06_MR	g3142328	BLASTN	910	3e-34	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18140	GM_M31_A2_E03_MF	g4038056	BLASTX	200	5e-14	41	(AC005897) putative transposon [Arabidopsis thaliana]
18141	GM_M31_A2_E04_MR	g507910	BLASTN	439	3e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18142	GM_M31_A2_E09_MF	g2673917	BLASTX	186	5e-12	65	(AC002561) putative ATP-dependent RNA helicase [Arabidopsis thaliana]
18143	GM_M31_A2_E11_MF	g3845197	BLASTN	380	4e-10	65	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
18144	GM_M31_A2_E12_MF	g3777527	BLASTX	547	1e-50	89	(AF053008) gag-pol polyprotein [Glycine max]
18145	GM_M31_A2_E12_MR	g507910	BLASTN	356	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
18146	GM_M31_A2_F03_MF	g4063760	BLASTX	505	2e-46	73	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18147	GM_M31_A2_F03_MR	g343840	BLASTN	425	2e-12	63	Yeast (S.cerevisiae) strain B mitochondrial petite mutant b-1 ori1 region.
18148	GM_M31_A2_F05_MF	g3142328	BLASTN	1038	4e-40	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18149	GM_M31_A2_F10_MR	g4038056	BLASTX	356	9e-31	55	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18150	GM_M31_A2_G01_MF	g13373	BLASTN	384	3e-11	67	Terminal inverted repeat from Paramecium mitochondrion >gi 342968 gb J01432 PARMTDIN1 paramecium species 1 mitochondria dimer initiation region dna.
18151	GM_M31_A2_G04_MF	g507910	BLASTN	611	5e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
18152	GM_M31_A2_G04_MR	g4063760	BLASTX	239	4e-18	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18153	GM_M31_A2_G05_MF	g170029	BLASTN	370	1e-09	78	Glycine max cv. Dare nodulin 26 gene fragment.
18154	GM_M31_A2_G09_MR	g3319351	BLASTX	289	3e-23	40	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
18155	GM_M31_A2_G10_MF	g130405	BLASTX	115	3e-11	37	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 17.6) gi 74642 pir GNFF17 retrovirus-related pol polyprotein - fruit fly (Drosophila melanogaster) transposon 17.6 gi 1335613 gnl PID e1849 (X01472) ORF 2, pot. reverse transcriptase [Drosophila melanogaster] gi 224319 prf 1101404B ORF 2 [Drosophila melanogaster]
18156	GM_M31_A2_G10_MR	g3250695	BLASTX	166	8e-11	67	(AL024486) putative protein [Arabidopsis thaliana]
18157	GM_M31_A2_G11_MR	g2997694	BLASTX	226	5e-18	37	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
18158	GM_M31_A2_H03_MR	g905361	BLASTX	179	5e-12	32	(U22103) gag-protease polyprotein [Glycine max]
18159	GM_M31_A2_H06_MF	g3142379	BLASTX	265	8e-22	59	(AF053008) envelope-like [Glycine max]
18160	GM_M31_A2_H10_MR	g3777527	BLASTX	297	4e-24	46	(AF053008) gag-pol polyprotein [Glycine max]
18161	GM_M31_A2_H12_MF	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
18162	GM_M31_A2_H12_MR	g4092471	BLASTN	502	1e-15	69	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
18163	GM_M31_B1_A09_MF	g507910	BLASTN	410	6e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18164	GM_M31_B1_A09_MR	g507910	BLASTN	387	7e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
18165	GM_M31_B1_A11_MF	g4092471	BLASTN	378	5e-10	64	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
18166	GM_M31_B1_A11_MR	g3873174	BLASTN	399	6e-11	61	Genomic sequence for Arabidopsis thaliana BAC F14N23, complete sequence [Arabidopsis thaliana]
18167	GM_M31_B1_A12_MF	g100484	BLASTX	310	5e-26	55	hypothetical protein - garden snapdragon
18168	GM_M31_B1_B01_MF	g4063760	BLASTX	512	4e-47	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18169	GM_M31_B1_B01_MR	g3142328	BLASTN	833	9e-31	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18170	GM_M31_B1_B02_MF	g100484	BLASTX	184	2e-12	45	hypothetical protein - garden snapdragon

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18171	GM_M31_B1_B05_MF	g4063760	BLASTX	349	9e-30	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18172	GM_M31_B1_B05_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18173	GM_M31_B1_B10_MF	g3645899	BLASTX	182	5e-12	55	(U68408) 5' end not determined experimentally [Zea mays]
18174	GM_M31_B1_C04_MR	g3777527	BLASTX	631	7e-63	95	(AF053008) gag-pol polyprotein [Glycine max]
18175	GM_M31_B1_C05_MR	g2924732	BLASTN	778	4e-28	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUA2, complete sequence [Arabidopsis thaliana]
18176	GM_M31_B1_D03_MF	g1769898	BLASTX	254	4e-20	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18177	GM_M31_B1_D03_MR	g2522227	BLASTX	180	5e-13	60	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
18178	GM_M31_B1_D06_MF	g3097320	BLASTN	950	5e-36	76	Glycine max gene for Bd 30K, complete cds
18179	GM_M31_B1_D11_MF	g4038056	BLASTX	340	3e-30	54	(AC005897) putative transposon [Arabidopsis thaliana]
18180	GM_M31_B1_D11_MR	g4063760	BLASTX	350	8e-30	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18181	GM_M31_B1_D12_MR	g4063756	BLASTN	484	8e-15	70	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
18182	GM_M31_B1_E05_MR	g507910	BLASTN	396	3e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18183	GM_M31_B1_E06_MR	g3128228	BLASTX	463	4e-43	92	(AC004077) putative ribosomal protein L18A [Arabidopsis thaliana] gi 3337376 (AC004481) putative ribosomal protein L18A [Arabidopsis thaliana]
18184	GM_M31_B1_E07_MR	g3650039	BLASTX	279	9e-23	45	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
18185	GM_M31_B1_E08_MF	g1431738	BLASTN	863	2e-32	82	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
18186	GM_M31_B1_E12_MF	g2129618	BLASTX	148	3e-14	47	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18187	GM_M31_B1_F07_MF	g507910	BLASTN	460	4e-14	79	Glycine max BSR-101 satellite SB92 genomic sequence.
18188	GM_M31_B1_F10_MR	g18559	BLASTN	955	3e-36	76	G.max gene for catalase
18189	GM_M31_B1_G05_MR	g507910	BLASTN	578	2e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
18190	GM_M31_B1_G08_MR	g226407	BLASTX	332	7e-28	51	retrotransposon del1-46 [Lilium henryi]
18191	GM_M31_B1_G09_MR	g3810596	BLASTX	174	3e-11	31	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
18192	GM_M31_B1_G12_MR	g507910	BLASTN	394	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
18193	GM_M31_B1_H01_MF	g1944192	BLASTN	1050	1e-41	90	Soybean mRNA for nodulin 35, complete cds
18194	GM_M31_B1_H02_MR	g3021270	BLASTX	261	5e-31	77	(AL022347) serine/threonine kinase -like protein [Arabidopsis thaliana]
18195	GM_M31_B1_H05_MR	g905361	BLASTX	154	3e-09	29	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18196	GM_M31_B2_A08_MF	g4049332	BLASTN	367	9e-18	66	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)
18197	GM_M31_B2_A09_MF	g2264320	BLASTN	489	5e-15	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
18198	GM_M31_B2_A10_MF	g2344894	BLASTX	158	1e-12	67	(AC002388) hypothetical protein [Arabidopsis thaliana]
18199	GM_M31_B2_B01_MF	g507910	BLASTN	456	5e-14	77	Glycine max BSR-101 satellite SB92 genomic sequence.
18200	GM_M31_B2_C10_MF	g18559	BLASTN	497	2e-15	75	G.max gene for catalase
18201	GM_M31_B2_C11_MF	g3097320	BLASTN	892	2e-33	77	Glycine max gene for Bd 30K, complete cds
18202	GM_M31_B2_D01_MF	g507910	BLASTN	362	9e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
18203	GM_M31_B2_E02_MF	g4063760	BLASTX	462	7e-42	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18204	GM_M31_B2_E03_MF	g1326016	BLASTX	230	4e-17	41	TY3-2 orfB
18205	GM_M31_B2_E05_MF	g3643604	BLASTX	187	1e-12	37	(AC005395) receptor-like protein kinase [Arabidopsis thaliana]
18206	GM_M31_B2_E10_MF	g2827702	BLASTX	393	9e-36	71	(AL021684) predicted protein [Arabidopsis thaliana]
18207	GM_M31_B2_F03_MF	g498931	BLASTX	448	1e-41	68	(Z12825) ORF167; homologous to reverse transcriptases from retroviral-like transposons TNT 1-94 from tobacco and COPIA from Drosophila [Beta vulgaris]
18208	GM_M31_B2_G04_MF	g2270991	BLASTN	425	6e-13	84	Glycine max metallothionein-II protein mRNA, complete cds
18209	GM_M31_B2_G05_MF	g507910	BLASTN	383	1e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18210	GM_M31_B2_G08_MF	g4063760	BLASTX	531	3e-49	75	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18211	GM_M31_B2_H01_MF	g3142328	BLASTN	1437	3e-58	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18212	GM_M31_B2_H02_MF	g507910	BLASTN	702	4e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
18213	GM_M31_B2_H05_MF	g3645899	BLASTX	352	3e-30	55	(U68408) 5' end not determined experimentally [Zea mays]
18214	GM_M31_B2_H09_MF	g3096919	BLASTX	280	3e-23	49	(AL023094) putative serine/threonine protein kinase [Arabidopsis thaliana]
18215	GM_M31_B2_H11_MF	g3288442	BLASTN	467	5e-14	66	Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Ga...
18216	GM_M32_A1_A07_MF	g3142379	BLASTX	242	3e-19	72	(AF053008) envelope-like [Glycine max]
18217	GM_M32_A1_B04_MR	g3097320	BLASTN	492	3e-15	70	Glycine max gene for Bd 30K, complete cds
18218	GM_M32_A1_B05_MF	g3777527	BLASTX	180	1e-11	44	(AF053008) gag-pol polyprotein [Glycine max]
18219	GM_M32_A1_B05_MR	g2443899	BLASTN	397	7e-11	64	A. thaliana BAC T3F12 from chromsome IV, likely from the long arm, complete sequence [Arabidopsis thaliana]
18220	GM_M32_A1_B10_MF	g507910	BLASTN	592	4e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18221	GM_M32_A1_C02_MF	g905361	BLASTX	171	4e-11	35	(U22103) gag-protease polyprotein [Glycine max]
18222	GM_M32_A1_C06_MR	g3273387	BLASTN	426	3e-12	68	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
18223	GM_M32_A1_C07_MR	g507910	BLASTN	341	8e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18224	GM_M32_A1_C09_MF	g3097320	BLASTN	432	2e-12	73	Glycine max gene for Bd 30K, complete cds
18225	GM_M32_A1_C09_MR	g4063760	BLASTX	222	3e-16	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18226	GM_M32_A1_D04_MF	g3777527	BLASTX	604	9e-57	98	(AF053008) gag-pol polyprotein [Glycine max]
18227	GM_M32_A1_D10_MR	g3645899	BLASTX	307	2e-25	50	(U68408) 5' end not determined experimentally [Zea mays]
18228	GM_M32_A1_E01_MR	g2462134	BLASTX	171	3e-11	33	(Y13368) reverse transcriptase [Beta vulgaris]
18229	GM_M32_A1_E02_MF	g3779026	BLASTX	315	5e-26	49	(AC005171) putative retrotransposon [Arabidopsis thaliana]
18230	GM_M32_A1_E05_MR	g2121303	BLASTN	410	2e-11	61	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
18231	GM_M32_A1_E07_MF	g3688172	BLASTX	152	2e-10	49	(AL031804) putative protein [Arabidopsis thaliana]
18232	GM_M32_A1_E08_MF	g507910	BLASTN	353	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
18233	GM_M32_A1_E08_MR	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18234	GM_M32_A1_E09_MR	g4063760	BLASTX	280	2e-22	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18235	GM_M32_A1_E12_MF	g507910	BLASTN	597	2e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
18236	GM_M32_A1_E12_MR	g507910	BLASTN	395	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
18237	GM_M32_A1_F04_MF	g342963	BLASTN	378	2e-10	65	paramecium species 5,87 mt dna dimer: replication init. region.
18238	GM_M32_A1_F04_MR	g99755	BLASTX	289	6e-24	43	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
18239	GM_M32_A1_G08_MR	g4140712	BLASTX	252	8e-21	37	(AF110183) putative integrase [Oryza sativa]
18240	GM_M32_A1_G12_MR	g4063760	BLASTX	184	4e-12	42	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18241	GM_M32_A2_A10_MF	g18683	BLASTN	435	9e-13	77	G.max N-20t gene
18242	GM_M32_A2_A11_MF	g3859060	BLASTN	354	6e-09	62	Human DNA sequence from clone 769D20 on chromosome Xp21.1-21.3 Contains EST, GSS, complete sequence [Homo sapiens]
18243	GM_M32_A2_B03_MR	g629693	BLASTX	146	4e-11	41	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
18244	GM_M32_A2_B04_MF	g100484	BLASTX	97	4e-10	60	hypothetical protein - garden snapdragon
18245	GM_M32_A2_B05_MF	g18695	BLASTN	399	4e-11	72	Soybean nodulin 22 gene
18246	GM_M32_A2_B10_MF	g1142703	BLASTN	301	2e-17	77	Glycine max satellite STR120-B.1.
18247	GM_M32_A2_B12_MF	g3097320	BLASTN	1204	2e-47	83	Glycine max gene for Bd 30K, complete cds
18248	GM_M32_A2_C01_MF	g4038056	BLASTX	241	4e-24	57	(AC005897) putative transposon [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18249	GM_M32_A2_C02_MF	g4038056	BLASTX	223	9e-22	56	(AC005897) putative transposon [Arabidopsis thaliana]
18250	GM_M32_A2_C07_MR	g2462058	BLASTX	171	3e-12	55	(Y13389) reverse transcriptase [Antirrhinum majus]
18251	GM_M32_A2_C08_MR	g3142328	BLASTN	1093	1e-42	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18252	GM_M32_A2_D02_MF	g3097320	BLASTN	402	4e-11	71	Glycine max gene for Bd 30K, complete cds
18253	GM_M32_A2_D02_MR	g18559	BLASTN	402	3e-11	74	G.max gene for catalase
18254	GM_M32_A2_D06_MF	g3688172	BLASTX	168	1e-10	78	(AL031804) putative protein [Arabidopsis thaliana]
18255	GM_M32_A2_D10_MR	g2982538	BLASTN	309	7e-09	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-28, complete sequence [Plasmodium falciparum]
18256	GM_M32_A2_D11_MF	g2809207	BLASTX	154	2e-10	84	(AF042184) lysine-ketoglutarate reductase/saccharopine dehydrogenase [Brassica napus]
18257	GM_M32_A2_E07_MR	g3319362	BLASTX	184	2e-19	57	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
18258	GM_M32_A2_F03_MR	g3695395	BLASTX	191	2e-13	40	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
18259	GM_M32_A2_F04_MF	g507910	BLASTN	584	9e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
18260	GM_M32_A2_F04_MR	g507910	BLASTN	610	6e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
18261	GM_M32_A2_F07_MR	g3777527	BLASTX	725	9e-70	96	(AF053008) gag-pol polyprotein [Glycine max]
18262	GM_M32_A2_F12_MR	g3513745	BLASTX	164	7e-10	31	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
18263	GM_M32_A2_G01_MR	g4063760	BLASTX	536	9e-50	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18264	GM_M32_A2_G02_MR	g4063760	BLASTX	291	3e-33	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18265	GM_M32_A2_G03_MF	g343543	BLASTN	344	5e-09	62	T.brucei kinetoplast ATPase 6 edited mRNA, complete cds.
18266	GM_M32_A2_G05_MF	g2760837	BLASTX	139	1e-15	53	(AC003105) putative cytochrome P450 [Arabidopsis thaliana]
18267	GM_M32_A2_G05_MR	g2129618	BLASTX	201	4e-14	46	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18268	GM_M32_A2_G06_MR	g3779026	BLASTX	361	6e-31	50	(AC005171) putative retrotransposon [Arabidopsis thaliana]
18269	GM_M32_A2_G10_MF	g4063760	BLASTX	271	2e-21	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18270	GM_M32_A2_G11_MR	g3176811	BLASTN	397	7e-12	64	Homo sapiens allele 18 fragile site locus (FRA10B) minisatellite, 3' sequence
18271	GM_M32_A2_G12_MR	g3319362	BLASTX	282	9e-23	43	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
18272	GM_M32_A2_H02_MR	g1778438	BLASTX	120	2e-09	53	(U82399) putative protein kinase PK1 [Arabidopsis thaliana]
18273	GM_M32_A2_H03_MR	g507910	BLASTN	511	2e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18274	GM_M32_A2_H06_MF	g629693	BLASTX	146	4e-12	47	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
18275	GM_M32_A2_H12_MR	g3097320	BLASTN	451	2e-13	73	Glycine max gene for Bd 30K, complete cds
18276	GM_M32_B1_A02_MR	g3142328	BLASTN	614	8e-21	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18277	GM_M32_B1_A05_MF	g3550435	BLASTN	460	9e-14	63	Hordeum vulgare Hotr1 gene
18278	GM_M32_B1_A05_MR	g507910	BLASTN	668	1e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
18279	GM_M32_B1_A11_MR	g2129618	BLASTX	235	1e-17	45	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18280	GM_M32_B1_B01_MF	g3777527	BLASTX	166	3e-11	40	(AF053008) gag-pol polyprotein [Glycine max]
18281	GM_M32_B1_B02_MR	g4063760	BLASTX	243	9e-20	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18282	GM_M32_B1_B11_MR	g905361	BLASTX	239	2e-18	38	(U22103) gag-protease polyprotein [Glycine max]
18283	GM_M32_B1_B12_MR	g505129	BLASTN	385	1e-15	70	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
18284	GM_M32_B1_C01_MR	g3493214	BLASTX	140	2e-15	43	(AF056940) pol polyprotein [Drosophila virilis]
18285	GM_M32_B1_C04_MF	g3097320	BLASTN	793	7e-29	74	Glycine max gene for Bd 30K, complete cds
18286	GM_M32_B1_C05_MF	g170080	BLASTN	1000	4e-57	97	Soybean seed lectin gene transposable element tgm1.
18287	GM_M32_B1_C09_MF	g3142379	BLASTX	197	2e-14	72	(AF053008) envelope-like [Glycine max]
18288	GM_M32_B1_C09_MR	g3777527	BLASTX	435	5e-58	98	(AF053008) gag-pol polyprotein [Glycine max]
18289	GM_M32_B1_D01_MR	g629693	BLASTX	166	5e-11	30	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
18290	GM_M32_B1_D02_MR	g100484	BLASTX	376	4e-33	57	hypothetical protein - garden snapdragon
18291	GM_M32_B1_D05_MF	g3914056	BLASTX	118	5e-12	74	DNA MISMATCH REPAIR PROTEIN MSH2 >gi 2522362 (AF002706) MutS homolog 2 [Arabidopsis thaliana] >gi 2522364 (AF003005) MutS homolog 2 [Arabidopsis thaliana] >gi 2547236 (AF026549) DNA mismatch repair protein MSH2 [Arabidopsis thaliana]
18292	GM_M32_B1_D06_MR	g2995405	BLASTX	425	3e-38	71	(Y12432) polyprotein [Ananas comosus]
18293	GM_M32_B1_D07_MF	g3645899	BLASTX	221	4e-16	48	(U68408) 5' end not determined experimentally [Zea mays]
18294	GM_M32_B1_D10_MF	g905361	BLASTX	421	2e-38	93	(U22103) gag-protease polyprotein [Glycine max]
18295	GM_M32_B1_D12_MR	g3845197	BLASTN	483	8e-15	64	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
18296	GM_M32_B1_E01_MF	g1769897	BLASTX	164	2e-10	38	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18297	GM_M32_B1_E02_MR	g18559	BLASTN	693	2e-24	72	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18298	GM_M32_B1_E09_MR	g4006838	BLASTN	386	2e-10	68	Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence [Homo sapiens]
18299	GM_M32_B1_F01_MF	g1345644	BLASTX	176	7e-12	51	CYTOCHROME P450 LXXXVI gi 940446 (X90458) cytochrome p450 [Arabidopsis thaliana]
18300	GM_M32_B1_F02_MR	g4063760	BLASTX	483	4e-47	70	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18301	GM_M32_B1_F07_MR	g3522966	BLASTN	354	6e-09	65	Homo sapiens subtelomeric cosmid clone 5b-1, complete sequence [Homo sapiens]
18302	GM_M32_B1_F08_MR	g3935157	BLASTX	151	7e-09	63	(AC005106) T25N20.21 [Arabidopsis thaliana]
18303	GM_M32_B1_G02_MR	g3337395	BLASTN	426	3e-12	62	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
18304	GM_M32_B1_G04_MF	g3426038	BLASTX	271	5e-21	46	(AC005168) unknown protein [Arabidopsis thaliana]
18305	GM_M32_B1_G09_MF	g3930515	BLASTX	115	4e-10	46	(AF059674) putative gag protein [Nicotiana tabacum]
18306	GM_M32_B1_G11_MR	g18559	BLASTN	448	3e-13	76	G.max gene for catalase
18307	GM_M32_B1_H04_MF	g2264320	BLASTN	630	2e-21	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
18308	GM_M32_B1_H04_MR	g629693	BLASTX	151	2e-09	30	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
18309	GM_M32_B1_H05_MF	g2569940	BLASTX	197	5e-14	50	(Y15194) GRS protein [Arabidopsis thaliana]
18310	GM_M32_B1_H08_MR	g2997694	BLASTX	183	1e-13	33	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
18311	GM_M32_B1_H09_MF	g3930515	BLASTX	121	5e-10	47	(AF059674) putative gag protein [Nicotiana tabacum]
18312	GM_M32_B2_A02_MR	g3777527	BLASTX	325	5e-27	49	(AF053008) gag-pol polyprotein [Glycine max]
18313	GM_M32_B2_A05_MR	g2213582	BLASTX	206	2e-14	28	(AC000348) T7N9.2 [Arabidopsis thaliana]
18314	GM_M32_B2_B04_MR	g3928543	BLASTX	215	4e-16	45	(AB016819) UDP-glucose glucosyltransferase [Arabidopsis thaliana]
18315	GM_M32_B2_B10_MR	g3777527	BLASTX	177	3e-11	44	(AF053008) gag-pol polyprotein [Glycine max]
18316	GM_M32_B2_C01_MR	g507910	BLASTN	608	7e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
18317	GM_M32_B2_C03_MR	g2462134	BLASTX	163	2e-10	34	(Y13368) reverse transcriptase [Beta vulgaris]
18318	GM_M32_B2_C07_MR	g531389	BLASTX	175	4e-11	42	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
18319	GM_M32_B2_D04_MF	g3386533	BLASTN	490	3e-15	75	Glycine max mariner element Soymar1 transposase gene, complete cds
18320	GM_M32_B2_D04_MR	g3386533	BLASTN	1587	3e-65	97	Glycine max mariner element Soymar1 transposase gene, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18321	GM_M32_B2_D09_MF	g3142328	BLASTN	578	3e-19	67	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18322	GM_M32_B2_D10_MF	g3777527	BLASTX	297	4e-24	45	(AF053008) gag-pol polyprotein [Glycine max]
18323	GM_M32_B2_D12_MR	g4063760	BLASTX	452	9e-41	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18324	GM_M32_B2_F01_MR	g1236920	BLASTN	276	4e-10	62	Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.
18325	GM_M32_B2_F08_MR	g2995405	BLASTX	337	1e-28	46	(Y12432) polyprotein [Ananas comosus]
18326	GM_M32_B2_G06_MR	g587603	BLASTN	414	9e-12	61	P.falciparum gene for beta subunit RNA polymerase
18327	GM_M32_B2_H01_MR	g3097320	BLASTN	467	4e-14	76	Glycine max gene for Bd 30K, complete cds
18328	GM_M32_B2_H07_MR	g3142328	BLASTN	833	9e-31	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18329	GM_M32_B2_H11_MR	g4115365	BLASTX	169	1e-14	61	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
18330	GM_M33_A1_A09_MR	g905361	BLASTX	181	3e-12	34	(U22103) gag-protease polyprotein [Glycine max]
18331	GM_M33_A1_A10_MF	g2781345	BLASTX	154	4e-09	93	(AC003113) F24O1.2 [Arabidopsis thaliana]
18332	GM_M33_A1_A12_MR	g4115536	BLASTX	170	6e-12	39	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]
18333	GM_M33_A1_B02_MF	g3845197	BLASTN	373	8e-10	61	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
18334	GM_M33_A1_B03_MR	g840618	BLASTN	468	2e-14	60	Medicago sativa middle repetitive DNA (RPE15) gene, complete cds
18335	GM_M33_A1_B04_MR	g4006828	BLASTX	194	2e-13	30	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
18336	GM_M33_A1_B05_MF	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18337	GM_M33_A1_B05_MR	g507910	BLASTN	393	4e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18338	GM_M33_A1_C02_MR	g349405	BLASTN	386	2e-10	64	Brassica napus (clone BnNa) DNA sequence.
18339	GM_M33_A1_C04_MR	g3513744	BLASTX	164	2e-11	37	(AF080118) contains similarity to Medicago truncatula MtN3 (GB:Y08726) [Arabidopsis thaliana]
18340	GM_M33_A1_C05_MF	g170296	BLASTN	401	4e-13	80	Nicotiana plumbaginifolia plasma-membrane H+ ATPase (pma3) gene, exons 1-9.
18341	GM_M33_A1_C05_MR	g2281330	BLASTX	157	2e-10	51	(U85646) putative pectate lyase Nt59 [Nicotiana tabacum]
18342	GM_M33_A1_C10_MR	g4063760	BLASTX	554	1e-51	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18343	GM_M33_A1_C11_MF	g2522227	BLASTX	227	1e-20	45	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
18344	GM_M33_A1_C12_MF	g3777527	BLASTX	628	2e-59	96	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18345	GM_M33_A1_D02_MR	g2245082	BLASTX	166	4e-11	31	(Z97343) SCARECROW homolog [Arabidopsis thaliana]
18346	GM_M33_A1_D03_MF	g2443320	BLASTX	294	8e-24	46	(D85597) polyprotein [Oryza australiensis]
18347	GM_M33_A1_D05_MR	g3777527	BLASTX	741	2e-71	96	(AF053008) gag-pol polyprotein [Glycine max]
18348	GM_M33_A1_D10_MF	g18559	BLASTN	863	4e-32	76	G.max gene for catalase
18349	GM_M33_A1_D11_MF	g507910	BLASTN	552	2e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
18350	GM_M33_A1_D12_MF	g3820757	BLASTN	416	5e-12	63	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
18351	GM_M33_A1_E11_MR	g18559	BLASTN	677	1e-23	71	G.max gene for catalase
18352	GM_M33_A1_F10_MR	g2708743	BLASTX	254	1e-19	42	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
18353	GM_M33_A1_F11_MR	g905361	BLASTX	343	1e-29	93	(U22103) gag-protease polyprotein [Glycine max]
18354	GM_M33_A1_G03_MR	g4115536	BLASTX	172	3e-12	39	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]
18355	GM_M33_A1_G04_MR	g3142328	BLASTN	1253	7e-50	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18356	GM_M33_A1_G09_MF	g4063760	BLASTX	334	4e-28	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18357	GM_M33_A1_H02_MF	g2129618	BLASTX	191	4e-13	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18358	GM_M33_A1_H07_MR	g1167523	BLASTX	300	2e-24	47	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18359	GM_M33_A1_H09_MR	g2583112	BLASTX	167	2e-11	40	(AC002387) putative PD1-like DNA-binding protein [Arabidopsis thaliana]
18360	GM_M33_A1_H10_MF	g507910	BLASTN	586	7e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
18361	GM_M33_A2_A04_MF	g2414229	BLASTN	361	3e-09	64	Caenorhabditis elegans cosmid K03D10, complete sequence [Caenorhabditis elegans]
18362	GM_M33_A2_A07_MF	g2316016	BLASTX	397	1e-34	61	(U92650) MRP-like ABC transporter [Arabidopsis thaliana]
18363	GM_M33_A2_A08_MR	g4063760	BLASTX	326	3e-27	54	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18364	GM_M33_A2_A11_MF	g1769896	BLASTN	409	2e-11	64	A.thaliana lectin receptor kinase gene
18365	GM_M33_A2_B02_MR	g18559	BLASTN	552	5e-18	72	G.max gene for catalase
18366	GM_M33_A2_B09_MF	g1167523	BLASTX	115	2e-12	48	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18367	GM_M33_A2_B09_MR	g4160362	BLASTN	266	6e-12	69	Saccharomyces cerevisiae complete mitochondrial genome
18368	GM_M33_A2_B10_MF	g4038037	BLASTX	385	1e-33	60	(AC005936) hypothetical protein [Arabidopsis thaliana]
18369	GM_M33_A2_C01_MR	g18766	BLASTN	387	6e-11	80	Soybean Tgm5 transposable element
18370	GM_M33_A2_C03_MF	g3097320	BLASTN	817	6e-30	72	Glycine max gene for Bd 30K, complete cds
18371	GM_M33_A2_C03_MR	g3779021	BLASTX	165	4e-10	41	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18372	GM_M33_A2_C04_MF	g126406	BLASTX	278	7e-33	77	SEED LIPOXYGENASE-3 (L-3) gi 18677 (X06928) lipoxygenase [Glycine max]
18373	GM_M33_A2_C06_MF	g2961349	BLASTX	303	7e-25	49	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
18374	GM_M33_A2_C11_MR	g3451074	BLASTX	259	1e-20	50	(AL031326) putative protein [Arabidopsis thaliana]
18375	GM_M33_A2_D01_MF	g3337395	BLASTN	375	7e-10	61	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
18376	GM_M33_A2_D02_MR	g421955	BLASTX	164	8e-11	41	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
18377	GM_M33_A2_D04_MF	g2462134	BLASTX	347	8e-31	44	(Y13368) reverse transcriptase [Beta vulgaris]
18378	GM_M33_A2_D05_MF	g3513747	BLASTX	197	2e-13	47	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
18379	GM_M33_A2_D07_MF	g3982831	BLASTX	615	6e-59	100	(AF083343) 101 kDa heat shock protein; HSP101 [Nicotiana tabacum]
18380	GM_M33_A2_D10_MF	g3021280	BLASTX	249	1e-19	38	(AL022347) serine /threonine kinase - like protein [Arabidopsis thaliana]
18381	GM_M33_A2_D10_MR	g1769899	BLASTX	128	3e-17	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18382	GM_M33_A2_E05_MR	g2586082	BLASTX	159	2e-09	37	(U72725) retrofit [Oryza longistaminata]
18383	GM_M33_A2_E07_MR	g4063756	BLASTN	362	3e-09	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
18384	GM_M33_A2_E11_MF	g3779021	BLASTX	169	2e-10	34	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]
18385	GM_M33_A2_E12_MF	g4038056	BLASTX	234	1e-17	50	(AC005897) putative transposon [Arabidopsis thaliana]
18386	GM_M33_A2_F03_MF	g320565	BLASTX	189	4e-14	54	transposon TA1-1 KAS-1 - Arabidopsis thaliana (fragment)
18387	GM_M33_A2_F05_MF	g18559	BLASTN	953	3e-36	76	G.max gene for catalase
18388	GM_M33_A2_F07_MF	g4038056	BLASTX	279	2e-22	47	(AC005897) putative transposon [Arabidopsis thaliana]
18389	GM_M33_A2_F08_MF	g905361	BLASTX	149	9e-09	83	(U22103) gag-protease polyprotein [Glycine max]
18390	GM_M33_A2_F10_MF	g2104679	BLASTX	238	4e-30	86	(X97906) transcription factor [Vicia faba]
18391	GM_M33_A2_G03_MR	g3426334	BLASTN	563	2e-18	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
18392	GM_M33_A2_G05_MF	g2443320	BLASTX	316	4e-26	52	(D85597) polyprotein [Oryza australiensis]
18393	GM_M33_A2_G07_MF	g2245029	BLASTX	159	1e-09	55	(Z97341) limonene cyclase homolog [Arabidopsis thaliana]
18394	GM_M33_A2_G08_MR	g4038056	BLASTX	358	6e-31	53	(AC005897) putative transposon [Arabidopsis thaliana]
18395	GM_M33_A2_G10_MR	g100484	BLASTX	343	1e-29	51	hypothetical protein - garden snapdragon
18396	GM_M33_A2_H02_MF	g507910	BLASTN	376	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
18397	GM_M33_A2_H02_MR	g4063760	BLASTX	314	5e-26	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18398	GM_M33_A2_H04_MF	g507910	BLASTN	558	1e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18399	GM_M33_B1_B01_MF	g507910	BLASTN	644	2e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
18400	GM_M33_B1_C11_MF	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
18401	GM_M33_B1_D09_MF	g3980359	BLASTN	360	3e-09	65	Human DNA sequence from clone 344I7 on chromosome Xp11.21-11.3. Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8, KRT8) pseudogene, ESTs and a GSS, complete sequence [Homo sapiens]
18402	GM_M33_B1_F06_MF	g498167	BLASTN	536	4e-18	94	Soybean mRNA for leginsulin, complete cds
18403	GM_M33_B1_G09_MF	g507910	BLASTN	353	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18404	GM_M33_B1_H07_MF	g507910	BLASTN	650	9e-23	84	Glycine max BSR-101 satellite SB92 genomic sequence.
18405	GM_M33_B1_H11_MF	g2995405	BLASTX	332	3e-28	61	(Y12432) polyprotein [Ananas comosus]
18406	GM_M33_B2_E07_MR	g1817728	BLASTN	414	1e-11	72	Cloning vector pBeloBAC11
18407	GM_M34_A1_A04_MR	g18768	BLASTN	510	1e-16	69	Soybean Tgm6 transposable element 3' end
18408	GM_M34_A1_A05_MR	g3142328	BLASTN	1221	2e-48	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18409	GM_M34_A1_A12_MF	g218269	BLASTX	205	7e-16	52	(D12839) reverse transcriptase [Glycine max]
18410	GM_M34_A1_B01_MF	g3980412	BLASTX	185	2e-12	44	(AC004561) pumilio-like protein [Arabidopsis thaliana]
18411	GM_M34_A1_B01_MR	g22741	BLASTN	285	4e-11	86	G.max mitochondrial pseudo-atpA.
18412	GM_M34_A1_B02_MF	g3176795	BLASTN	391	3e-11	63	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
18413	GM_M34_A1_B02_MR	g3845298	BLASTN	391	1e-10	62	Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence
18414	GM_M34_A1_B03_MR	g2129618	BLASTX	251	2e-19	47	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18415	GM_M34_A1_B04_MF	g1688074	BLASTX	146	4e-09	35	(U46570) tetratricopeptide repeat protein [Homo sapiens]
18416	GM_M34_A1_B06_MF	g99922	BLASTX	396	8e-43	66	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
18417	GM_M34_A1_B07_MR	g3746069	BLASTX	206	2e-14	43	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
18418	GM_M34_A1_B11_MF	g1666236	BLASTX	148	3e-09	30	(U76261) unknown [Hordeum vulgare]
18419	GM_M34_A1_B12_MF	g1334366	BLASTX	172	3e-12	80	(X02441) gtg start [Nicotiana tabacum]
18420	GM_M34_A1_C01_MF	g2190548	BLASTX	193	1e-14	71	(AC001229) EST gb ATTS1121 comes from this gene. [Arabidopsis thaliana]
18421	GM_M34_A1_C01_MR	g2995405	BLASTX	273	1e-23	43	(Y12432) polyprotein [Ananas comosus]
18422	GM_M34_A1_C02_MF	g3402758	BLASTX	256	4e-21	69	(AL031187) serine/threonine kinase - like protein [Arabidopsis thaliana]
18423	GM_M34_A1_C03_MF	g2995405	BLASTX	109	1e-12	41	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18424	GM_M34_A1_C06_MR	g1167523	BLASTX	249	5e-19	47	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18425	GM_M34_A1_C11_MR	g2351069	BLASTN	403	4e-11	68	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MSH12
18426	GM_M34_A1_C12_MF	g507910	BLASTN	422	2e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18427	GM_M34_A1_C12_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18428	GM_M34_A1_D02_MR	g2995405	BLASTX	479	4e-44	61	(Y12432) polyprotein [Ananas comosus]
18429	GM_M34_A1_D04_MR	g2330651	BLASTX	301	2e-24	72	(Y14559) topoisomerase II [Pisum sativum]
18430	GM_M34_A1_D08_MF	g3142328	BLASTN	768	8e-28	78	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18431	GM_M34_A1_D09_MR	g2129618	BLASTX	179	9e-12	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18432	GM_M34_A1_E07_MF	g3426334	BLASTN	357	4e-09	59	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
18433	GM_M34_A1_F06_MF	g4063760	BLASTX	211	2e-16	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18434	GM_M34_A1_F07_MF	g1785701	BLASTX	89	1e-10	48	(Y08501) orf154 [Arabidopsis thaliana]
18435	GM_M34_A1_F08_MF	g2995405	BLASTX	200	2e-22	48	(Y12432) polyprotein [Ananas comosus]
18436	GM_M34_A1_F10_MF	g3319362	BLASTX	191	1e-15	47	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
18437	GM_M34_A1_F10_MR	g1167523	BLASTX	378	8e-33	51	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18438	GM_M34_A1_F12_MF	g3810596	BLASTX	218	1e-20	41	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
18439	GM_M34_A1_G01_MF	g18559	BLASTN	360	3e-09	73	G.max gene for catalase
18440	GM_M34_A1_G04_MF	g3513747	BLASTX	244	2e-18	54	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
18441	GM_M34_A1_G06_MF	g558922	BLASTN	627	5e-22	76	Lupinus albus farnesyl pyrophosphate synthase (fps1) mRNA, complete cds.
18442	GM_M34_A1_G07_MR	g3097320	BLASTN	356	4e-09	66	Glycine max gene for Bd 30K, complete cds
18443	GM_M34_A1_G11_MF	g4092471	BLASTN	469	4e-14	71	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
18444	GM_M34_A1_H01_MF	g99730	BLASTX	328	1e-28	50	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
18445	GM_M34_A1_H01_MR	g3142328	BLASTN	1951	9e-82	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18446	GM_M34_A1_H02_MF	g1091678	BLASTX	143	8e-13	34	activator-like transposable element [Pennisetum glaucum]
18447	GM_M34_A1_H04_MF	g3779021	BLASTX	172	6e-12	40	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18448	GM_M34_A1_H05_MR	g1899158	BLASTN	382	2e-10	61	Saccharomyces cerevisiae synthetic green fluorescent protein (cox3::GFPm) gene, mitochondrial gene construct, complete cds
18449	GM_M34_A1_H11_MR	g3426038	BLASTX	278	9e-22	91	(AC005168) unknown protein [Arabidopsis thaliana]
18450	GM_M34_A1_H12_MR	g2085783	BLASTN	386	2e-10	62	Human BAC clone GS113D04 from 5p15.2, complete sequence [Homo sapiens]
18451	GM_M34_A2_A08_MF	g3135269	BLASTX	219	6e-16	45	(AC003058) unknown protein [Arabidopsis thaliana]
18452	GM_M34_A2_A12_MF	g2995405	BLASTX	338	8e-29	55	(Y12432) polyprotein [Ananas comosus]
18453	GM_M34_A2_C12_MF	g507910	BLASTN	580	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
18454	GM_M34_A2_D02_MF	g3142328	BLASTN	961	1e-36	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18455	GM_M34_A2_D06_MF	g3142328	BLASTN	1001	2e-38	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18456	GM_M34_A2_F04_MF	g1769897	BLASTX	311	1e-29	62	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18457	GM_M34_A2_F08_MF	g4050011	BLASTN	666	4e-23	66	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
18458	GM_M34_A2_G03_MF	g18683	BLASTN	489	3e-15	72	G.max N-20t gene
18459	GM_M34_A2_G11_MF	g507910	BLASTN	343	7e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18460	GM_M34_A2_H01_MF	g3415117	BLASTX	219	5e-16	70	(AF081203) villin 3 [Arabidopsis thaliana]
18461	GM_M34_A2_H02_MF	g2258317	BLASTX	137	7e-12	42	(AF004879) resistance complex protein I2C-2 [Lycopersicon esculentum]
18462	GM_M34_A2_H10_MF	g161840	BLASTN	360	2e-09	64	T.thermophila micronuclear region R DNA.
18463	GM_M34_B1_A04_MR	g4038056	BLASTX	378	4e-33	51	(AC005897) putative transposon [Arabidopsis thaliana]
18464	GM_M34_B1_A05_MR	g2129618	BLASTX	191	5e-13	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18465	GM_M34_B1_A08_MR	g4038056	BLASTX	285	5e-25	43	(AC005897) putative transposon [Arabidopsis thaliana]
18466	GM_M34_B1_B01_MR	g728483	BLASTX	238	4e-20	59	(L41046) endo-1,4-beta-glucanase [Pisum sativum]
18467	GM_M34_B1_B02_MF	g3293503	BLASTN	379	6e-11	64	Ephedrus persicae NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds
18468	GM_M34_B1_B02_MR	g2791289	BLASTX	227	1e-16	37	(AJ000387) protease [Drosophila melanogaster]
18469	GM_M34_B1_B11_MR	g3097320	BLASTN	473	2e-14	72	Glycine max gene for Bd 30K, complete cds
18470	GM_M34_B1_C06_MR	g18559	BLASTN	988	9e-38	77	G.max gene for catalase
18471	GM_M34_B1_C10_MR	g507910	BLASTN	390	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18472	GM_M34_B1_D02_MR	g1769898	BLASTX	237	3e-18	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18473	GM_M34_B1_D04_MR	g3777527	BLASTX	255	1e-19	39	(AF053008) gag-pol polyprotein [Glycine max]
18474	GM_M34_B1_D06_MF	g2995405	BLASTX	247	5e-25	50	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18475	GM_M34_B1_D08_MF	g130582	BLASTX	323	6e-27	48	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
18476	GM_M34_B1_D10_MF	g3176671	BLASTX	256	5e-20	67	(AC004393) Contains similarity to hypothetical gene B0495.7 gb 687822 from C. elegans cosmid gb U21317. [Arabidopsis thaliana]
18477	GM_M34_B1_D11_MR	g1431738	BLASTN	655	8e-23	93	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
18478	GM_M34_B1_E03_MF	g2264320	BLASTN	547	1e-17	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
18479	GM_M34_B1_E05_MF	g1769897	BLASTX	171	3e-11	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18480	GM_M34_B1_E08_MR	g130188	BLASTX	529	4e-49	86	PHYTOCHROME A gi 81937 pir S06856 phytochrome - garden pea gi 169132 (M37217) phytochrome [Pisum sativum] gi 295830 (X14077) phytochrome apoprotein [Pisum sativum] gi 226757 prf 1604466A phytochrome [Pisum sativum]
18481	GM_M34_B1_E09_MR	g3377848	BLASTX	169	2e-16	50	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
18482	GM_M34_B1_F05_MR	g1769897	BLASTX	292	7e-28	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18483	GM_M34_B1_F10_MF	g82231	BLASTX	165	1e-11	96	hypothetical protein 82 - common tobacco chloroplast gi 225200 prf 1211235AE ORF 82 [Nicotiana tabacum]
18484	GM_M34_B1_G07_MF	g3142328	BLASTN	1602	9e-66	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18485	GM_M34_B1_G09_MF	g18588	BLASTN	364	2e-09	74	Soybean gene 3 for chalcone synthetase protein
18486	GM_M34_B1_H04_MR	g18559	BLASTN	976	3e-37	77	G.max gene for catalase
18487	GM_M34_B1_H05_MF	g18559	BLASTN	666	4e-23	76	G.max gene for catalase
18488	GM_M34_B1_H06_MR	g2213582	BLASTX	161	1e-09	27	(AC000348) T7N9.2 [Arabidopsis thaliana]
18489	GM_M34_B1_H08_MR	g531389	BLASTX	246	1e-18	50	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
18490	GM_M34_B1_H12_MR	g4063760	BLASTX	395	1e-34	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18491	GM_M34_B2_A12_MF	g1817728	BLASTN	612	1e-20	69	Cloning vector pBeloBAC11
18492	GM_M34_B2_B02_MF	g2579906	BLASTN	467	4e-15	70	Homo sapiens genomic DNA, 21q region, clone: Q6F8BG5
18493	GM_M34_B2_B03_MR	g2462058	BLASTX	214	9e-17	61	(Y13389) reverse transcriptase [Antirrhinum majus]
18494	GM_M34_B2_B09_MR	g3142328	BLASTN	938	2e-35	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18495	GM_M34_B2_B12_MR	g3097320	BLASTN	431	2e-12	70	Glycine max gene for Bd 30K, complete cds
18496	GM_M34_B2_C09_MR	g3924609	BLASTX	201	7e-14	56	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
18497	GM_M34_B2_D10_MR	g100484	BLASTX	195	1e-23	63	hypothetical protein - garden snapdragon
18498	GM_M34_B2_E11_MR	g3820757	BLASTN	382	2e-10	63	Caenorhabditis elegans cosmid Y53C12D, complete sequence [Caenorhabditis elegans]
18499	GM_M34_B2_F08_MR	g1170031	BLASTX	671	3e-65	97	GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE PRECURSOR (GSA) (GLUTAMATE-1-SEMIALDEHYDE AMINOTRANSFERASE) (GSA-AT) gi 541940 pir JQ2263 glutamate 1-semialdehyde aminotransferase (EC 2.6.1.-) precursor - soybean gi 310567 (L12453) glutamate 1-semialdehyde aminotransferase [Glycine max] gi 747968 (U20260) glutamate 1-semialdehyde aminotransferase [Glycine max]
18500	GM_M34_B2_F12_MR	g3142328	BLASTN	839	5e-31	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18501	GM_M34_B2_G05_MF	g3777526	BLASTN	487	5e-15	74	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
18502	GM_M34_B2_G07_MR	g4063756	BLASTN	454	2e-13	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
18503	GM_M34_B2_G08_MR	g1732513	BLASTX	182	2e-13	68	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]
18504	GM_M34_B2_G11_MR	g3513747	BLASTX	310	2e-25	51	(AF080118) contains similarity to reverse transcriptases (Pfam; rvt.hmm, score: 11.19) [Arabidopsis thaliana]
18505	GM_M35_A2_A05_MF	g507910	BLASTN	638	3e-22	86	Glycine max BSR-101 satellite SB92 genomic sequence.
18506	GM_M35_A2_A05_MR	g507910	BLASTN	551	3e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
18507	GM_M35_A2_A07_MR	g342952	BLASTN	392	1e-11	63	paramecium species 1,168 mt dna dimer: replication init. region.
18508	GM_M35_A2_A11_MF	g4115365	BLASTX	129	2e-09	54	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
18509	GM_M35_A2_A12_MF	g3600034	BLASTX	249	2e-20	52	(AF080119) No definition line found [Arabidopsis thaliana]
18510	GM_M35_A2_B03_MF	g1091678	BLASTX	135	1e-11	30	activator-like transposable element [Pennisetum glaucum]
18511	GM_M35_A2_B10_MF	g2129618	BLASTX	223	2e-16	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18512	GM_M35_A2_C01_MR	g4150930	BLASTN	375	7e-10	64	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18513	GM_M35_A2_C05_MF	g3687828	BLASTN	370	1e-09	64	Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence [Homo sapiens]
18514	GM_M35_A2_C06_MR	g117519	BLASTX	138	2e-10	66	PHYTOENE DEHYDROGENASE PRECURSOR (PHYTOENE DESATURASE) gi 99945 pir A39597 phytoene dehydrogenase (EC 1.3.-.-) - soybean gi 170044 (M64704) phytoene desaturase [Glycine max]
18515	GM_M35_A2_C09_MR	g3901012	BLASTX	238	2e-19	66	(AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]
18516	GM_M35_A2_C10_MR	g3907448	BLASTN	401	5e-11	60	Homo sapiens chromosome 18, clone hRPK.24_A_23, complete sequence [Homo sapiens]
18517	GM_M35_A2_C12_MF	g4115365	BLASTX	293	1e-23	49	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
18518	GM_M35_A2_D06_MR	g3645899	BLASTX	154	5e-11	34	(U68408) 5' end not determined experimentally [Zea mays]
18519	GM_M35_A2_D07_MF	g3599669	BLASTN	356	4e-09	64	Dictyostelium discoideum gene for TRFA, complete cds
18520	GM_M35_A2_D08_MF	g4038056	BLASTX	220	4e-26	51	(AC005897) putative transposon [Arabidopsis thaliana]
18521	GM_M35_A2_D09_MF	g1769898	BLASTX	366	2e-32	52	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18522	GM_M35_A2_D11_MF	g3097320	BLASTN	818	5e-30	78	Glycine max gene for Bd 30K, complete cds
18523	GM_M35_A2_E08_MR	g3142303	BLASTX	516	2e-47	77	(AC002411) Strong similarity to MRP-like ABC transporter gb U92650 from A. thaliana and canalicular multi-drug resistance protein gb L49379 from Rattus norvegicus. [Arabidopsis thaliana]
18524	GM_M35_A2_F09_MF	g421955	BLASTX	155	1e-11	40	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
18525	GM_M35_A2_F09_MR	g2244749	BLASTX	248	8e-20	48	(Z97335) hydroxymethyltransferase [Arabidopsis thaliana]
18526	GM_M35_A2_G01_MF	g4138581	BLASTX	168	1e-13	45	(X98474) mitochondrial energy transfer protein [Solanum tuberosum]
18527	GM_M35_A2_G04_MF	g18559	BLASTN	651	2e-22	67	G.max gene for catalase
18528	GM_M35_A2_G09_MF	g507910	BLASTN	655	6e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
18529	GM_M35_A2_G11_MF	g3777527	BLASTX	225	2e-16	64	(AF053008) gag-pol polyprotein [Glycine max]
18530	GM_M35_A2_G12_MF	g3645899	BLASTX	338	7e-33	58	(U68408) 5' end not determined experimentally [Zea mays]
18531	GM_M35_A2_H04_MR	g3193290	BLASTX	227	4e-17	49	(AF069298) contains similarity to a protein kinase domain (Pfam: pkinase.hmm, score: 165.48), to legume lectins beta domain (Pfam: lectin_legB.hmm, score: 125.64) and legume lectins alpha domain (Pfam: lectin_legA.hmm, score: 16.72) [Arabido...
18532	GM_M35_A2_H05_MF	g2642158	BLASTX	166	6e-11	41	(AC003000) hypothetical protein [Arabidopsis thaliana]
18533	GM_M35_A2_H06_MR	g4063760	BLASTX	277	5e-22	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18534	GM_M35_A2_H07_MR	g2995405	BLASTX	474	2e-43	55	(Y12432) polyprotein [Ananas comosus]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18535	GM_M35_A2_H08_MF	g507910	BLASTN	382	1e-10	74	Glycine max BSR-101 satellite SB92 genomic sequence.
18536	GM_M35_B1_A05_MF	g441205	BLASTN	410	2e-11	73	Soybean lox1gm4 gene encoding lipxygenase L-4
18537	GM_M35_B1_A06_MF	g2462732	BLASTX	275	2e-22	67	(AC002292) Hypothetical Protein [Arabidopsis thaliana]
18538	GM_M35_B1_A07_MF	g2995405	BLASTX	220	3e-16	40	(Y12432) polyprotein [Ananas comosus]
18539	GM_M35_B1_B04_MR	g3142328	BLASTN	1040	4e-40	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18540	GM_M35_B1_B09_MF	g170605	BLASTN	488	2e-15	64	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
18541	GM_M35_B1_C02_MR	g3650039	BLASTX	271	7e-22	39	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
18542	GM_M35_B1_C10_MF	g3142328	BLASTN	804	2e-29	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18543	GM_M35_B1_C11_MR	g3273387	BLASTN	363	2e-09	67	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
18544	GM_M35_B1_D03_MF	g3097320	BLASTN	1092	2e-42	79	Glycine max gene for Bd 30K, complete cds
18545	GM_M35_B1_E02_MR	g114532	BLASTX	592	7e-59	91	ATP SYNTHASE ALPHA CHAIN gi 67824 pir PWNTA H+-transporting ATP synthase (EC 3.6.1.34) alpha chain - common tobacco chloroplast gi 11769 (V00162) alpha subunit of ATPase [Nicotiana tabacum] gi 11811 (Z00044) ATPase alpha subunit [Nicotiana tabacum] gi 225270 prf 1211235E ATPase alpha [Nicotiana tabacum]
18546	GM_M35_B1_F03_MR	g3645899	BLASTX	158	3e-21	40	(U68408) 5' end not determined experimentally [Zea mays]
18547	GM_M35_B1_F10_MR	g2443320	BLASTX	260	3e-20	48	(D85597) polyprotein [Oryza australiensis]
18548	GM_M35_B1_G03_MF	g209631	BLASTN	373	8e-10	66	Amsacta entomopoxvirus spheroidin gene, complete cds, and four vaccinia related orfs. >gi 1251578 gb I16670 I16670 Sequence 1 from patent US 5476781
18549	GM_M35_B1_G05_MR	g2264302	BLASTN	655	1e-22	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]
18550	GM_M35_B1_G08_MR	g3176777	BLASTN	425	3e-13	62	Homo sapiens allele 4 fragile site locus (FRA10B) minisatellite, 3' sequence
18551	GM_M35_B2_A03_MF	g2764526	BLASTN	367	1e-09	59	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
18552	GM_M35_B2_A03_MR	g100484	BLASTX	202	2e-14	48	hypothetical protein - garden snapdragon
18553	GM_M35_B2_A04_MF	g3461846	BLASTX	266	8e-21	48	(AC005315) putative zinc-finger protein [Arabidopsis thaliana]
18554	GM_M35_B2_A07_MF	g531389	BLASTX	230	4e-22	50	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18555	GM_M35_B2_A10_MR	g4063760	BLASTX	209	7e-15	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18556	GM_M35_B2_B01_MF	g505129	BLASTN	371	8e-10	74	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
18557	GM_M35_B2_B01_MR	g3510344	BLASTN	467	5e-14	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MJG14, complete sequence [Arabidopsis thaliana]
18558	GM_M35_B2_B02_MR	g170606	BLASTN	726	3e-26	66	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
18559	GM_M35_B2_B03_MF	g1169198	BLASTX	144	5e-09	76	DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR gi 479738 pir S35270 hypothetical protein - Arabidopsis thaliana gi 166926 (L11367) [Arabidopsis thaliana unidentified mRNA sequence, complete cds.], gene product [Arabidopsis thaliana]
18560	GM_M35_B2_C05_MR	g4056476	BLASTN	350	9e-09	66	Arabidopsis thaliana chromosome II BAC F3G5 genomic sequence, complete sequence [Arabidopsis thaliana]
18561	GM_M35_B2_D01_MF	g3142328	BLASTN	520	1e-16	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18562	GM_M35_B2_D02_MF	g4063760	BLASTX	418	4e-37	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18563	GM_M35_B2_D03_MR	g507910	BLASTN	341	8e-09	68	Glycine max BSR-101 satellite SB92 genomic sequence.
18564	GM_M35_B2_D04_MR	g170080	BLASTN	455	1e-13	87	Soybean seed lectin gene transposable element tgm1.
18565	GM_M35_B2_D07_MF	g3645899	BLASTX	174	4e-11	56	(U68408) 5' end not determined experimentally [Zea mays]
18566	GM_M35_B2_D11_MF	g1769897	BLASTX	331	1e-28	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18567	GM_M35_B2_E01_MF	g4063760	BLASTX	590	2e-55	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18568	GM_M35_B2_E04_MF	g3176795	BLASTN	377	1e-10	63	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
18569	GM_M35_B2_F04_MF	g4115365	BLASTX	329	2e-27	49	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
18570	GM_M35_B2_F07_MR	g2443320	BLASTX	136	2e-15	41	(D85597) polyprotein [Oryza australiensis]
18571	GM_M35_B2_F08_MR	g3142328	BLASTN	642	4e-22	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18572	GM_M35_B2_F09_MF	g2564750	BLASTN	384	3e-10	61	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
18573	GM_M35_B2_G06_MF	g100484	BLASTX	384	5e-34	54	hypothetical protein - garden snapdragon
18574	GM_M35_B2_G06_MR	g3603175	BLASTX	125	1e-09	50	(AF025374) TIRC7 [Homo sapiens]
18575	GM_M35_B2_G08_MF	g1707364	BLASTX	226	3e-17	83	(X94626) AATP2 [Arabidopsis thaliana]
18576	GM_M35_B2_H01_MR	g2522228	BLASTX	204	3e-15	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
18577	GM_M35_B2_H08_MF	g2462134	BLASTX	268	7e-22	36	(Y13368) reverse transcriptase [Beta vulgaris]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18578	GM_M35_B2_H09_MF	g507910	BLASTN	362	9e-10	69	Glycine max BSR-101 satellite SB92 genomic sequence.
18579	GM_M35_B2_H09_MR	g507910	BLASTN	379	2e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18580	GM_M36_A1_B01_MR	g4050011	BLASTN	460	9e-14	68	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
18581	GM_M36_A1_B03_MR	g2129618	BLASTX	180	7e-12	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18582	GM_M36_A1_B07_MR	g3047068	BLASTX	190	5e-13	35	(AF058825) similar to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
18583	GM_M36_A1_B10_MR	g4038056	BLASTX	279	2e-22	45	(AC005897) putative transposon [Arabidopsis thaliana]
18584	GM_M36_A1_C06_MR	g2213632	BLASTX	135	3e-13	40	(AC000103) F21J9.24 [Arabidopsis thaliana]
18585	GM_M36_A1_D01_MR	g18559	BLASTN	772	6e-28	72	G.max gene for catalase
18586	GM_M36_A1_D10_MR	g2765817	BLASTX	147	1e-08	54	(Z95352) AtMlo-h1 [Arabidopsis thaliana]
18587	GM_M36_A1_D11_MR	g2213632	BLASTX	170	1e-22	46	(AC000103) F21J9.24 [Arabidopsis thaliana]
18588	GM_M36_A1_F01_MR	g905361	BLASTX	109	3e-13	47	(U22103) gag-protease polyprotein [Glycine max]
18589	GM_M36_A1_F12_MR	g2522228	BLASTX	171	2e-21	80	(AB007466) reverse transcriptase-like protein [Vicia faba]
18590	GM_M36_A1_G01_MR	g2586082	BLASTX	203	1e-28	67	(U72725) retrofit [Oryza longistaminata]
18591	GM_M36_A1_H07_MR	g507910	BLASTN	367	6e-10	69	Glycine max BSR-101 satellite SB92 genomic sequence.
18592	GM_M36_A1_H08_MR	g18559	BLASTN	848	2e-31	73	G.max gene for catalase
18593	GM_M36_A1_H12_MR	g905361	BLASTX	381	2e-42	79	(U22103) gag-protease polyprotein [Glycine max]
18594	GM_M36_B1_A01_MR	g3367520	BLASTX	219	1e-16	59	(AC004392) Similar to protein kinase APK1A, tyrosine-serine-threonine kinase gb D12522 from A. thaliana. [Arabidopsis thaliana]
18595	GM_M36_B1_B03_MR	g507910	BLASTN	543	6e-18	78	Glycine max BSR-101 satellite SB92 genomic sequence.
18596	GM_M36_B1_B10_MR	g4063760	BLASTX	212	4e-15	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18597	GM_M36_B1_C06_MR	g4063760	BLASTX	156	3e-09	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18598	GM_M36_B1_C07_MR	g1769898	BLASTX	182	3e-15	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18599	GM_M36_B1_C08_MR	g2462935	BLASTX	188	1e-12	40	(Y12321) open reading frame 1 [Brassica oleracea]
18600	GM_M36_B1_D06_MR	g3319362	BLASTX	174	3e-11	37	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
18601	GM_M36_B1_D08_MR	g18559	BLASTN	857	8e-32	71	G.max gene for catalase
18602	GM_M36_B1_D09_MR	g3777527	BLASTX	218	1e-15	40	(AF053008) gag-pol polyprotein [Glycine max]
18603	GM_M36_B1_E07_MR	g3283026	BLASTX	220	2e-16	40	putative transposase [Arabidopsis thaliana]
18604	GM_M36_B1_E10_MR	g3695401	BLASTX	98	2e-10	39	(AF096373) No definition line found [Arabidopsis thaliana]
18605	GM_M36_B1_F01_MR	g3377834	BLASTX	153	4e-09	30	(AF075598) No definition line found [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18606	GM_M36_B1_F03_MR	g13774	BLASTN	428	1e-12	61	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
18607	GM_M36_B1_F04_MR	g2281647	BLASTX	214	8e-17	47	(AF003104) AP2 domain containing protein RAP2.11 [Arabidopsis thaliana]
18608	GM_M36_B1_F08_MR	g2281647	BLASTX	203	1e-15	50	(AF003104) AP2 domain containing protein RAP2.11 [Arabidopsis thaliana]
18609	GM_M36_B1_F09_MR	g3695395	BLASTX	197	8e-16	40	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
18610	GM_M36_B1_G11_MR	g629693	BLASTX	209	8e-16	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
18611	GM_M36_B2_A01_MF	g905360	BLASTN	458	8e-14	65	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds
18612	GM_M36_B2_A04_MR	g4063760	BLASTX	412	2e-36	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18613	GM_M36_B2_B06_MR	g507910	BLASTN	475	7e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
18614	GM_M36_B2_C01_MR	g3097320	BLASTN	1073	1e-41	85	Glycine max gene for Bd 30K, complete cds
18615	GM_M36_B2_C03_MR	g2351065	BLASTN	410	2e-11	86	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MHF15
18616	GM_M36_B2_D02_MR	g3142328	BLASTN	701	9e-25	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18617	GM_M36_B2_D07_MR	g3142328	BLASTN	561	2e-18	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18618	GM_M36_B2_E01_MR	g3097320	BLASTN	440	7e-13	71	Glycine max gene for Bd 30K, complete cds
18619	GM_M37_A1_B03_MF	g4063756	BLASTN	443	6e-13	69	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
18620	GM_M37_A1_B06_MF	g1769897	BLASTX	178	5e-12	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18621	GM_M37_A1_B12_MF	g100484	BLASTX	161	5e-10	37	hypothetical protein - garden snapdragon
18622	GM_M37_A1_C01_MR	g4038055	BLASTX	249	2e-35	61	(AC005897) putative cytochrome P450 [Arabidopsis thaliana]
18623	GM_M37_A1_C03_MF	g3201680	BLASTX	203	2e-15	60	(AF060941) extra-large G-protein [Arabidopsis thaliana]
18624	GM_M37_A1_C03_MR	g18559	BLASTN	991	6e-38	76	G.max gene for catalase
18625	GM_M37_A1_C04_MF	g3599418	BLASTN	1031	9e-40	75	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
18626	GM_M37_A1_C11_MR	g2429543	BLASTX	136	3e-10	35	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18627	GM_M37_A1_C12_MF	g4063760	BLASTX	445	5e-40	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18628	GM_M37_A1_D01_MF	g629693	BLASTX	131	5e-11	34	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
18629	GM_M37_A1_D04_MF	g1621467	BLASTX	448	1e-41	80	(U73106) laccase [Liriodendron tulipifera]
18630	GM_M37_A1_D04_MR	g3193320	BLASTX	217	5e-16	52	(AF069299) contains similarity to the subtilase family of serine proteases (Pfam: subtilase.hmm, score: 47.57); strong similarity to Cucumis melo (muskmelon) cucumisin (GB:D32206) [Arabidopsis thaliana]
18631	GM_M37_A1_D07_MF	g3650035	BLASTX	267	5e-21	47	(AC005396) putative reverse transcriptase [Arabidopsis thaliana]
18632	GM_M37_A1_D11_MR	g2995405	BLASTX	276	3e-22	43	(Y12432) polyprotein [Ananas comosus]
18633	GM_M37_A1_D12_MR	g18559	BLASTN	867	3e-32	74	G.max gene for catalase
18634	GM_M37_A1_F01_MR	g629693	BLASTX	243	1e-19	51	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
18635	GM_M37_A1_F06_MF	g4063735	BLASTN	399	6e-11	66	Arabidopsis thaliana BAC F18G18 from chromosome V near 60.5 cM, complete sequence [Arabidopsis thaliana]
18636	GM_M37_A1_F07_MF	g507910	BLASTN	405	1e-11	76	Glycine max BSR-101 satellite SB92 genomic sequence.
18637	GM_M37_A1_G01_MF	g2522228	BLASTX	321	1e-40	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
18638	GM_M37_A1_G01_MR	g3560029	BLASTN	474	1e-14	66	Schistosoma intercalatum ribosomal intergenic spacer DNA (2169 bp)
18639	GM_M37_A1_G10_MF	g122105	BLASTX	169	5e-12	53	HISTONE H4 gi 81288 pir S00939 histone H4 - Volvox carteri gi 21984 (X06963) put. histone H4 [Volvox carteri] gi 21987 (X06964) put. histone H4 [Volvox carteri]
18640	GM_M37_A1_G11_MR	g3777527	BLASTX	634	3e-62	95	(AF053008) gag-pol polyprotein [Glycine max]
18641	GM_M37_A1_G12_MR	g2129618	BLASTX	165	1e-11	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18642	GM_M37_A1_H01_MR	g3461813	BLASTX	220	2e-30	81	(AC004138) putative sucrose/H+ symporter [Arabidopsis thaliana]
18643	GM_M37_A1_H05_MF	g905361	BLASTX	176	1e-11	34	(U22103) gag-protease polyprotein [Glycine max]
18644	GM_M37_A1_H06_MF	g1666236	BLASTX	157	3e-10	29	(U76261) unknown [Hordeum vulgare]
18645	GM_M37_A1_H07_MF	g2924729	BLASTN	654	2e-22	71	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MNA5, complete sequence [Arabidopsis thaliana]
18646	GM_M37_A1_H10_MF	g3777527	BLASTX	175	5e-11	35	(AF053008) gag-pol polyprotein [Glycine max]
18647	GM_M37_A1_H11_MR	g3834315	BLASTX	238	1e-18	46	(AC005679) F9K20.15 [Arabidopsis thaliana]
18648	GM_M37_A1_H12_MF	g4115365	BLASTX	218	2e-19	49	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18649	GM_M37_B1_A02_MR	g3142328	BLASTN	728	5e-26	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18650	GM_M37_B1_A03_MR	g3885341	BLASTX	427	2e-38	53	(AC005623) unknown protein [Arabidopsis thaliana]
18651	GM_M37_B1_A08_MF	g3142328	BLASTN	764	1e-27	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18652	GM_M37_B1_A08_MR	g18559	BLASTN	901	8e-34	73	G.max gene for catalase
18653	GM_M37_B1_A10_MR	g3097320	BLASTN	407	2e-11	77	Glycine max gene for Bd 30K, complete cds
18654	GM_M37_B1_A11_MR	g3142328	BLASTN	427	3e-12	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18655	GM_M37_B1_B03_MF	g3142328	BLASTN	630	1e-21	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18656	GM_M37_B1_B03_MR	g3645899	BLASTX	263	2e-32	50	(U68408) 5' end not determined experimentally [Zea mays]
18657	GM_M37_B1_B05_MF	g1769898	BLASTX	144	2e-11	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18658	GM_M37_B1_B07_MF	g1666236	BLASTX	144	9e-09	31	(U76261) unknown [Hordeum vulgare]
18659	GM_M37_B1_B10_MR	g3097320	BLASTN	460	8e-14	66	Glycine max gene for Bd 30K, complete cds
18660	GM_M37_B1_C01_MR	g4006838	BLASTN	432	2e-12	64	Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence [Homo sapiens]
18661	GM_M37_B1_C04_MR	g3426334	BLASTN	520	2e-16	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
18662	GM_M37_B1_C05_MF	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18663	GM_M37_B1_C05_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18664	GM_M37_B1_C06_MR	g3810596	BLASTX	296	3e-24	41	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
18665	GM_M37_B1_C10_MF	g508826	BLASTN	350	8e-09	60	Drosophila melanogaster Oregon-R mitochondrial A+T region.
18666	GM_M37_B1_D03_MF	g3645899	BLASTX	344	3e-29	52	(U68408) 5' end not determined experimentally [Zea mays]
18667	GM_M37_B1_D05_MR	g3171875	BLASTN	438	9e-13	67	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.1...
18668	GM_M37_B1_D07_MR	g2522227	BLASTX	112	4e-09	36	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
18669	GM_M37_B1_D09_MR	g4063760	BLASTX	161	1e-18	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18670	GM_M37_B1_E01_MF	g3822223	BLASTX	175	1e-16	57	(AF077955) branched-chain alpha keto-acid dehydrogenase E1 alpha subunit [Arabidopsis thaliana]
18671	GM_M37_B1_E02_MR	g3785992	BLASTN	380	4e-10	64	Arabidopsis thaliana chromosome II BAC T6A23 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18672	GM_M37_B1_E03_MR	g905361	BLASTX	238	2e-18	35	(U22103) gag-protease polyprotein [Glycine max]
18673	GM_M37_B1_E07_MF	g3845197	BLASTN	405	3e-11	64	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
18674	GM_M37_B1_E07_MR	g2764525	BLASTN	467	3e-14	64	Pisum sativum genomic DNA encoding truncated Ty3/Gypsy-like retroelement Cyclops-1
18675	GM_M37_B1_E08_MR	g3142328	BLASTN	858	7e-32	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18676	GM_M37_B1_E09_MR	g3406033	BLASTN	350	9e-09	58	Homo sapiens 12p13.3 RPCI4-773N5 (Roswell Park Cancer Institute Human PAC library) complete sequence [Homo sapiens]
18677	GM_M37_B1_F01_MF	g3777527	BLASTX	612	1e-57	93	(AF053008) gag-pol polyprotein [Glycine max]
18678	GM_M37_B1_F02_MF	g3377856	BLASTX	305	4e-25	49	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 19.54) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 12.35) [Arabidopsis thaliana]
18679	GM_M37_B1_F02_MR	g2522227	BLASTX	193	1e-14	48	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
18680	GM_M37_B1_F03_MF	g2129618	BLASTX	230	3e-17	44	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18681	GM_M37_B1_F07_MR	g4150930	BLASTN	400	5e-11	64	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
18682	GM_M37_B1_F08_MF	g100226	BLASTX	336	5e-29	47	hypothetical protein - tomato gi 19275 (Z12127) protein of unknown function [Lycopersicon esculentum] gi 445619 prf 1909366A Leu zipper protein [Lycopersicon esculentum]
18683	GM_M37_B1_F09_MR	g3097836	BLASTN	471	3e-14	66	Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H148), complete sequence [Homo sapiens]
18684	GM_M37_B1_F10_MF	g3860246	BLASTX	147	4e-09	30	(AC005824) putative reverse-transcriptase protein [Arabidopsis thaliana]
18685	GM_M37_B1_F12_MR	g1076581	BLASTX	164	9e-13	40	cf-9 protein precursor - tomato gi 563233 (U15936) Cf-9 precursor [Lycopersicon pimpinellifolium] gi 2792186 gnl PID e1240191 (AJ002236) Cf-9 [Lycopersicon pimpinellifolium]
18686	GM_M37_B1_G08_MR	g3810596	BLASTX	269	2e-21	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
18687	GM_M37_B1_H01_MF	g3810595	BLASTX	272	2e-21	43	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
18688	GM_M37_B1_H05_MR	g2522230	BLASTX	290	7e-25	40	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18689	GM_M37_B1_H08_MR	g2194136	BLASTX	256	8e-20	45	(AC002062) Strong similarity to Zea mays retrotransposon Hopscotch polyprotein (gb U12626). [Arabidopsis thaliana]
18690	GM_M37_B2_A04_MR	g3319362	BLASTX	158	2e-16	39	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
18691	GM_M37_B2_A07_MF	g3810596	BLASTX	200	5e-14	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
18692	GM_M37_B2_A08_MR	g3777527	BLASTX	352	6e-30	76	(AF053008) gag-pol polyprotein [Glycine max]
18693	GM_M37_B2_A11_MF	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18694	GM_M37_B2_A11_MR	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18695	GM_M37_B2_B10_MF	g507910	BLASTN	412	5e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18696	GM_M37_B2_B10_MR	g507910	BLASTN	454	7e-14	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18697	GM_M37_B2_C01_MF	g22102	BLASTN	572	7e-19	62	Zea mays A1 gene for 40.1kd A1 protein (NADPH-dependent reductase).
18698	GM_M37_B2_C01_MR	g3894211	BLASTN	411	2e-11	66	Homo sapiens PAC clone DJ0888A21 from 7q31, complete sequence [Homo sapiens]
18699	GM_M37_B2_C03_MF	g320565	BLASTX	114	1e-09	59	transposon TA1-1 KAS-1 - Arabidopsis thaliana (fragment)
18700	GM_M37_B2_C04_MF	g507910	BLASTN	575	2e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
18701	GM_M37_B2_C10_MF	g2104945	BLASTN	386	2e-10	61	Glycine max copia-like retrotransposon Tgmr, complete sequence
18702	GM_M37_B2_C11_MF	g3985952	BLASTN	896	2e-33	73	Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MRC8, complete sequence [Arabidopsis thaliana]
18703	GM_M37_B2_D05_MF	g3777527	BLASTX	309	3e-25	43	(AF053008) gag-pol polyprotein [Glycine max]
18704	GM_M37_B2_D05_MR	g1769898	BLASTX	289	6e-24	51	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18705	GM_M37_B2_D09_MF	g505129	BLASTN	360	3e-09	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
18706	GM_M37_B2_D09_MR	g3273387	BLASTN	417	8e-12	64	Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence [Homo sapiens]
18707	GM_M37_B2_E04_MR	g1370171	BLASTN	572	1e-19	75	L.japonicus mRNA for small GTP-binding protein, RAB1X.
18708	GM_M37_B2_F01_MF	g3294467	BLASTX	159	3e-23	89	(U89341) phosphoglucomutase 1 [Zea mays]
18709	GM_M37_B2_F06_MF	g4063760	BLASTX	108	8e-09	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18710	GM_M37_B2_F10_MF	g13774	BLASTN	387	9e-11	68	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
18711	GM_M37_B2_F11_MR	g3142328	BLASTN	2117	2e-89	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18712	GM_M37_B2_G01_MF	g3142379	BLASTX	220	7e-17	57	(AF053008) envelope-like [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18713	GM_M37_B2_G03_MF	g1843447	BLASTN	420	6e-12	63	Human DNA sequence from PAC 345P10 on chromosome 22q12-qter contains ESTs and STS and polymorphic CA repeat D22S927
18714	GM_M37_B2_G04_MR	g2522228	BLASTX	233	2e-18	42	(AB007466) reverse transcriptase-like protein [Vicia faba]
18715	GM_M37_B2_G06_MF	g18559	BLASTN	782	2e-28	75	G.max gene for catalase
18716	GM_M37_B2_G09_MF	g3097320	BLASTN	492	3e-15	70	Glycine max gene for Bd 30K, complete cds
18717	GM_M37_B2_H01_MR	g3510505	BLASTX	251	3e-19	39	(AF030881) pol polyprotein [Fugu rubripes]
18718	GM_M37_B2_H02_MF	g531389	BLASTX	256	6e-24	48	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
18719	GM_M37_B2_H05_MF	g2505874	BLASTX	284	8e-24	42	(Y12776) putative kinase [Arabidopsis thaliana]
18720	GM_M37_B2_H05_MR	g20749	BLASTN	512	5e-17	73	Pea PSU2 gene for U2 snRNA
18721	GM_M37_B2_H06_MR	g1769898	BLASTX	149	8e-09	31	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18722	GM_M37_B2_H09_MR	g170080	BLASTN	398	5e-11	68	Soybean seed lectin gene transposable element tgm1.
18723	GM_M37_B2_H11_MR	g2264308	BLASTN	321	5e-09	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MIK22, complete sequence.
18724	GM_M38_A2_A02_MR	g18559	BLASTN	691	3e-24	70	G.max gene for catalase
18725	GM_M38_A2_A08_MR	g4063760	BLASTX	497	1e-45	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18726	GM_M38_A2_B03_MF	g3004545	BLASTX	308	3e-25	43	(AC003673) putative reverse transcriptase [Arabidopsis thaliana]
18727	GM_M38_A2_B05_MR	g507910	BLASTN	395	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18728	GM_M38_A2_B06_MR	g3097320	BLASTN	378	4e-10	65	Glycine max gene for Bd 30K, complete cds
18729	GM_M38_A2_B10_MF	g507910	BLASTN	573	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
18730	GM_M38_A2_B10_MR	g4038056	BLASTX	398	3e-35	53	(AC005897) putative transposon [Arabidopsis thaliana]
18731	GM_M38_A2_B11_MR	g507910	BLASTN	453	7e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
18732	GM_M38_A2_B12_MR	g18588	BLASTN	370	1e-09	73	Soybean gene 3 for chalcone synthetase protein
18733	GM_M38_A2_C01_MF	g3142328	BLASTN	1170	4e-46	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18734	GM_M38_A2_C01_MR	g3510505	BLASTX	239	5e-18	41	(AF030881) pol polyprotein [Fugu rubripes]
18735	GM_M38_A2_C04_MF	g3135282	BLASTN	388	2e-10	60	Homo sapiens PAC clone DJ1107K12 from 7p12-p14, complete sequence [Homo sapiens]
18736	GM_M38_A2_C04_MR	g3097320	BLASTN	450	2e-13	73	Glycine max gene for Bd 30K, complete cds
18737	GM_M38_A2_C05_MF	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18738	GM_M38_A2_C08_MF	g3810596	BLASTX	264	8e-21	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
18739	GM_M38_A2_C10_MF	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18740	GM_M38_A2_C10_MR	g507910	BLASTN	355	2e-09	69	Glycine max BSR-101 satellite SB92 genomic sequence.
18741	GM_M38_A2_C11_MF	g4063760	BLASTX	216	1e-15	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18742	GM_M38_A2_D01_MF	g3021268	BLASTX	135	4e-13	69	(AL022347) putative protein [Arabidopsis thaliana]
18743	GM_M38_A2_D02_MR	g99729	BLASTX	162	1e-19	48	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
18744	GM_M38_A2_D04_MF	g1480927	BLASTN	1129	8e-45	93	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
18745	GM_M38_A2_D04_MR	g18559	BLASTN	729	5e-26	68	G.max gene for catalase
18746	GM_M38_A2_D06_MR	g3819164	BLASTX	237	2e-18	62	(AJ012318) cytosolic chaperonin, delta-subunit [Glycine max]
18747	GM_M38_A2_D07_MF	g99922	BLASTX	565	6e-54	84	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
18748	GM_M38_A2_D07_MR	g100484	BLASTX	340	3e-29	48	hypothetical protein - garden snapdragon
18749	GM_M38_A2_D08_MR	g3097320	BLASTN	748	8e-27	81	Glycine max gene for Bd 30K, complete cds
18750	GM_M38_A2_D11_MF	g3935167	BLASTX	171	3e-12	57	(AC004557) F17L21.10 [Arabidopsis thaliana]
18751	GM_M38_A2_D12_MF	g507910	BLASTN	592	4e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
18752	GM_M38_A2_D12_MR	g18559	BLASTN	943	1e-35	74	G.max gene for catalase
18753	GM_M38_A2_E02_MR	g2194126	BLASTX	201	2e-17	52	(AC002062) EST gb T43335 comes from this gene. [Arabidopsis thaliana]
18754	GM_M38_A2_E04_MF	g507910	BLASTN	386	8e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18755	GM_M38_A2_E04_MR	g507910	BLASTN	377	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18756	GM_M38_A2_E06_MF	g507910	BLASTN	374	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18757	GM_M38_A2_G01_MR	g507910	BLASTN	488	2e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
18758	GM_M38_A2_G04_MR	g2811096	BLASTN	360	3e-09	62	Homo sapiens Xp22 BAC GSHB-257G1 (Genome Systems BAC Library) complete sequence [Homo sapiens]
18759	GM_M38_A2_G10_MF	g3097320	BLASTN	532	5e-17	67	Glycine max gene for Bd 30K, complete cds
18760	GM_M38_A2_G11_MF	g2244802	BLASTX	185	4e-15	33	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
18761	GM_M38_A2_G11_MR	g3779030	BLASTX	174	1e-12	29	(AC005171) putative gag-protease polyprotein [Arabidopsis thaliana]
18762	GM_M38_A2_G12_MR	g905361	BLASTX	621	6e-60	83	(U22103) gag-protease polyprotein [Glycine max]
18763	GM_M38_A2_H01_MR	g1350625	BLASTX	253	6e-21	80	CHLOROPLAST 50S RIBOSOMAL PROTEIN L1 PRECURSOR gi 577089 (X82776) chloroplast ribosomal protein L1 [Pisum sativum]
18764	GM_M38_A2_H04_MR	g4063760	BLASTX	283	9e-23	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18765	GM_M38_A2_H06_MR	g4063756	BLASTN	449	3e-13	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18766	GM_M38_A2_H10_MF	g4063760	BLASTX	482	5e-44	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18767	GM_M38_B1_A01_MF	g2586082	BLASTX	205	2e-14	40	(U72725) retrofit [Oryza longistaminata]
18768	GM_M38_B1_A04_MR	g2160179	BLASTX	154	1e-09	55	(AC000132) No definition line found [Arabidopsis thaliana]
18769	GM_M38_B1_A07_MF	g1769899	BLASTX	153	4e-20	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18770	GM_M38_B1_A08_MF	g3097320	BLASTN	410	2e-11	72	Glycine max gene for Bd 30K, complete cds
18771	GM_M38_B1_A09_MF	g3097320	BLASTN	1015	6e-39	81	Glycine max gene for Bd 30K, complete cds
18772	GM_M38_B1_A12_MR	g2245104	BLASTX	212	5e-15	37	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
18773	GM_M38_B1_B07_MR	g3097320	BLASTN	435	1e-12	72	Glycine max gene for Bd 30K, complete cds
18774	GM_M38_B1_B12_MF	g4063770	BLASTX	207	7e-15	40	(AB004906) transposase [Ipomoea purpurea]
18775	GM_M38_B1_C04_MR	g2833389	BLASTX	220	6e-16	86	SOLUBLE GLYCOGEN (STARCH) SYNTHASE PRECURSOR (SS III) gi 1200154 gnl PID e223347 (X95759) glycogen (starch) synthase [Solanum tuberosum]
18776	GM_M38_B1_C05_MF	g2832657	BLASTX	330	1e-30	60	(AL021710) putative protein [Arabidopsis thaliana]
18777	GM_M38_B1_C05_MR	g342965	BLASTN	408	5e-12	63	paramecium species 7,227 mt dna dimer: replication init. region.
18778	GM_M38_B1_C06_MF	g3250687	BLASTX	188	7e-14	46	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
18779	GM_M38_B1_C06_MR	g13773	BLASTN	365	5e-10	65	Torulopsis glabrata mitochondrial genes for tRNAs -Tyr, -Asn, -Ala, -Ile -Trp (from Var1-LrRNA intergenic region) >gi 343959 gb M11906 YSLMTIG09 Yeast (T.glabrata) mitochondrial DNA between var1 and L rRNA genes.
18780	GM_M38_B1_C10_MR	g507910	BLASTN	593	3e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
18781	GM_M38_B1_D02_MR	g1580757	BLASTN	416	9e-13	67	C.arietinum urate oxidase gene (partial).
18782	GM_M38_B1_D04_MR	g905361	BLASTX	255	3e-20	36	(U22103) gag-protease polyprotein [Glycine max]
18783	GM_M38_B1_D08_MR	g2660669	BLASTX	332	2e-27	67	(AC002342) human Mi-2 autoantigen-like protein [Arabidopsis thaliana]
18784	GM_M38_B1_D12_MR	g905361	BLASTX	229	2e-17	35	(U22103) gag-protease polyprotein [Glycine max]
18785	GM_M38_B1_E09_MF	g2995405	BLASTX	154	6e-19	46	(Y12432) polyprotein [Ananas comosus]
18786	GM_M38_B1_E10_MR	g158813	BLASTN	375	2e-10	64	Drosophila hydei Y chromosome lampbrush loop transcribed repeats.
18787	GM_M38_B1_F01_MF	g905361	BLASTX	660	5e-64	96	(U22103) gag-protease polyprotein [Glycine max]
18788	GM_M38_B1_F02_MR	g507910	BLASTN	637	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
18789	GM_M38_B1_F05_MF	g507910	BLASTN	600	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
18790	GM_M38_B1_F05_MR	g507910	BLASTN	580	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
18791	GM_M38_B1_F07_MF	g2995405	BLASTX	202	1e-22	43	(Y12432) polyprotein [Ananas comosus]

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18792	GM_M38_B1_F09_MF	g2801423	BLASTN	398	6e-11	63	Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence [Homo sapiens]
18793	GM_M38_B1_F12_MF	g905361	BLASTX	219	3e-16	40	(U22103) gag-protease polyprotein [Glycine max]
18794	GM_M38_B1_F12_MR	g507910	BLASTN	363	8e-10	77	Glycine max BSR-101 satellite SB92 genomic sequence.
18795	GM_M38_B1_G01_MR	g2129559	BLASTX	190	1e-18	53	cellulase homolog OR16pep - Arabidopsis thaliana gi 1022807 (U37702) cellulase [Arabidopsis thaliana] gi 3493633 (AF074092) cellulase [Arabidopsis thaliana] gi 3598956 (AF074375) cellulase [Arabidopsis thaliana]
18796	GM_M38_B1_G04_MF	g12628	BLASTN	416	5e-12	62	Aedes albopictus mit-gene for large ribosomal subunit RNA (LSU)
18797	GM_M38_B1_G04_MR	g2342681	BLASTX	251	2e-19	56	(AC000106) F7G19.9 [Arabidopsis thaliana]
18798	GM_M38_B1_G06_MF	g3176689	BLASTX	170	2e-10	44	(AC003671) Contains similarity to ubiquitin carboxyl-terminal hydrolase 14 gb Z35927 from S. cerevisiae. [Arabidopsis thaliana]
18799	GM_M38_B1_G07_MR	g4150933	BLASTN	395	8e-11	64	Homo sapiens BAC clone NH0520M18 from 7q31.1-q31.2, complete sequence [Homo sapiens]
18800	GM_M38_B1_G08_MF	g1142702	BLASTN	351	2e-09	74	Glycine max satellite STR120-A.4.
18801	GM_M38_B1_H03_MF	g507910	BLASTN	553	2e-18	80	Glycine max BSR-101 satellite SB92 genomic sequence.
18802	GM_M38_B1_H10_MF	g99729	BLASTX	179	4e-13	41	hypothetical protein 2 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345511 gnl PID e73214 (X53975) orf 2 [Arabidopsis thaliana]
18803	GM_M38_B1_H12_MR	g226407	BLASTX	217	1e-15	39	retrotransposon del1-46 [Lilium henryi]
18804	GM_M39_A2_A02_MR	g2655314	BLASTN	309	3e-11	65	Bactrocera xanthodes strain Vanuatu mitochondrial D-loop region, complete sequence
18805	GM_M39_A2_A03_MF	g3097320	BLASTN	515	3e-16	73	Glycine max gene for Bd 30K, complete cds
18806	GM_M39_A2_A12_MR	g2924257	BLASTN	423	4e-12	66	Tobacco chloroplast genome DNA
18807	GM_M39_A2_B04_MF	g507910	BLASTN	358	1e-09	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18808	GM_M39_A2_B09_MR	g2997694	BLASTX	299	8e-26	41	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
18809	GM_M39_A2_B10_MF	g905361	BLASTX	208	4e-15	33	(U22103) gag-protease polyprotein [Glycine max]
18810	GM_M39_A2_B10_MR	g2522228	BLASTX	216	2e-16	35	(AB007466) reverse transcriptase-like protein [Vicia faba]
18811	GM_M39_A2_B11_MR	g3513301	BLASTN	365	2e-09	64	Homo sapiens chromosome 19, cosmid R26894, complete sequence [Homo sapiens]
18812	GM_M39_A2_C04_MR	g2911393	BLASTX	190	3e-14	85	(AF045927) cell division cycle protein 48 [Hordeum vulgare]
18813	GM_M39_A2_C06_MF	g2522228	BLASTX	172	2e-23	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
18814	GM_M39_A2_C06_MR	g3056582	BLASTX	108	5e-12	45	(AC004255) T1F9.3 [Arabidopsis thaliana]
18815	GM_M39_A2_C10_MR	g905361	BLASTX	222	1e-16	39	(U22103) gag-protease polyprotein [Glycine max]

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18816	GM_M39_A2_D02_MR	g3269291	BLASTX	165	1e-21	82	(AL030978) putative receptor protein kinase [Arabidopsis thaliana]
18817	GM_M39_A2_D04_MF	g2462936	BLASTX	326	1e-28	48	(Y12321) open reading frame 2 [Brassica oleracea]
18818	GM_M39_A2_D05_MR	g531389	BLASTX	149	6e-18	34	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
18819	GM_M39_A2_D10_MR	g4063770	BLASTX	155	3e-11	34	(AB004906) transposase [Ipomoea purpurea]
18820	GM_M39_A2_D12_MR	g3036785	BLASTN	363	2e-09	61	Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains histone genes H2A/l,H2B.1A,H4,H2A.1b,H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG island
18821	GM_M39_A2_E12_MR	g18559	BLASTN	376	5e-10	73	G.max gene for catalase
18822	GM_M39_A2_F01_MF	g3142328	BLASTN	1008	1e-38	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18823	GM_M39_A2_F01_MR	g3142330	BLASTX	733	9e-72	92	(U96295) envelope-like [Glycine max]
18824	GM_M39_A2_F02_MR	g3805853	BLASTX	561	2e-53	68	(AL031986) putative protein [Arabidopsis thaliana]
18825	GM_M39_A2_F10_MR	g3859610	BLASTN	726	9e-26	67	Arabidopsis thaliana BAC T9E19
18826	GM_M39_A2_F12_MF	g2462745	BLASTX	293	3e-24	44	(AC002292) Hypothetical protein [Arabidopsis thaliana]
18827	GM_M39_A2_G05_MR	g3777527	BLASTX	173	7e-11	32	(AF053008) gag-pol polyprotein [Glycine max]
18828	GM_M39_A2_G08_MR	g3777527	BLASTX	201	1e-29	67	(AF053008) gag-pol polyprotein [Glycine max]
18829	GM_M39_A2_G09_MR	g2760839	BLASTX	316	9e-27	52	(AC003105) putative receptor kinase [Arabidopsis thaliana]
18830	GM_M39_A2_G12_MR	g99922	BLASTX	375	2e-55	71	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
18831	GM_M39_A2_H02_MR	g2764526	BLASTN	379	4e-10	65	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
18832	GM_M39_A2_H03_MF	g4063760	BLASTX	222	3e-16	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18833	GM_M39_A2_H04_MF	g4063760	BLASTX	229	6e-17	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18834	GM_M39_A2_H07_MR	g2160185	BLASTX	420	6e-38	51	(AC000132) Similar to S. pombe ISP4 (gb D83992). [Arabidopsis thaliana]
18835	GM_M39_A2_H08_MF	g3645899	BLASTX	274	4e-25	59	(U68408) 5' end not determined experimentally [Zea mays]
18836	GM_M39_A2_H10_MR	g2842490	BLASTX	225	7e-18	72	(AL021749) heat-shock protein [Arabidopsis thaliana]
18837	GM_M39_B2_A01_MF	g1769899	BLASTX	282	5e-24	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18838	GM_M39_B2_A03_MR	g505129	BLASTN	351	7e-09	68	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
18839	GM_M39_B2_A05_MR	g3789709	BLASTN	359	3e-09	61	Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence [Homo sapiens]
18840	GM_M39_B2_A11_MF	g507910	BLASTN	595	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.

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18841	GM_M39_B2_A12_MF	g3056590	BLASTX	253	9e-20	69	(AC004255) T1F9.11 [Arabidopsis thaliana]
18842	GM_M39_B2_A12_MR	g4038056	BLASTX	214	5e-30	54	(AC005897) putative transposon [Arabidopsis thaliana]
18843	GM_M39_B2_B01_MF	g3859610	BLASTN	488	5e-15	63	Arabidopsis thaliana BAC T9E19
18844	GM_M39_B2_B02_MF	g2073447	BLASTN	358	4e-09	71	L.japonicus gln1, pge1 & krm genes
18845	GM_M39_B2_B04_MR	g3746069	BLASTX	277	5e-22	44	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
18846	GM_M39_B2_B05_MR	g130398	BLASTX	218	7e-16	41	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON 297) gi 85089 pir B24872 retrovirus-related pol polyprotein homolog - fruit fly (Drosophila melanogaster) transposon 297
18847	GM_M39_B2_B06_MF	g3097320	BLASTN	455	1e-13	69	Glycine max gene for Bd 30K, complete cds
18848	GM_M39_B2_B08_MR	g3047073	BLASTX	176	9e-12	37	(AF058825) contains similarity to retrotransposon-like proteins [Arabidopsis thaliana]
18849	GM_M39_B2_B10_MR	g3097320	BLASTN	760	2e-27	76	Glycine max gene for Bd 30K, complete cds
18850	GM_M39_B2_C05_MR	g1841475	BLASTX	153	3e-10	56	(Y11105) Myb26 [Pisum sativum]
18851	GM_M39_B2_C10_MF	g169934	BLASTN	1514	4e-62	99	G.max (soybean) atpH gene encoding CFO-ATPase subunit III, chloroplast gene encoding chloroplast protein, complete cds.
18852	GM_M39_B2_C12_MR	g1769897	BLASTX	335	2e-32	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18853	GM_M39_B2_D05_MR	g3319362	BLASTX	193	4e-21	57	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
18854	GM_M39_B2_D07_MR	g2462058	BLASTX	102	9e-13	37	(Y13389) reverse transcriptase [Antirrhinum majus]
18855	GM_M39_B2_D11_MF	g4063760	BLASTX	251	2e-19	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18856	GM_M39_B2_E03_MF	g131289	BLASTX	573	4e-60	89	PHOTOSYSTEM II 44 KD REACTION CENTRE PROTEIN (P6 PROTEIN) (CP43) gi 72709 pir F2NT44 photosystem II chlorophyll a-binding protein psbC - common tobacco chloroplast gi 225285 prf 1211235W photosystem II 44kD protein [Nicotiana tabacum]
18857	GM_M39_B2_E05_MR	g18559	BLASTN	829	1e-30	81	G.max gene for catalase
18858	GM_M39_B2_E11_MF	g130582	BLASTX	303	9e-25	47	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
18859	GM_M39_B2_F02_MR	g3283026	BLASTX	180	5e-14	30	putative transposase [Arabidopsis thaliana]
18860	GM_M39_B2_F05_MF	g507910	BLASTN	594	3e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.

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18861	GM_M39_B2_F07_MR	g3777527	BLASTX	746	6e-72	97	(AF053008) gag-pol polyprotein [Glycine max]
18862	GM_M39_B2_F08_MR	g1167523	BLASTX	187	5e-24	52	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18863	GM_M39_B2_F12_MR	g3738114	BLASTN	360	3e-09	62	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]
18864	GM_M39_B2_G03_MF	g99755	BLASTX	209	5e-26	45	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
18865	GM_M39_B2_G06_MF	g2564750	BLASTN	498	2e-15	66	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
18866	GM_M39_B2_G07_MF	g507910	BLASTN	386	8e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18867	GM_M39_B2_G07_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18868	GM_M39_B2_G10_MF	g479805	BLASTX	120	6e-12	46	SNF2 protein homolog - human (fragment) gi 292498 (M89907) transcription activator [Homo sapiens]
18869	GM_M39_B2_H02_MR	g3377855	BLASTX	355	9e-32	49	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
18870	GM_M39_B2_H03_MR	g507910	BLASTN	394	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18871	GM_M39_B2_H08_MR	g3402690	BLASTX	235	9e-19	33	(AC004697) hypothetical protein, 3' partial [Arabidopsis thaliana]
18872	GM_M40_A1_A04_MF	g507910	BLASTN	507	3e-16	78	Glycine max BSR-101 satellite SB92 genomic sequence.
18873	GM_M40_A1_A05_MR	g13619	BLASTN	378	5e-11	64	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
18874	GM_M40_A1_B01_MF	g507910	BLASTN	363	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
18875	GM_M40_A1_B04_MF	g4150930	BLASTN	407	2e-11	62	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
18876	GM_M40_A1_B07_MF	g99922	BLASTX	469	9e-54	86	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
18877	GM_M40_A1_C12_MR	g3142328	BLASTN	995	4e-38	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18878	GM_M40_A1_D01_MF	g2462058	BLASTX	230	2e-18	57	(Y13389) reverse transcriptase [Antirrhinum majus]
18879	GM_M40_A1_D07_MR	g3097320	BLASTN	625	3e-21	74	Glycine max gene for Bd 30K, complete cds
18880	GM_M40_A1_D12_MR	g2213608	BLASTX	250	3e-19	42	(AC000103) F21J9.2 [Arabidopsis thaliana]
18881	GM_M40_A1_E04_MF	g18559	BLASTN	596	3e-22	69	G.max gene for catalase
18882	GM_M40_A1_E05_MR	g3777527	BLASTX	175	9e-31	92	(AF053008) gag-pol polyprotein [Glycine max]
18883	GM_M40_A1_F01_MR	g2443320	BLASTX	121	1e-09	58	(D85597) polyprotein [Oryza australiensis]
18884	GM_M40_A1_F12_MF	g3287269	BLASTN	390	1e-10	66	S.tuberosum mRNA for protein involved in starch metabolism

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18885	GM_M40_A1_G10_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18886	GM_M40_A1_H06_MF	g100484	BLASTX	381	1e-33	57	hypothetical protein - garden snapdragon
18887	GM_M40_A1_H07_MF	g4063760	BLASTX	286	3e-35	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18888	GM_M40_A1_H08_MR	g3142328	BLASTN	1422	1e-57	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18889	GM_M40_A1_H12_MR	g3097320	BLASTN	903	7e-34	77	Glycine max gene for Bd 30K, complete cds
18890	GM_M40_A2_A07_MF	g130582	BLASTX	202	5e-14	67	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
18891	GM_M40_A2_A09_MF	g507910	BLASTN	561	1e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
18892	GM_M40_A2_A10_MF	g507910	BLASTN	623	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
18893	GM_M40_A2_B01_MR	g3845213	BLASTN	355	5e-09	63	Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence
18894	GM_M40_A2_B02_MR	g3176771	BLASTN	405	3e-12	65	Homo sapiens allele 2 fragile site locus (FRA10B) minisatellite, 3' sequence
18895	GM_M40_A2_B03_MR	g3097320	BLASTN	394	8e-11	71	Glycine max gene for Bd 30K, complete cds
18896	GM_M40_A2_B10_MR	g3142328	BLASTN	1721	3e-71	96	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18897	GM_M40_A2_C01_MR	g3777527	BLASTX	693	3e-66	93	(AF053008) gag-pol polyprotein [Glycine max]
18898	GM_M40_A2_D02_MF	g1431738	BLASTN	744	7e-27	88	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
18899	GM_M40_A2_D10_MF	g507910	BLASTN	624	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
18900	GM_M40_A2_F07_MF	g295355	BLASTX	174	4e-12	48	(L13653) peroxidase [Lycopersicon esculentum]
18901	GM_M40_A2_G09_MR	g3142328	BLASTN	807	1e-29	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18902	GM_M40_A2_H01_MF	g4063760	BLASTX	254	1e-19	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18903	GM_M40_A2_H07_MF	g4063756	BLASTN	412	1e-11	74	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
18904	GM_M40_B1_A07_MF	g3777527	BLASTX	209	1e-14	79	(AF053008) gag-pol polyprotein [Glycine max]
18905	GM_M40_B1_A08_MF	g4063760	BLASTX	315	4e-26	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18906	GM_M40_B1_A10_MR	g1167523	BLASTX	228	9e-17	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
18907	GM_M40_B1_A12_MF	g3142379	BLASTX	382	1e-34	86	(AF053008) envelope-like [Glycine max]
18908	GM_M40_B1_B09_MF	g3097320	BLASTN	1083	5e-42	81	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18909	GM_M40_B1_B12_MR	g4140712	BLASTX	145	2e-09	40	(AF110183) putative integrase [Oryza sativa]
18910	GM_M40_B1_C02_MF	g2462935	BLASTX	126	3e-13	38	(Y12321) open reading frame 1 [Brassica oleracea]
18911	GM_M40_B1_C08_MF	g507910	BLASTN	445	2e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18912	GM_M40_B1_C09_MR	g2982452	BLASTX	353	3e-30	60	(AL022223) receptor protein kinase - like protein [Arabidopsis thaliana]
18913	GM_M40_B1_C12_MR	g3777527	BLASTX	230	6e-17	86	(AF053008) gag-pol polyprotein [Glycine max]
18914	GM_M40_B1_D06_MR	g507910	BLASTN	349	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18915	GM_M40_B1_D11_MF	g2815075	BLASTN	391	1e-10	61	Caenorhabditis elegans cosmid Y38H8A, complete sequence [Caenorhabditis elegans]
18916	GM_M40_B1_D12_MR	g3421038	BLASTN	405	3e-11	63	Human DNA sequence from clone 35C21 on chromosome 1q23-24. Contains STSs, complete sequence [Homo sapiens]
18917	GM_M40_B1_E04_MR	g507910	BLASTN	633	5e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
18918	GM_M40_B1_E05_MR	g3033389	BLASTX	173	4e-11	36	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
18919	GM_M40_B1_E07_MR	g3097320	BLASTN	467	4e-14	70	Glycine max gene for Bd 30K, complete cds
18920	GM_M40_B1_E09_MR	g3142328	BLASTN	1100	7e-43	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18921	GM_M40_B1_E11_MF	g4006849	BLASTN	379	4e-10	73	Arabidopsis thaliana DNA chromosome 4, ESSA I AP2 contig fragment No. 1
18922	GM_M40_B1_F08_MR	g18559	BLASTN	653	1e-22	76	G.max gene for catalase
18923	GM_M40_B1_G01_MF	g3097320	BLASTN	360	3e-09	67	Glycine max gene for Bd 30K, complete cds
18924	GM_M40_B1_G03_MF	g3021268	BLASTX	158	1e-21	67	(AL022347) putative protein [Arabidopsis thaliana]
18925	GM_M40_B1_G06_MF	g13619	BLASTN	360	5e-10	62	Saccharomyces douglasii mitDNA for tRNA(f)Met and put. tRNA synthesis locus (TSL)
18926	GM_M40_B1_H01_MF	g13774	BLASTN	356	2e-09	59	Torulopsis glabrata mitochondrial gene for ribosomal protein var1 gi 343958 lcl X02893 Yeast (T.glabrata) mitochondrial gene for ribosomal protein VAR1.
18927	GM_M40_B2_B06_MF	g226407	BLASTX	242	3e-18	43	retrotransposon del1-46 [Lilium henryi]
18928	GM_M40_B2_C03_MF	g3738293	BLASTX	255	3e-21	67	(AC005309) putative CCAAT-binding transcription factor subunit A (CBF-A) [Arabidopsis thaliana]
18929	GM_M40_B2_C05_MF	g1769898	BLASTX	312	2e-26	52	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18930	GM_M40_B2_D02_MR	g18768	BLASTN	518	5e-17	65	Soybean Tgm6 transposable element 3' end
18931	GM_M40_B2_D10_MF	g976284	BLASTX	133	2e-19	45	reverse transcriptase [Arabidopsis thaliana]
18932	GM_M40_B2_D11_MR	g2465923	BLASTX	171	7e-11	52	(AF024648) receptor-like serine/threonine kinase [Arabidopsis thaliana]
18933	GM_M40_B2_E02_MR	g3142330	BLASTX	185	6e-22	80	(U96295) envelope-like [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18934	GM_M40_B2_E06_MF	g18559	BLASTN	713	3e-25	85	G.max gene for catalase
18935	GM_M40_B2_E08_MF	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
18936	GM_M40_B2_F01_MR	g4063760	BLASTX	437	4e-39	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18937	GM_M40_B2_F02_MR	g4092471	BLASTN	448	3e-13	70	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
18938	GM_M40_B2_F03_MR	g13597	BLASTN	371	7e-10	59	Yeast mitochondrial tRNA genes for tRNA-Ala, tRNA-Tyr and tRNA-Ile
18939	GM_M40_B2_F05_MF	g6940	BLASTN	420	1e-12	67	C.elegans repetitive DNA
18940	GM_M40_B2_F09_MF	g2129618	BLASTX	213	2e-15	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18941	GM_M40_B2_G01_MR	g1769898	BLASTX	256	3e-20	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18942	GM_M40_B2_G02_MR	g4056462	BLASTX	179	2e-19	72	(AC005990) Strong similarity to gb Y09876 aldehyde dehydrogenase (NAD+) from Nicotiana tabacum and a member of the aldehyde dehydrogenase family PF 00171. ESTs gb F15117, gb R83958 and gb 586262 come from this gene. [Arabidopsis thaliana]
18943	GM_M40_B2_G12_MF	g507910	BLASTN	550	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
18944	GM_M40_B2_H03_MR	g905361	BLASTX	212	1e-15	34	(U22103) gag-protease polyprotein [Glycine max]
18945	GM_M40_B2_H04_MF	g507910	BLASTN	422	2e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
18946	GM_M40_B2_H04_MR	g507910	BLASTN	408	8e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18947	GM_M40_B2_H12_MF	g2281115	BLASTX	206	5e-18	93	(AC002330) putative cullin-like 1 protein [Arabidopsis thaliana]
18948	GM_M41_A1_A04_MR	g507910	BLASTN	617	3e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
18949	GM_M41_A1_A09_MR	g3341679	BLASTX	154	2e-09	65	(AC003672) dynamin-like protein phragmoplastin 12 [Arabidopsis thaliana]
18950	GM_M41_A1_B09_MR	g3645899	BLASTX	218	2e-20	48	(U68408) 5' end not determined experimentally [Zea mays]
18951	GM_M41_A1_B10_MF	g3522943	BLASTX	474	4e-43	71	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]
18952	GM_M41_A1_B12_MF	g2832304	BLASTX	353	2e-31	65	(AF044489) receptor-like protein kinase [Oryza sativa]
18953	GM_M41_A1_C07_MF	g4063760	BLASTX	498	1e-45	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18954	GM_M41_A1_C11_MF	g4063760	BLASTX	293	9e-24	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
18955	GM_M41_A1_D01_MF	g1666236	BLASTX	187	1e-13	30	(U76261) unknown [Hordeum vulgare]
18956	GM_M41_A1_D03_MR	g905361	BLASTX	108	1e-11	45	(U22103) gag-protease polyprotein [Glycine max]
18957	GM_M41_A1_D04_MR	g3738114	BLASTN	378	5e-10	61	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18958	GM_M41_A1_D06_MR	g130582	BLASTX	392	3e-34	62	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
18959	GM_M41_A1_D10_MR	g3142328	BLASTN	597	2e-43	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18960	GM_M41_A1_D12_MR	g507910	BLASTN	729	3e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
18961	GM_M41_A1_E08_MR	g507910	BLASTN	438	4e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
18962	GM_M41_A1_F02_MR	g1076763	BLASTX	161	3e-10	38	AWJL218 protein - wheat gi 551212 (X81369) AWJL218 gene product [Triticum aestivum]
18963	GM_M41_A1_F04_MR	g2129618	BLASTX	266	5e-21	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18964	GM_M41_A1_F05_MF	g421954	BLASTX	178	4e-13	38	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
18965	GM_M41_A1_F05_MR	g3582328	BLASTX	211	2e-24	43	(AC005496) hypothetical protein [Arabidopsis thaliana]
18966	GM_M41_A1_F10_MF	g3513745	BLASTX	156	5e-09	31	(AF080118) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 42.57) [Arabidopsis thaliana]
18967	GM_M41_A1_G04_MF	g507910	BLASTN	380	1e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
18968	GM_M41_A1_G06_MR	g2864621	BLASTX	218	1e-16	38	hypothetical protein [Arabidopsis thaliana]
18969	GM_M41_A1_G09_MF	g3426039	BLASTX	414	5e-38	60	(AC005168) unknown protein [Arabidopsis thaliana]
18970	GM_M41_A1_H01_MF	g1438880	BLASTN	450	1e-13	80	Glycine max choline kinase GmCK2p mRNA, complete cds
18971	GM_M41_A1_H02_MF	g3779026	BLASTX	119	8e-16	34	(AC005171) putative retrotransposon [Arabidopsis thaliana]
18972	GM_M41_A1_H02_MR	g3777527	BLASTX	214	3e-15	32	(AF053008) gag-pol polyprotein [Glycine max]
18973	GM_M41_A1_H05_MF	g3142328	BLASTN	855	9e-32	83	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
18974	GM_M41_A1_H05_MR	g3599418	BLASTN	369	1e-09	69	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
18975	GM_M41_A1_H12_MR	g507910	BLASTN	733	2e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
18976	GM_M41_A2_A01_MR	g401237	BLASTX	144	2e-12	62	UBIQUITIN-ACTIVATING ENZYME E1 2 gi 170684 (M90663) ubiquitin activating enyme [Triticum aestivum]
18977	GM_M41_A2_A02_MF	g2655314	BLASTN	373	4e-10	59	Bactrocera xanthodes strain Vanuatu mitochondrial D-loop region, complete sequence
18978	GM_M41_A2_A02_MR	g1040717	BLASTN	343	2e-09	65	D.polychroa microsatellite sequence (clone Dp ch1 F3)
18979	GM_M41_A2_A05_MR	g2996576	BLASTN	380	4e-10	59	Homo sapiens DNA sequence from PAC 29C18 on chromosome 22

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
18980	GM_M41_A2_A07_MR	g3377848	BLASTX	172	7e-19	44	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
18981	GM_M41_A2_A11_MF	g3097320	BLASTN	918	1e-34	81	Glycine max gene for Bd 30K, complete cds
18982	GM_M41_A2_B01_MR	g3645899	BLASTX	162	4e-23	63	(U68408) 5' end not determined experimentally [Zea mays]
18983	GM_M41_A2_B03_MR	g1769899	BLASTX	192	2e-14	49	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
18984	GM_M41_A2_B06_MR	g507910	BLASTN	581	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
18985	GM_M41_A2_B07_MR	g2129618	BLASTX	237	6e-18	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
18986	GM_M41_A2_B08_MF	g2443320	BLASTX	246	1e-18	38	(D85597) polyprotein [Oryza australiensis]
18987	GM_M41_A2_B09_MF	g905361	BLASTX	582	8e-56	91	(U22103) gag-protease polyprotein [Glycine max]
18988	GM_M41_A2_B10_MF	g4006828	BLASTX	193	3e-13	34	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
18989	GM_M41_A2_C04_MR	g3319351	BLASTX	262	2e-20	44	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
18990	GM_M41_A2_C05_MR	g114734	BLASTX	388	3e-35	97	AUXIN-INDUCED PROTEIN AUX28 gi 81759 pir A28993 aux28 protein - soybean gi 169921 (J03919) auxin-regulated protein (Aux28) [Glycine max]
18991	GM_M41_A2_C11_MF	g3097320	BLASTN	623	4e-21	80	Glycine max gene for Bd 30K, complete cds
18992	GM_M41_A2_D02_MR	g3845255	BLASTN	403	4e-11	66	Plasmodium falciparum chromosome 2, section 50 of 73 of the complete sequence
18993	GM_M41_A2_D04_MF	g170080	BLASTN	391	4e-13	79	Soybean seed lectin gene transposable element tgm1.
18994	GM_M41_A2_D08_MF	g2995405	BLASTX	237	5e-18	44	(Y12432) polyprotein [Ananas comosus]
18995	GM_M41_A2_D10_MR	g507910	BLASTN	376	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
18996	GM_M41_A2_D12_MF	g507910	BLASTN	678	5e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
18997	GM_M41_A2_E01_MR	g507910	BLASTN	725	4e-26	89	Glycine max BSR-101 satellite SB92 genomic sequence.
18998	GM_M41_A2_E02_MF	g1617470	BLASTN	429	2e-12	61	Z.diploperennis DNA for Grande1-4 retrotransposon.
18999	GM_M41_A2_E07_MR	g3142328	BLASTN	551	6e-18	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19000	GM_M41_A2_E09_MF	g3845234	BLASTN	390	1e-10	63	Plasmodium falciparum chromosome 2, section 44 of 73 of the complete sequence
19001	GM_M41_A2_E09_MR	g3777527	BLASTX	195	4e-13	46	(AF053008) gag-pol polyprotein [Glycine max]
19002	GM_M41_A2_E11_MF	g1871187	BLASTX	222	3e-16	51	(U90439) unknown protein [Arabidopsis thaliana]
19003	GM_M41_A2_F01_MF	g2522228	BLASTX	370	2e-33	69	(AB007466) reverse transcriptase-like protein [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19004	GM_M41_A2_F01_MR	g548533	BLASTX	218	1e-38	78	2,3-BISPHOSPHOGLYCERATE-INDEPENDENT PHOSPHOGLYCERATE MUTASE (PHOSPHOGLYCEROMUTASE) (BPG-INDEPENDENT PGAM) gi 1076631 pir S49646 phosphoglycerate mutase (EC 5.4.2.1) - common tobacco gi 474168 (X70651) phosphoglycerate mutase [Nicotiana tabacum]
19005	GM_M41_A2_F02_MF	g3810596	BLASTX	168	1e-10	33	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19006	GM_M41_A2_F05_MR	g13581	BLASTN	380	6e-11	70	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTCG10 Saccharomyces cerevisiae mitochondrion DNA segment.
19007	GM_M41_A2_F06_MF	g4063756	BLASTN	405	3e-11	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19008	GM_M41_A2_F09_MF	g3845094	BLASTN	422	5e-12	60	Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence
19009	GM_M41_A2_F12_MR	g2765091	BLASTX	347	1e-30	64	(Y10982) putative cytochrome P450 [Glycine max]
19010	GM_M41_A2_G03_MR	g18559	BLASTN	788	1e-28	75	G.max gene for catalase
19011	GM_M41_A2_G04_MR	g507910	BLASTN	432	6e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19012	GM_M41_A2_G05_MF	g4063760	BLASTX	306	4e-25	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19013	GM_M41_A2_G07_MF	g4063760	BLASTX	165	8e-16	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19014	GM_M41_A2_G08_MR	g1709919	BLASTX	499	4e-47	82	AMIDOPHOSPHORIBOSYLTRANSFERASE PRECURSOR (GLUTAMINE PHOSPHORIBOSYLPYROPHOSPHATE AMIDOTRANSFERASE) (ATASE) (GPAT) gi 439105 (L23834) glutamine phosphoribosylpyrophosphate amidotransferase [Vigna aconitifolia]
19015	GM_M41_A2_H02_MR	g4063760	BLASTX	204	3e-14	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19016	GM_M41_A2_H04_MR	g3135969	BLASTN	423	4e-12	62	Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family prot...
19017	GM_M41_A2_H06_MF	g3746069	BLASTX	158	2e-10	37	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
19018	GM_M41_A2_H10_MF	g4063760	BLASTX	375	2e-32	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19019	GM_M41_B1_A02_MR	g3097320	BLASTN	569	1e-18	78	Glycine max gene for Bd 30K, complete cds
19020	GM_M41_B1_A03_MF	g507910	BLASTN	538	1e-17	82	Glycine max BSR-101 satellite SB92 genomic sequence.
19021	GM_M41_B1_A04_MF	g905361	BLASTX	592	8e-57	88	(U22103) gag-protease polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19022	GM_M41_B1_A04_MR	g1142699	BLASTN	1233	2e-49	87	Glycine max satellite STR120-A.1.
19023	GM_M41_B1_A05_MF	g550452	BLASTX	132	5e-12	76	(U08469) 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]
19024	GM_M41_B1_A06_MR	g99922	BLASTX	527	6e-50	74	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
19025	GM_M41_B1_A10_MF	g995751	BLASTN	365	1e-09	66	Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence
19026	GM_M41_B1_B07_MR	g100484	BLASTX	219	3e-16	44	hypothetical protein - garden snapdragon
19027	GM_M41_B1_B08_MF	g507910	BLASTN	392	4e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19028	GM_M41_B1_B08_MR	g507910	BLASTN	375	2e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19029	GM_M41_B1_C07_MF	g2827715	BLASTX	351	4e-30	69	(AL021684) receptor protein kinase - like protein [Arabidopsis thaliana]
19030	GM_M41_B1_C08_MR	g387902	BLASTX	170	3e-23	41	(L23524) ORF [Hordeum vulgare]
19031	GM_M41_B1_D02_MF	g2626751	BLASTN	349	8e-09	63	Triticum aestivum retrotransposon Tar1, partial sequence.
19032	GM_M41_B1_D06_MF	g3319362	BLASTX	256	6e-20	46	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
19033	GM_M41_B1_D06_MR	g3599418	BLASTN	493	2e-15	84	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
19034	GM_M41_B1_D08_MF	g507910	BLASTN	635	4e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
19035	GM_M41_B1_D08_MR	g507910	BLASTN	545	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
19036	GM_M41_B1_D11_MF	g4063756	BLASTN	454	2e-13	63	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19037	GM_M41_B1_D11_MR	g507910	BLASTN	570	4e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
19038	GM_M41_B1_D12_MF	g130582	BLASTX	199	9e-14	32	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
19039	GM_M41_B1_E03_MR	g462013	BLASTX	116	2e-10	80	ENDOPLASMIN HOMOLOG PRECURSOR (GRP94 HOMOLOG) gi 542022 pir S39558 HSP90 homolog - Madagascar periwinkle gi 348696 (L14594) heat shock protein 90 [Catharanthus roseus]
19040	GM_M41_B1_E10_MR	g4038056	BLASTX	353	2e-30	50	(AC005897) putative transposon [Arabidopsis thaliana]
19041	GM_M41_B1_F05_MR	g507910	BLASTN	506	3e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19042	GM_M41_B1_F06_MF	g538067	BLASTX	213	6e-16	45	(M77661) putative pol polyprotein [Magnaporthe grisea]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19043	GM_M41_B1_F10_MR	g2522228	BLASTX	304	7e-38	60	(AB007466) reverse transcriptase-like protein [Vicia faba]
19044	GM_M41_B1_F12_MR	g3860312	BLASTN	624	3e-22	73	Cicer arietinum mRNA for hypothetical protein, clone Can144
19045	GM_M41_B1_G01_MF	g507910	BLASTN	644	2e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
19046	GM_M41_B1_G01_MR	g905361	BLASTX	424	9e-39	95	(U22103) gag-protease polyprotein [Glycine max]
19047	GM_M41_B1_G03_MR	g169110	BLASTN	415	3e-12	71	Pea lox2-like lipoxygenase gene, 5' flank.
19048	GM_M41_B1_H01_MF	g3687234	BLASTX	179	1e-11	35	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
19049	GM_M41_B1_H03_MR	g2995405	BLASTX	378	4e-33	45	(Y12432) polyprotein [Ananas comosus]
19050	GM_M41_B1_H09_MR	g2522227	BLASTX	199	3e-15	47	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
19051	GM_M41_B1_H10_MR	g505129	BLASTN	325	3e-10	68	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
19052	GM_M41_B1_H11_MF	g1142702	BLASTN	345	4e-09	74	Glycine max satellite STR120-A.4.
19053	GM_M41_B2_A07_MR	g342964	BLASTN	370	1e-10	62	paramecium species 5,311 mt dna dimer: replication init. region.
19054	GM_M41_B2_A10_MR	g226407	BLASTX	409	4e-36	54	retrotransposon del1-46 [Lilium henryi]
19055	GM_M41_B2_A12_MR	g3097320	BLASTN	558	3e-18	73	Glycine max gene for Bd 30K, complete cds
19056	GM_M41_B2_B02_MR	g507910	BLASTN	600	2e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
19057	GM_M41_B2_B05_MR	g3097320	BLASTN	1280	6e-51	81	Glycine max gene for Bd 30K, complete cds
19058	GM_M41_B2_B07_MR	g2827718	BLASTX	197	1e-13	34	(AL021684) retrotransposon - like protein [Arabidopsis thaliana]
19059	GM_M41_B2_C02_MR	g728868	BLASTX	139	1e-13	37	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG (PROTEIN CEX) gi 99824 pir S16748 proline-rich protein - rape (fragment) gi 22597 (X60376) proline-rich protein [Brassica napus]
19060	GM_M41_B2_C03_MR	g3599418	BLASTN	354	5e-09	64	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
19061	GM_M41_B2_C07_MR	g1666236	BLASTX	116	4e-12	30	(U76261) unknown [Hordeum vulgare]
19062	GM_M41_B2_C12_MR	g3097320	BLASTN	948	7e-36	88	Glycine max gene for Bd 30K, complete cds
19063	GM_M41_B2_D03_MR	g2129618	BLASTX	178	1e-11	33	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19064	GM_M41_B2_D04_MR	g3097320	BLASTN	587	1e-19	74	Glycine max gene for Bd 30K, complete cds
19065	GM_M41_B2_D05_MR	g2961380	BLASTX	167	7e-11	36	(AL022141) putative protein [Arabidopsis thaliana]
19066	GM_M41_B2_E10_MR	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
19067	GM_M41_B2_E11_MR	g2801677	BLASTN	579	5e-20	64	Glycine max telomere-associated sequence STAS6
19068	GM_M41_B2_F03_MR	g4115365	BLASTX	309	2e-25	59	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19069	GM_M41_B2_F04_MR	g1345132	BLASTX	180	8e-12	36	(U47029) ERECTA [Arabidopsis thaliana] gi 1389566 gnl PID d1012536 (D83257) receptor protein kinase [Arabidopsis thaliana] gi 3075386 (AC004484) receptor protein kinase, ERECTA [Arabidopsis thaliana]
19070	GM_M41_B2_F05_MR	g3810596	BLASTX	195	2e-13	35	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19071	GM_M41_B2_G03_MR	g3645899	BLASTX	379	4e-33	62	(U68408) 5' end not determined experimentally [Zea mays]
19072	GM_M41_B2_G05_MR	g3810595	BLASTX	179	5e-16	43	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
19073	GM_M41_B2_G08_MR	g1769897	BLASTX	177	6e-12	32	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19074	GM_M41_B2_G10_MR	g3097320	BLASTN	1329	4e-53	82	Glycine max gene for Bd 30K, complete cds
19075	GM_M41_B2_H03_MR	g226407	BLASTX	495	3e-45	67	retrotransposon del1-46 [Lilium henryi]
19076	GM_M41_B2_H09_MR	g507910	BLASTN	411	6e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
19077	GM_M41_B2_H12_MR	g2982545	BLASTN	450	3e-13	62	Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-52, complete sequence [Plasmodium falciparum]
19078	GM_M42_A1_A04_MF	g3097320	BLASTN	452	2e-13	69	Glycine max gene for Bd 30K, complete cds
19079	GM_M42_A1_A06_MR	g4063760	BLASTX	100	8e-14	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19080	GM_M42_A1_A08_MF	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19081	GM_M42_A1_A12_MF	g1706130	BLASTX	124	4e-10	68	CDPK-RELATED PROTEIN KINASE (PK421) gi 2129917 pir S60052 calcium-dependent protein kinase homolog - carrot gi 1103386 (X83869) CDPK-related protein kinase [Daucus carota]
19082	GM_M42_A1_B02_MF	g2558658	BLASTX	192	2e-14	41	(AC002354) No definition line found [Arabidopsis thaliana]
19083	GM_M42_A1_B10_MR	g218269	BLASTX	235	5e-19	66	(D12839) reverse transcriptase [Glycine max]
19084	GM_M42_A1_B11_MF	g2588629	BLASTN	392	1e-10	64	Human BAC clone GS303P24 from 7q21-22, complete sequence [Homo sapiens]
19085	GM_M42_A1_B12_MR	g100484	BLASTX	365	6e-32	53	hypothetical protein - garden snapdragon
19086	GM_M42_A1_C03_MR	g3695395	BLASTX	237	3e-18	50	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
19087	GM_M42_A1_C05_MF	g507910	BLASTN	398	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19088	GM_M42_A1_C05_MR	g507910	BLASTN	371	4e-10	69	Glycine max BSR-101 satellite SB92 genomic sequence.
19089	GM_M42_A1_C10_MF	g507910	BLASTN	344	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19090	GM_M42_A1_C12_MR	g3645899	BLASTX	343	3e-29	54	(U68408) 5' end not determined experimentally [Zea mays]
19091	GM_M42_A1_D02_MR	g3779021	BLASTX	195	3e-13	35	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]
19092	GM_M42_A1_D04_MF	g3283026	BLASTX	257	3e-20	40	putative transposase [Arabidopsis thaliana]
19093	GM_M42_A1_D07_MF	g2522227	BLASTX	187	8e-14	51	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19094	GM_M42_A1_D11_MF	g3142328	BLASTN	814	7e-30	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19095	GM_M42_A1_E04_MR	g2121303	BLASTN	420	6e-12	63	Homo sapiens cosmids Qc5E3, LC1833, IC0177, Qc12F11 and Qc18D10 from Xq28, complete sequence [Homo sapiens]
19096	GM_M42_A1_E08_MF	g170603	BLASTN	477	3e-15	67	Broad bean (V.faba) BamHI repetitive element, 990 bp family.
19097	GM_M42_A1_F04_MF	g3097320	BLASTN	1056	9e-41	80	Glycine max gene for Bd 30K, complete cds
19098	GM_M42_A1_F11_MF	g507910	BLASTN	408	8e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19099	GM_M42_A1_G08_MF	g18559	BLASTN	817	5e-30	75	G.max gene for catalase
19100	GM_M42_A1_G09_MR	g99922	BLASTX	334	4e-34	72	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
19101	GM_M42_A1_G11_MR	g2588611	BLASTN	360	3e-09	62	Human BAC clone RG335O22 from 7q21-q22, complete sequence [Homo sapiens]
19102	GM_M42_A1_G12_MR	g2191136	BLASTX	163	1e-10	36	(AF007269) Similar to UTP-Glucose Glucosyltransferase; coded for by A. thaliana cDNA T46230; coded for by A. thaliana cDNA H76538; coded for by A. thaliana cDNA H76290 [Arabidopsis thaliana]
19103	GM_M42_A1_H01_MR	g3645899	BLASTX	201	2e-29	41	(U68408) 5' end not determined experimentally [Zea mays]
19104	GM_M42_A1_H03_MR	g3201680	BLASTX	176	1e-13	63	(AF060941) extra-large G-protein [Arabidopsis thaliana]
19105	GM_M42_A1_H04_MR	g507910	BLASTN	572	3e-19	81	Glycine max BSR-101 satellite SB92 genomic sequence.
19106	GM_M42_A1_H07_MR	g2829902	BLASTX	246	3e-19	64	(AC002311) Putative sulphate transporter protein#protein [Arabidopsis thaliana]
19107	GM_M42_A1_H11_MR	g3097320	BLASTN	506	7e-16	69	Glycine max gene for Bd 30K, complete cds
19108	GM_M42_B1_A12_MF	g13096	BLASTN	459	8e-14	64	Leishmania tarentolae maxicircle DNA fragment
19109	GM_M42_B1_B01_MF	g507910	BLASTN	379	2e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19110	GM_M42_B1_B02_MF	g3097320	BLASTN	500	1e-15	72	Glycine max gene for Bd 30K, complete cds
19111	GM_M42_B1_B06_MF	g507910	BLASTN	523	5e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
19112	GM_M42_B1_B11_MF	g3901012	BLASTX	255	4e-21	73	(AJ130885) xyloglucan endotransglycosylase 1 [Fagus sylvatica]
19113	GM_M42_B1_C02_MF	g1184075	BLASTX	228	2e-19	43	(U42444) Cf-2.1 [Lycopersicon pimpinellifolium] gi 1587673 prf 2207203A Cf-2 gene [Lycopersicon esculentum]
19114	GM_M42_B1_C07_MF	g3645899	BLASTX	377	7e-33	57	(U68408) 5' end not determined experimentally [Zea mays]
19115	GM_M42_B1_C09_MF	g507910	BLASTN	362	9e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19116	GM_M42_B1_C10_MF	g2281086	BLASTX	153	2e-09	37	(AC002333) indole-3-acetate beta-glucosyltransferase isolog [Arabidopsis thaliana]
19117	GM_M42_B1_C11_MF	g3894383	BLASTX	230	8e-20	43	(AF053993) disease resistance protein [Lycopersicon esculentum]
19118	GM_M42_B1_D01_MF	g1769897	BLASTX	260	6e-21	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19119	GM_M42_B1_D08_MF	g507910	BLASTN	594	3e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
19120	GM_M42_B1_D09_MF	g507910	BLASTN	461	3e-14	77	Glycine max BSR-101 satellite SB92 genomic sequence.
19121	GM_M42_B1_F01_MF	g3142328	BLASTN	966	8e-37	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19122	GM_M42_B1_F11_MF	g1666236	BLASTX	192	4e-14	38	(U76261) unknown [Hordeum vulgare]
19123	GM_M42_B1_G02_MF	g462627	BLASTX	131	2e-14	61	MSP1 PROTEIN (TAT-BINDING HOMOLOG 4) gi 1362427 pir A49506 MSP1 protein - yeast (Saccharomyces cerevisiae) gi 404217 (X68055) MSP1 protein [Saccharomyces cerevisiae] gi 531756 (X81069) probable regulatory subunit of 26S protease [Saccharomyces cerevisiae] gi 1323004 gnl PID e243375 (Z72813) ORF YGR028w [Saccharomyces cerevisiae]
19124	GM_M42_B1_G03_MF	g2522230	BLASTX	267	2e-22	38	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
19125	GM_M42_B1_G06_MF	g3250687	BLASTX	284	3e-24	42	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
19126	GM_M42_B1_H08_MF	g3319351	BLASTX	216	2e-15	38	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
19127	GM_M42_B1_H09_MF	g3097320	BLASTN	860	6e-32	76	Glycine max gene for Bd 30K, complete cds
19128	GM_M42_B1_H10_MF	g4063760	BLASTX	484	3e-44	72	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19129	GM_M43_A1_A11_MF	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19130	GM_M43_A1_A12_MR	g1658457	BLASTX	175	9e-13	70	(U75248) reverse transcriptase [Gossypium barbadense]
19131	GM_M43_A1_B02_MR	g3461813	BLASTX	136	4e-11	89	(AC004138) putative sucrose/H+ symporter [Arabidopsis thaliana]
19132	GM_M43_A1_B03_MF	g18559	BLASTN	645	3e-22	69	G.max gene for catalase
19133	GM_M43_A1_B11_MF	g3142328	BLASTN	741	1e-26	92	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19134	GM_M43_A1_C01_MR	g3142379	BLASTX	286	3e-24	66	(AF053008) envelope-like [Glycine max]
19135	GM_M43_A1_C04_MF	g4063760	BLASTX	210	7e-28	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19136	GM_M43_A1_C07_MR	g3142328	BLASTN	1209	7e-48	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19137	GM_M43_A1_D02_MF	g3777527	BLASTX	669	1e-63	97	(AF053008) gag-pol polyprotein [Glycine max]
19138	GM_M43_A1_D02_MR	g507910	BLASTN	392	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19139	GM_M43_A1_D07_MF	g4063756	BLASTN	526	1e-16	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19140	GM_M43_A1_D08_MF	g2244915	BLASTX	165	4e-17	41	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19141	GM_M43_A1_E08_MF	g2129618	BLASTX	170	9e-11	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19142	GM_M43_A1_E08_MR	g2764526	BLASTN	415	1e-11	63	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
19143	GM_M43_A1_E09_MR	g100484	BLASTX	207	6e-15	33	hypothetical protein - garden snapdragon
19144	GM_M43_A1_E11_MF	g2522227	BLASTX	156	3e-10	41	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
19145	GM_M43_A1_F07_MR	g2995405	BLASTX	218	2e-32	51	(Y12432) polyprotein [Ananas comosus]
19146	GM_M43_A1_F08_MF	g4038056	BLASTX	368	5e-32	54	(AC005897) putative transposon [Arabidopsis thaliana]
19147	GM_M43_A1_F08_MR	g3810595	BLASTX	144	9e-18	41	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
19148	GM_M43_A1_F09_MF	g3006139	BLASTX	265	4e-22	43	(AL022299) hypothetical protein [Schizosaccharomyces pombe]
19149	GM_M43_A1_G03_MF	g3777527	BLASTX	645	4e-61	93	(AF053008) gag-pol polyprotein [Glycine max]
19150	GM_M43_A1_G03_MR	g4038056	BLASTX	169	9e-11	43	(AC005897) putative transposon [Arabidopsis thaliana]
19151	GM_M43_A1_G05_MR	g3212102	BLASTN	608	2e-20	62	Arabidopsis Thaliana BAC F6A4, Chromosome IV, near 60.5 cM, complete sequence [Arabidopsis thaliana]
19152	GM_M43_A1_G08_MF	g507910	BLASTN	529	3e-17	79	Glycine max BSR-101 satellite SB92 genomic sequence.
19153	GM_M43_A1_G09_MR	g3928116	BLASTN	395	8e-11	63	, complete sequence [Homo sapiens]
19154	GM_M43_A1_G12_MF	g2129618	BLASTX	228	5e-17	43	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19155	GM_M43_A1_H03_MR	g2522228	BLASTX	207	2e-28	50	(AB007466) reverse transcriptase-like protein [Vicia faba]
19156	GM_M43_A1_H05_MF	g3265161	BLASTN	369	6e-10	63	Glossina morsitans morsitans 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence
19157	GM_M43_A1_H07_MR	g18559	BLASTN	980	2e-37	79	G.max gene for catalase
19158	GM_M43_A2_A04_MF	g3142328	BLASTN	1030	1e-39	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19159	GM_M43_A2_A12_MF	g507910	BLASTN	415	4e-12	74	Glycine max BSR-101 satellite SB92 genomic sequence.
19160	GM_M43_A2_A12_MR	g4063760	BLASTX	184	2e-19	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19161	GM_M43_A2_B01_MF	g8540	BLASTN	449	4e-14	66	Drosophila satellite DNA fragment 1.672-614 >gi 158379 gb M29744 DROSAT02 Drosophila satellite DNA fragment 1.672-614.
19162	GM_M43_A2_B04_MR	g4063760	BLASTX	228	6e-31	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19163	GM_M43_A2_B05_MF	g905361	BLASTX	423	1e-38	92	(U22103) gag-protease polyprotein [Glycine max]
19164	GM_M43_A2_B05_MR	g507910	BLASTN	392	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19165	GM_M43_A2_B07_MF	g3702691	BLASTX	156	7e-29	80	(AB005902) AtPIP5K1 [Arabidopsis thaliana]
19166	GM_M43_A2_B07_MR	g1905774	BLASTN	411	1e-11	69	A.thaliana mRNA for protein kinase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19167	GM_M43_A2_B10_MF	g3777527	BLASTX	403	4e-44	89	(AF053008) gag-pol polyprotein [Glycine max]
19168	GM_M43_A2_B12_MF	g2499535	BLASTX	158	8e-10	70	2-OXOGLUTARATE/MALATE TRANSLOCATOR PRECURSOR gi 595681 (U13238) 2-oxoglutarate/malate translocator [Spinacia oleracea]
19169	GM_M43_A2_C01_MR	g2052034	BLASTN	414	1e-11	63	Human DNA sequence from PAC 450C20 on chromosome X
19170	GM_M43_A2_C04_MF	g2129618	BLASTX	138	4e-13	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19171	GM_M43_A2_C05_MF	g507910	BLASTN	363	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19172	GM_M43_A2_C05_MR	g507910	BLASTN	347	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19173	GM_M43_A2_C06_MR	g3319362	BLASTX	136	9e-22	59	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
19174	GM_M43_A2_D01_MF	g4150930	BLASTN	400	5e-11	64	Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence [Homo sapiens]
19175	GM_M43_A2_D01_MR	g905361	BLASTX	114	1e-11	45	(U22103) gag-protease polyprotein [Glycine max]
19176	GM_M43_A2_D07_MF	g2576343	BLASTN	351	8e-09	63	Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence [Homo sapiens]
19177	GM_M43_A2_D10_MR	g3930515	BLASTX	132	8e-12	52	(AF059674) putative gag protein [Nicotiana tabacum]
19178	GM_M43_A2_E08_MF	g3142328	BLASTN	1455	4e-59	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19179	GM_M43_A2_E10_MR	g3097320	BLASTN	828	2e-30	72	Glycine max gene for Bd 30K, complete cds
19180	GM_M43_A2_E11_MF	g2129473	BLASTX	205	7e-16	42	arabinogalactan-like protein - loblolly pine gi 607774 (U09556) arabinogalactan-like protein [Pinus taeda]
19181	GM_M43_A2_F01_MR	g1244652	BLASTN	373	8e-10	60	Zea mays copia-type retroelement PREM-2 gag gene, complete cds.
19182	GM_M43_A2_F02_MR	g1244652	BLASTN	357	4e-09	59	Zea mays copia-type retroelement PREM-2 gag gene, complete cds.
19183	GM_M43_A2_F06_MF	g507910	BLASTN	354	2e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19184	GM_M43_A2_G07_MR	g3142328	BLASTN	1415	3e-57	85	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19185	GM_M43_A2_G08_MF	g559261	BLASTN	392	3e-11	67	Saccharomyces cerevisiae mitochondrion 21S R2 ribosomal RNA, 3' end.
19186	GM_M43_A2_G09_MR	g903472	BLASTN	341	3e-09	66	Stealth virus clone C16290 T3.
19187	GM_M43_A2_H01_MR	g3142328	BLASTN	645	3e-22	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19188	GM_M43_A2_H05_MF	g507910	BLASTN	500	6e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19189	GM_M43_A2_H09_MR	g3142328	BLASTN	480	1e-14	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19190	GM_M43_A2_H12_MR	g2129473	BLASTX	331	3e-29	47	arabinogalactan-like protein - loblolly pine gi 607774 (U09556) arabinogalactan-like protein [Pinus taeda]
19191	GM_M43_B1_A03_MF	g2997591	BLASTX	353	2e-31	85	(AF020814) glucose-6-phosphate/phosphate-translocator precursor [Pisum sativum]
19192	GM_M43_B1_A04_MR	g1144550	BLASTN	405	3e-12	60	Anopheles gambiae 12S ribosomal RNA, D-loop, and tRNA-Ile mitochondrial genes, partial sequence.
19193	GM_M43_B1_A05_MR	g2864610	BLASTX	152	3e-18	55	(AL021811) putative protein [Arabidopsis thaliana]
19194	GM_M43_B1_A09_MR	g4063760	BLASTX	459	2e-42	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19195	GM_M43_B1_A10_MR	g1142701	BLASTN	1359	4e-55	85	Glycine max satellite STR120-A.3.
19196	GM_M43_B1_A11_MF	g3600059	BLASTX	348	5e-31	77	(AF080120) contains similarity to WB domains, G-beta repeats (Pfam: G-beta.hmm, score: 14.83 and 23.03) [Arabidopsis thaliana]
19197	GM_M43_B1_A11_MR	g2829275	BLASTX	178	5e-26	77	(AF044265) nucleoside diphosphate kinase 3 [Arabidopsis thaliana] gi 3513740 (AF080118) contains similarity to nucleoside diphosphate kinases (Pfam: NDK.hmm, score: 301.12) [Arabidopsis thaliana]
19198	GM_M43_B1_B02_MR	g1769898	BLASTX	223	9e-17	31	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19199	GM_M43_B1_B06_MR	g1216393	BLASTN	422	5e-13	61	Trypanosoma cruzi ATPase subunit 6 mRNA, complete cds
19200	GM_M43_B1_B07_MR	g4063760	BLASTX	487	2e-44	62	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19201	GM_M43_B1_B11_MR	g3377834	BLASTX	154	3e-09	28	(AF075598) No definition line found [Arabidopsis thaliana]
19202	GM_M43_B1_C05_MR	g3777527	BLASTX	772	9e-75	93	(AF053008) gag-pol polyprotein [Glycine max]
19203	GM_M43_B1_C09_MF	g1769897	BLASTX	334	3e-32	66	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19204	GM_M43_B1_E02_MR	g3142328	BLASTN	905	5e-34	90	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19205	GM_M43_B1_E03_MR	g3097320	BLASTN	501	1e-15	69	Glycine max gene for Bd 30K, complete cds
19206	GM_M43_B1_E09_MR	g507910	BLASTN	468	1e-14	74	Glycine max BSR-101 satellite SB92 genomic sequence.
19207	GM_M43_B1_E10_MF	g2842524	BLASTX	126	6e-13	36	(AL021746) retrotransposable element [Schizosaccharomyces pombe]
19208	GM_M43_B1_E10_MR	g2760844	BLASTX	178	4e-12	78	(AC003105) hypothetical protein [Arabidopsis thaliana]
19209	GM_M43_B1_E11_MR	g3283026	BLASTX	168	9e-11	30	putative transposase [Arabidopsis thaliana]
19210	GM_M43_B1_F02_MF	g1666236	BLASTX	195	2e-14	30	(U76261) unknown [Hordeum vulgare]
19211	GM_M43_B1_F04_MR	g2832625	BLASTX	250	1e-19	78	(AL021711) putative protein [Arabidopsis thaliana]
19212	GM_M43_B1_F05_MR	g3097320	BLASTN	429	2e-12	72	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19213	GM_M43_B1_F07_MR	g130582	BLASTX	346	2e-29	49	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
19214	GM_M43_B1_F12_MR	g1785729	BLASTN	325	2e-14	67	A.thaliana mitochondrial genome, part B
19215	GM_M43_B1_G01_MR	g3142328	BLASTN	668	3e-23	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19216	GM_M43_B1_G03_MF	g1769897	BLASTX	376	6e-34	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19217	GM_M43_B1_G04_MF	g133913	BLASTX	525	9e-50	76	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 gi 70858 pir R3PM2 ribosomal protein S2 - garden pea chloroplast gi 12138 (X03912) ORF (aa 1-236) with homology to ribosomal protein S2; pid:g12138 [Pisum sativum]
19218	GM_M43_B1_G04_MR	g11748	BLASTN	1586	4e-66	89	Nicotiana debneyi chloroplast DNA for tRNA-Ile and ribosomal protein L2
19219	GM_M43_B1_G06_MR	g2792220	BLASTX	293	2e-24	38	(AF032688) NBS-LRR type resistance protein [Oryza sativa]
19220	GM_M43_B1_G07_MR	g3810595	BLASTX	461	1e-41	50	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
19221	GM_M43_B1_G08_MF	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19222	GM_M43_B1_G08_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19223	GM_M43_B1_G11_MF	g3777527	BLASTX	167	1e-17	40	(AF053008) gag-pol polyprotein [Glycine max]
19224	GM_M43_B1_G11_MR	g1769898	BLASTX	239	5e-20	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19225	GM_M43_B2_A03_MR	g2522226	BLASTN	440	6e-13	66	Vicia faba mRNA for reverse transcriptase-like protein, complete cds
19226	GM_M43_B2_A07_MR	g18559	BLASTN	436	1e-12	74	G.max gene for catalase
19227	GM_M43_B2_A10_MF	g2052034	BLASTN	410	2e-11	64	Human DNA sequence from PAC 450C20 on chromosome X
19228	GM_M43_B2_A11_MF	g3142328	BLASTN	1022	2e-39	75	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19229	GM_M43_B2_A11_MR	g478084	BLASTX	147	1e-09	53	reverse transcriptase (copia-like retrotransposon) - Liriodendron tulipifera (fragment) gi 168310 (M94479) reverse transcriptase [Liriodendron tulipifera]
19230	GM_M43_B2_B04_MF	g507910	BLASTN	650	9e-23	84	Glycine max BSR-101 satellite SB92 genomic sequence.
19231	GM_M43_B2_B10_MR	g1673405	BLASTN	675	8e-24	76	C.annuum mRNA for xanthophyll epoxidase.
19232	GM_M43_B2_C01_MR	g2969943	BLASTN	411	2e-11	71	Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS
19233	GM_M43_B2_C10_MF	g507910	BLASTN	397	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19234	GM_M43_B2_C10_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19235	GM_M43_B2_D04_MR	g3097320	BLASTN	691	3e-24	72	Glycine max gene for Bd 30K, complete cds
19236	GM_M43_B2_D10_MF	g421955	BLASTX	180	2e-12	44	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
19237	GM_M43_B2_E08_MF	g2809247	BLASTX	159	7e-10	27	(AC002560) F21B7.16 [Arabidopsis thaliana]
19238	GM_M43_B2_E09_MF	g4063760	BLASTX	461	1e-41	65	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19239	GM_M43_B2_E12_MR	g133916	BLASTX	140	8e-09	57	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 gi 70857 pir R3SP2 ribosomal protein S2 - spinach chloroplast gi 12256 (X05916) rps2 protein (AA 1-236) [Spinacia oleracea]
19240	GM_M43_B2_F05_MR	g4092470	BLASTN	512	2e-16	74	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
19241	GM_M43_B2_F07_MF	g18559	BLASTN	479	1e-14	67	G.max gene for catalase
19242	GM_M43_B2_F07_MR	g3777527	BLASTX	139	3e-11	58	(AF053008) gag-pol polyprotein [Glycine max]
19243	GM_M43_B2_F09_MR	g1167523	BLASTX	222	4e-16	43	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
19244	GM_M43_B2_F12_MR	g1142701	BLASTN	1086	9e-43	85	Glycine max satellite STR120-A.3.
19245	GM_M43_B2_G01_MF	g3142328	BLASTN	868	2e-32	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19246	GM_M43_B2_G03_MR	g3449334	BLASTN	364	2e-09	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYH9, complete sequence [Arabidopsis thaliana]
19247	GM_M43_B2_G05_MF	g1946279	BLASTX	309	7e-27	42	(Y12433) polyprotein; reverse transcriptase, RNase H [pineapple bacilliform virus]
19248	GM_M43_B2_G06_MR	g1769899	BLASTX	198	4e-15	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19249	GM_M43_B2_G10_MR	g2995405	BLASTX	176	3e-13	67	(Y12432) polyprotein [Ananas comosus]
19250	GM_M43_B2_G12_MF	g2995405	BLASTX	485	1e-44	61	(Y12432) polyprotein [Ananas comosus]
19251	GM_M43_B2_H06_MR	g629693	BLASTX	325	1e-28	58	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
19252	GM_M43_B2_H09_MF	g421955	BLASTX	180	2e-12	44	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
19253	GM_M44_A1_A02_MR	g3097320	BLASTN	758	2e-41	76	Glycine max gene for Bd 30K, complete cds
19254	GM_M44_A1_A11_MR	g3777527	BLASTX	360	1e-34	76	(AF053008) gag-pol polyprotein [Glycine max]
19255	GM_M44_A1_B02_MR	g905361	BLASTX	119	6e-12	47	(U22103) gag-protease polyprotein [Glycine max]
19256	GM_M44_A1_B04_MR	g3097320	BLASTN	1085	7e-50	79	Glycine max gene for Bd 30K, complete cds
19257	GM_M44_A1_B09_MR	g3426334	BLASTN	357	4e-09	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
19258	GM_M44_A1_C03_MF	g3738114	BLASTN	376	6e-10	60	Homo sapiens chromosome Y, clone 264,M,20, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19259	GM_M44_A1_C07_MR	g3582335	BLASTX	379	1e-33	72	(AC005496) unknown protein [Arabidopsis thaliana]
19260	GM_M44_A1_C08_MR	g3097320	BLASTN	795	6e-45	77	Glycine max gene for Bd 30K, complete cds
19261	GM_M44_A1_D02_MR	g2764526	BLASTN	605	3e-20	67	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
19262	GM_M44_A1_D04_MF	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19263	GM_M44_A1_D04_MR	g507910	BLASTN	348	4e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19264	GM_M44_A1_D07_MF	g130582	BLASTX	208	3e-29	55	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
19265	GM_M44_A1_D09_MR	g3522938	BLASTX	158	4e-10	50	(AC004411) unknown protein [Arabidopsis thaliana]
19266	GM_M44_A1_D11_MR	g4063760	BLASTX	274	1e-21	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19267	GM_M44_A1_D12_MR	g3142379	BLASTX	197	3e-14	58	(AF053008) envelope-like [Glycine max]
19268	GM_M44_A1_E03_MF	g4115536	BLASTX	229	2e-18	50	(AB012115) UDP-glycose:flavonoid glycosyltransferase [Vigna mungo]
19269	GM_M44_A1_E12_MF	g13773	BLASTN	391	3e-11	61	Torulopsis glabrata mitochondrial genes for tRNAs -Tyr, -Asn, -Ala, -Ile -Trp (from Var1-LrRNA intergenic region) >gi 343959 gb M11906 YSLMTIG09 Yeast (T.glabrata) mitochondrial DNA between var1 and L rRNA genes.
19270	GM_M44_A1_F02_MF	g1769898	BLASTX	232	9e-18	43	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19271	GM_M44_A1_F05_MF	g3212861	BLASTX	165	5e-11	43	(AC004005) unknown protein [Arabidopsis thaliana]
19272	GM_M44_A1_F07_MF	g507910	BLASTN	427	1e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19273	GM_M44_A1_G05_MF	g425194	BLASTX	134	1e-11	51	(L26243) heat shock protein [Spinacia oleracea] gi 2660772 (AF034618) cytosolic heat shock 70 protein [Spinacia oleracea]
19274	GM_M44_A1_G09_MF	g3142328	BLASTN	1535	1e-62	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19275	GM_M44_A1_G09_MR	g3097320	BLASTN	606	2e-20	74	Glycine max gene for Bd 30K, complete cds
19276	GM_M44_A1_H06_MR	g170080	BLASTN	416	7e-12	69	Soybean seed lectin gene transposable element tgm1.
19277	GM_M44_A1_H09_MR	g3777527	BLASTX	155	6e-11	50	(AF053008) gag-pol polyprotein [Glycine max]
19278	GM_M44_A2_C02_MR	g2462134	BLASTX	114	3e-10	29	(Y13368) reverse transcriptase [Beta vulgaris]
19279	GM_M44_A2_C07_MR	g4063760	BLASTX	167	1e-17	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19280	GM_M44_A2_D11_MR	g629693	BLASTX	295	2e-25	60	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
19281	GM_M44_A2_E11_MR	g3777527	BLASTX	358	2e-60	95	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19282	GM_M44_A2_F09_MR	g3142328	BLASTN	2085	5e-88	95	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19283	GM_M44_A2_G03_MR	g3845197	BLASTN	308	6e-10	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
19284	GM_M44_A2_G07_MR	g1588265	BLASTX	181	4e-12	80	100RNP protein [Spinacia oleracea]
19285	GM_M44_A2_G09_MR	g2264320	BLASTN	601	4e-20	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX110, complete sequence [Arabidopsis thaliana]
19286	GM_M44_A2_G11_MR	g226407	BLASTX	268	7e-38	58	retrotransposon del1-46 [Lilium henryi]
19287	GM_M44_A2_H12_MR	g2335097	BLASTX	179	8e-12	62	(AC002339) putative receptor-like protein kinase [Arabidopsis thaliana]
19288	GM_M44_B1_A10_MF	g2529683	BLASTX	467	1e-43	70	(AC002535) unknown protein [Arabidopsis thaliana]
19289	GM_M44_B1_A12_MF	g3676469	BLASTX	161	4e-10	34	(AF053884) (R)-(+)-mandelonitrile lyase isoform MDL4 precursor [Prunus serotina] gi 3676471 (AF053885) (R)-(+)-mandelonitrile lyase isoform MDL4 precursor [Prunus serotina]
19290	GM_M44_B1_C04_MF	g477280	BLASTX	157	9e-10	83	mitochondrial processing peptidase (EC 3.4.99.41) 55K protein precursor - potato gi 410633 bbs 136740 cytochrome c reductase-processing peptidase subunit I, MPP subunit I, P55 [potatoes, var. Marfona, tuber, Peptide Mitochondrial, 534 aa]
19291	GM_M44_B1_D01_MF	g18559	BLASTN	880	7e-33	74	G.max gene for catalase
19292	GM_M44_B1_E03_MF	g2708743	BLASTX	218	1e-15	34	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
19293	GM_M44_B1_E07_MF	g507910	BLASTN	626	1e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.
19294	GM_M44_B1_E10_MF	g170606	BLASTN	759	8e-28	69	Broad bean (V.faba) BamHI repetitive element, 1750 bp family.
19295	GM_M44_B1_F08_MF	g2832625	BLASTX	158	8e-10	47	(AL021711) putative protein [Arabidopsis thaliana]
19296	GM_M44_B1_G04_MF	g3510336	BLASTN	435	1e-12	65	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K18J17, complete sequence [Arabidopsis thaliana]
19297	GM_M44_B1_G08_MF	g3860271	BLASTX	210	4e-15	31	(AC005824) putative selenium-binding protein [Arabidopsis thaliana]
19298	GM_M44_B1_G09_MF	g2522230	BLASTX	210	2e-16	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
19299	GM_M44_B1_H02_MF	g18695	BLASTN	508	4e-16	75	Soybean nodulin 22 gene
19300	GM_M44_B1_H03_MF	g2073447	BLASTN	362	3e-09	65	L.japonicus gln1, pge1 & krm genes
19301	GM_M44_B1_H04_MF	g99755	BLASTX	342	8e-30	47	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19302	GM_M44_B2_A10_MF	g507910	BLASTN	545	5e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
19303	GM_M44_B2_B07_MF	g3645899	BLASTX	183	2e-15	54	(U68408) 5' end not determined experimentally [Zea mays]
19304	GM_M44_B2_C01_MF	g3142379	BLASTX	238	5e-22	85	(AF053008) envelope-like [Glycine max]
19305	GM_M44_B2_C03_MR	g100484	BLASTX	313	2e-26	58	hypothetical protein - garden snapdragon
19306	GM_M44_B2_D02_MF	g3645899	BLASTX	156	3e-09	43	(U68408) 5' end not determined experimentally [Zea mays]
19307	GM_M44_B2_D05_MR	g3142328	BLASTN	772	5e-28	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19308	GM_M44_B2_E02_MF	g2104945	BLASTN	1187	8e-47	83	Glycine max copia-like retrotransposon Tgmr, complete sequence
19309	GM_M44_B2_E12_MF	g3097320	BLASTN	584	2e-19	80	Glycine max gene for Bd 30K, complete cds
19310	GM_M44_B2_F07_MF	g422418	BLASTX	159	1e-09	36	pol protein - fruit fly (Drosophila ananassae) transposon Tom (fragment) gi 394705 (Z24451) pol protein [Drosophila ananassae]
19311	GM_M44_B2_F12_MF	g2264317	BLASTN	445	5e-13	77	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MUG13, complete sequence [Arabidopsis thaliana]
19312	GM_M44_B2_G01_MF	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19313	GM_M44_B2_G06_MF	g4063760	BLASTX	168	2e-10	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19314	GM_M44_B2_G07_MF	g2129618	BLASTX	174	3e-11	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19315	GM_M44_B2_G10_MR	g3599418	BLASTN	1194	4e-47	86	Glycine max alternative oxidase precursor (Aox1) gene, nuclear gene encoding mitochondrial protein, complete cds
19316	GM_M44_B2_G12_MF	g4050011	BLASTN	477	1e-14	68	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
19317	GM_M44_B2_H04_MF	g3763850	BLASTN	457	1e-13	82	Glycine max GmENOD93 gene for early nodulin, complete cds
19318	GM_M44_B2_H06_MF	g3063445	BLASTX	186	2e-12	46	(AC003981) F22O13.7 [Arabidopsis thaliana]
19319	GM_M44_B2_H08_MF	g3142328	BLASTN	562	2e-18	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19320	GM_M45_A1_A05_MF	g4063770	BLASTX	189	6e-13	41	(AB004906) transposase [Ipomoea purpurea]
19321	GM_M45_A1_A07_MR	g3777527	BLASTX	382	4e-33	87	(AF053008) gag-pol polyprotein [Glycine max]
19322	GM_M45_A1_A10_MF	g3810596	BLASTX	278	2e-22	52	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19323	GM_M45_A1_D04_MF	g133917	BLASTX	160	4e-11	93	CHLOROPLAST 30S RIBOSOMAL PROTEIN S2 gi 70856 pir R3NT2 ribosomal protein S2 - common tobacco chloroplast gi 11814 (Z00044) ribosomal protein S2 [Nicotiana tabacum] gi 225274 prf 1211235J ribosomal protein S2 [Nicotiana tabacum]
19324	GM_M45_A1_D11_MR	g3097320	BLASTN	697	2e-24	76	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19325	GM_M45_A1_E02_MF	g3142328	BLASTN	736	2e-26	87	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19326	GM_M45_A1_E07_MF	g3319351	BLASTX	86	8e-10	47	(AF077407) contains similarity to reverse transcriptases (PFam: rvt.hmm, score: 116.22) [Arabidopsis thaliana]
19327	GM_M45_A1_E09_MF	g18559	BLASTN	756	3e-27	75	G.max gene for catalase
19328	GM_M45_A1_F02_MF	g3142328	BLASTN	736	2e-26	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19329	GM_M45_A1_G02_MF	g3142328	BLASTN	1485	2e-60	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19330	GM_M45_A2_A08_MR	g3746069	BLASTX	161	1e-10	58	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
19331	GM_M45_A2_B07_MF	g4063760	BLASTX	401	3e-35	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19332	GM_M45_A2_B09_MF	g322662	BLASTX	147	8e-14	82	S-receptor kinase-related protein - Chinese kale gi 17915 (Z18883) S-receptor kinase related protein [Brassica oleracea]
19333	GM_M45_A2_C06_MR	g507910	BLASTN	472	1e-14	78	Glycine max BSR-101 satellite SB92 genomic sequence.
19334	GM_M45_A2_C08_MF	g1769898	BLASTX	334	9e-29	55	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19335	GM_M45_A2_C08_MR	g1769898	BLASTX	327	5e-28	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19336	GM_M45_A2_C10_MF	g2464905	BLASTX	171	2e-20	64	(Z99708) minor allergen [Arabidopsis thaliana]
19337	GM_M45_A2_D02_MR	g3510505	BLASTX	212	4e-15	35	(AF030881) pol polyprotein [Fugu rubripes]
19338	GM_M45_A2_D04_MF	g3645899	BLASTX	270	6e-28	66	(U68408) 5' end not determined experimentally [Zea mays]
19339	GM_M45_A2_D05_MF	g507910	BLASTN	586	7e-20	81	Glycine max BSR-101 satellite SB92 genomic sequence.
19340	GM_M45_A2_D06_MF	g507910	BLASTN	424	2e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19341	GM_M45_A2_D10_MF	g18559	BLASTN	519	2e-16	72	G.max gene for catalase
19342	GM_M45_A2_F10_MF	g3250687	BLASTX	198	4e-15	37	(AL024486) putative LTR retrotransposon (fragment) [Arabidopsis thaliana]
19343	GM_M45_A2_G03_MF	g3845197	BLASTN	375	6e-10	66	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
19344	GM_M45_A2_G05_MF	g507910	BLASTN	500	6e-16	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19345	GM_M45_A2_G08_MF	g507910	BLASTN	419	3e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19346	GM_M45_A2_G09_MR	g3645899	BLASTX	140	2e-09	38	(U68408) 5' end not determined experimentally [Zea mays]
19347	GM_M45_B1_B02_MF	g3097320	BLASTN	492	3e-15	73	Glycine max gene for Bd 30K, complete cds
19348	GM_M45_B1_B03_MR	g2522230	BLASTX	108	2e-14	37	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
19349	GM_M45_B1_B04_MR	g3810596	BLASTX	245	8e-19	43	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19350	GM_M45_B1_B05_MF	g507910	BLASTN	653	7e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19351	GM_M45_B1_C02_MR	g2924771	BLASTX	192	9e-14	47	(AC002334) putative dimethylaniline monooxygenase [Arabidopsis thaliana]
19352	GM_M45_B1_C06_MF	g3176707	BLASTX	175	4e-12	58	(AC002392) putative proline-rich protein APG [Arabidopsis thaliana]
19353	GM_M45_B1_C08_MF	g507910	BLASTN	481	4e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19354	GM_M45_B1_C12_MR	g18559	BLASTN	690	3e-24	74	G.max gene for catalase
19355	GM_M45_B1_D01_MF	g2264302	BLASTN	430	2e-12	63	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAC12, complete sequence [Arabidopsis thaliana]
19356	GM_M45_B1_D02_MR	g4063760	BLASTX	157	3e-09	49	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19357	GM_M45_B1_D09_MF	g226407	BLASTX	238	5e-23	41	retrotransposon del1-46 [Lilium henryi]
19358	GM_M45_B1_E01_MR	g3860246	BLASTX	143	1e-08	37	(AC005824) putative reverse-transcriptase protein [Arabidopsis thaliana]
19359	GM_M45_B1_E03_MF	g4006831	BLASTX	266	7e-21	44	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
19360	GM_M45_B1_E08_MF	g905361	BLASTX	558	3e-53	91	(U22103) gag-protease polyprotein [Glycine max]
19361	GM_M45_B1_F01_MR	g1769899	BLASTX	305	2e-26	67	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19362	GM_M45_B1_F02_MR	g1076545	BLASTX	233	8e-19	85	guanine nucleotide regulatory protein - fava bean gi 547478 (Z37503) guanine nucleotide regulatory protein [Vicia faba] gi 1098297 prf 2115367E small GTP-binding protein [Vicia faba]
19363	GM_M45_B1_F03_MF	g507910	BLASTN	370	4e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19364	GM_M45_B1_F03_MR	g507910	BLASTN	345	6e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19365	GM_M45_B1_F05_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19366	GM_M45_B1_F10_MF	g1256945	BLASTN	369	1e-09	65	Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete transcribed region and flanks.
19367	GM_M45_B1_F11_MF	g82207	BLASTX	234	3e-17	74	hypothetical protein 1708 - common tobacco chloroplast
19368	GM_M45_B1_F11_MR	g18559	BLASTN	769	8e-28	72	G.max gene for catalase
19369	GM_M45_B1_G02_MF	g3142328	BLASTN	653	1e-22	71	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19370	GM_M45_B1_G04_MR	g18768	BLASTN	353	1e-09	65	Soybean Tgm6 transposable element 3' end
19371	GM_M45_B1_G11_MF	g4038056	BLASTX	265	5e-21	38	(AC005897) putative transposon [Arabidopsis thaliana]
19372	GM_M45_B1_H02_MF	g3912919	BLASTX	150	8e-09	85	(AF001308) hypothetical protein [Arabidopsis thaliana]
19373	GM_M45_B1_H03_MF	g2781345	BLASTX	231	2e-17	69	(AC003113) F24O1.2 [Arabidopsis thaliana]
19374	GM_M45_B1_H09_MF	g2462134	BLASTX	260	5e-21	46	(Y13368) reverse transcriptase [Beta vulgaris]
19375	GM_M45_B1_H09_MR	g2351060	BLASTX	311	4e-27	78	(AB006660) sucrose-phosphate synthase [Citrus unshiu]
19376	GM_M45_B1_H10_MF	g3142328	BLASTN	1150	4e-45	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19377	GM_M45_B1_H12_MR	g2827663	BLASTX	188	6e-13	39	(AL021637) membrane-associated salt-inducible-like protein [Arabidopsis thaliana]
19378	GM_M45_B2_A01_MF	g3600044	BLASTX	175	1e-12	49	(AF080119) contains similarity to proteases [Arabidopsis thaliana]
19379	GM_M45_B2_A05_MR	g975703	BLASTN	722	1e-25	80	P.sativum GR gene
19380	GM_M45_B2_A09_MF	g507910	BLASTN	430	8e-13	77	Glycine max BSR-101 satellite SB92 genomic sequence.
19381	GM_M45_B2_A09_MR	g507910	BLASTN	412	5e-12	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19382	GM_M45_B2_B05_MF	g507910	BLASTN	395	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19383	GM_M45_B2_B07_MF	g3377848	BLASTX	258	3e-21	44	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
19384	GM_M45_B2_B08_MR	g4006831	BLASTX	192	5e-13	27	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
19385	GM_M45_B2_B10_MR	g13581	BLASTN	338	4e-09	62	Yeast mitochondrial ori(o) repeat unit of petite mutant 3 (petite strain a-10/3/2/B11) >gi 559270 gb L36894 YSCMTCG10 Saccharomyces cerevisiae mitochondrion DNA segment.
19386	GM_M45_B2_C01_MF	g507910	BLASTN	368	5e-10	69	Glycine max BSR-101 satellite SB92 genomic sequence.
19387	GM_M45_B2_C01_MR	g507910	BLASTN	362	9e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19388	GM_M45_B2_C04_MR	g421955	BLASTX	146	8e-09	50	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
19389	GM_M45_B2_C05_MF	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19390	GM_M45_B2_C05_MR	g507910	BLASTN	410	6e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19391	GM_M45_B2_C07_MR	g4063760	BLASTX	488	1e-44	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19392	GM_M45_B2_D03_MF	g507910	BLASTN	436	4e-13	74	Glycine max BSR-101 satellite SB92 genomic sequence.
19393	GM_M45_B2_D06_MF	g3777527	BLASTX	206	2e-14	33	(AF053008) gag-pol polyprotein [Glycine max]
19394	GM_M45_B2_D10_MF	g3283026	BLASTX	169	8e-11	40	putative transposase [Arabidopsis thaliana]
19395	GM_M45_B2_D11_MR	g2129618	BLASTX	160	9e-10	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19396	GM_M45_B2_E05_MR	g2997694	BLASTX	172	2e-12	42	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
19397	GM_M45_B2_F04_MF	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19398	GM_M45_B2_F04_MR	g507910	BLASTN	357	2e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19399	GM_M45_B2_F08_MF	g1769896	BLASTN	370	1e-09	72	A.thaliana lectin receptor kinase gene
19400	GM_M45_B2_F12_MR	g3777527	BLASTX	167	3e-10	32	(AF053008) gag-pol polyprotein [Glycine max]
19401	GM_M45_B2_G03_MF	g629693	BLASTX	205	2e-15	53	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
19402	GM_M45_B2_G03_MR	g3142379	BLASTX	117	8e-13	67	(AF053008) envelope-like [Glycine max]
19403	GM_M45_B2_G07_MR	g3859610	BLASTN	528	8e-17	65	Arabidopsis thaliana BAC T9E19

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19404	GM_M45_B2_H06_MF	g2129618	BLASTX	200	5e-14	40	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19405	GM_M45_B2_H07_MF	g2245104	BLASTX	166	4e-10	41	(Z97343) LTR retrotransposon [Arabidopsis thaliana]
19406	GM_M45_B2_H08_MR	g507910	BLASTN	555	2e-18	81	Glycine max BSR-101 satellite SB92 genomic sequence.
19407	GM_M45_B2_H10_MF	g18559	BLASTN	736	2e-26	73	G.max gene for catalase
19408	GM_M45_B2_H10_MR	g1040717	BLASTN	410	2e-12	63	D.polychroa microsatellite sequence (clone Dp ch1 F3)
19409	GM_M45_B2_H11_MR	g2979554	BLASTX	163	1e-09	38	(AC003680) CDC4 like protein [Arabidopsis thaliana]
19410	GM_M45_B2_H12_MF	g905361	BLASTX	158	2e-14	32	(U22103) gag-protease polyprotein [Glycine max]
19411	GM_M46_A1_B04_MF	g3176798	BLASTN	398	8e-12	65	Homo sapiens allele 14 fragile site locus (FRA10B) minisatellite, 5' sequence
19412	GM_M46_A1_C04_MF	g4063760	BLASTX	223	9e-26	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19413	GM_M46_A1_D11_MF	g1769898	BLASTX	266	4e-24	57	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19414	GM_M46_A1_F03_MF	g18559	BLASTN	760	2e-27	74	G.max gene for catalase
19415	GM_M46_A1_G06_MF	g4063760	BLASTX	177	1e-25	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19416	GM_M46_A1_H05_MF	g1076313	BLASTX	194	9e-22	56	cyclin delta-3 - Arabidopsis thaliana
19417	GM_M46_A1_H08_MF	g2443320	BLASTX	198	2e-23	45	(D85597) polyprotein [Oryza australiensis]
19418	GM_M46_A2_B01_MR	g507910	BLASTN	409	7e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19419	GM_M46_A2_B05_MR	g3142328	BLASTN	1325	4e-53	91	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19420	GM_M46_A2_B06_MR	g536873	BLASTX	313	7e-26	43	(M34549) POL3 gene product [Saccharomyces cerevisiae]
19421	GM_M46_A2_B11_MR	g1171577	BLASTX	199	6e-26	51	(X95343) hypersensitivity-related gene [Nicotiana tabacum]
19422	GM_M46_A2_C12_MF	g2104945	BLASTN	516	2e-16	79	Glycine max copia-like retrotransposon Tgmr, complete sequence
19423	GM_M46_A2_D04_MR	g1769898	BLASTX	525	9e-50	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19424	GM_M46_A2_D08_MF	g507910	BLASTN	400	2e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19425	GM_M46_A2_D09_MR	g3097320	BLASTN	709	5e-25	69	Glycine max gene for Bd 30K, complete cds
19426	GM_M46_A2_D10_MR	g1666236	BLASTX	211	3e-16	31	(U76261) unknown [Hordeum vulgare]
19427	GM_M46_A2_D12_MF	g3894387	BLASTX	275	5e-22	47	(AF053995) Hcr2-0B [Lycopersicon esculentum]
19428	GM_M46_A2_F02_MR	g3777527	BLASTX	704	2e-67	94	(AF053008) gag-pol polyprotein [Glycine max]
19429	GM_M46_A2_F04_MR	g2522228	BLASTX	460	7e-43	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
19430	GM_M46_A2_F10_MF	g170605	BLASTN	471	1e-14	62	Broad bean (V.faba) BamHI repetitive element, 1500 bp family.
19431	GM_M46_A2_G01_MR	g3377848	BLASTX	108	1e-11	42	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
19432	GM_M46_A2_G02_MR	g507910	BLASTN	628	9e-22	85	Glycine max BSR-101 satellite SB92 genomic sequence.
19433	GM_M46_A2_G04_MR	g1840106	BLASTN	433	2e-13	63	Human fragile site locus (FRA16B) minisatellite repeat
19434	GM_M46_A2_G06_MR	g20749	BLASTN	592	1e-20	74	Pea PSU2 gene for U2 snRNA

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19435	GM_M46_A2_G07_MF	g3650039	BLASTX	260	1e-20	42	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
19436	GM_M46_A2_G09_MF	g2696018	BLASTN	447	4e-13	71	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXC9
19437	GM_M46_A2_G09_MR	g18559	BLASTN	808	1e-29	70	G.max gene for catalase
19438	GM_M46_A2_G12_MR	g170029	BLASTN	382	3e-10	60	Glycine max cv. Dare nodulin 26 gene fragment.
19439	GM_M46_A2_H03_MF	g4063760	BLASTX	165	3e-11	39	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19440	GM_M46_A2_H08_MF	g4063760	BLASTX	262	1e-20	43	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19441	GM_M46_A2_H08_MR	g3273825	BLASTN	352	6e-09	63	Glycine max nodule-enhanced malate dehydrogenase (Mdh) gene, promoter region
19442	GM_M46_A2_H11_MR	g3123908	BLASTX	405	5e-37	54	(AF038392) pre-mRNA splicing factor [Homo sapiens]
19443	GM_M46_B1_A02_MR	g3810596	BLASTX	208	4e-23	35	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19444	GM_M46_B1_A05_MR	g3097320	BLASTN	984	2e-37	81	Glycine max gene for Bd 30K, complete cds
19445	GM_M46_B1_A06_MR	g3142328	BLASTN	954	3e-36	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19446	GM_M46_B1_A09_MR	g3985958	BLASTN	447	4e-13	65	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MZN1, complete sequence [Arabidopsis thaliana]
19447	GM_M46_B1_B01_MR	g3142328	BLASTN	964	1e-36	72	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19448	GM_M46_B1_B05_MR	g4103987	BLASTX	265	4e-29	85	(AF030516) 5,10-methylenetetrahydrofolate dehydrogenase-5,10-methenyltetrahydrofolate cyclohydrolase [Pisum sativum]
19449	GM_M46_B1_B10_MR	g3779021	BLASTX	236	1e-18	39	(AC005171) putative reverse transcriptase [Arabidopsis thaliana]
19450	GM_M46_B1_C05_MR	g18559	BLASTN	1082	5e-42	77	G.max gene for catalase
19451	GM_M46_B1_D09_MR	g4063760	BLASTX	364	2e-31	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19452	GM_M46_B1_E02_MR	g3097320	BLASTN	482	9e-15	68	Glycine max gene for Bd 30K, complete cds
19453	GM_M46_B1_E03_MR	g18559	BLASTN	999	3e-38	74	G.max gene for catalase
19454	GM_M46_B1_E04_MR	g130592	BLASTX	203	4e-28	48	ENZYMATIC POLYPROTEIN [CONTAINS: ASPARTIC PROTEASE ; ENDONUCLEASE; REVERSE TRANSCRIPTASE] >gi 75491 pir QQCV5 hypothetical protein 5 - cauliflower mosaic virus (strains Strasbourg, CM1841 and D/H) >gi 58826 (V00141) reading frame (V) [Cauliflower mosaic virus]
19455	GM_M46_B1_E07_MR	g507910	BLASTN	366	6e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19456	GM_M46_B1_E10_MR	g1706082	BLASTX	172	6e-25	68	serine carboxypeptidase II-3 precursor (CP-MII.3) gi 629787 pir S44191 serine-type carboxypeptidase (EC 3.4.16.1) II-3 - barley gi 619350 bbs 153536 CP-MII.3=serine carboxypeptidase [Hordeum vulgare=barley, cv. Alexis, aleurone, Peptide, 516 aa] gi 474392 (X78877) serine carboxylase II-3 [Hordeum vulgare]
19457	GM_M46_B1_F02_MR	g18559	BLASTN	328	2e-10	76	G.max gene for catalase
19458	GM_M46_B1_F07_MR	g4092470	BLASTN	439	9e-13	63	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
19459	GM_M46_B1_G06_MR	g3758836	BLASTN	298	4e-11	65	Plasmodium falciparum MAL3P6, complete sequence [Plasmodium falciparum]
19460	GM_M46_B1_G10_MR	g2708743	BLASTX	191	8e-13	36	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
19461	GM_M46_B1_G12_MR	g4063760	BLASTX	298	2e-50	61	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19462	GM_M46_B1_H01_MR	g3097320	BLASTN	414	1e-11	76	Glycine max gene for Bd 30K, complete cds
19463	GM_M46_B1_H03_MR	g4038056	BLASTX	310	8e-26	41	(AC005897) putative transposon [Arabidopsis thaliana]
19464	GM_M46_B1_H04_MR	g507910	BLASTN	610	6e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
19465	GM_M46_B1_H12_MR	g2995405	BLASTX	463	1e-43	58	(Y12432) polyprotein [Ananas comosus]
19466	GM_M46_B2_A02_MF	g170082	BLASTN	360	6e-10	83	Soybean Met-i-tRNA gene.
19467	GM_M46_B2_B01_MF	g3319366	BLASTX	137	1e-14	53	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
19468	GM_M46_B2_B02_MR	g3777527	BLASTX	693	5e-69	95	(AF053008) gag-pol polyprotein [Glycine max]
19469	GM_M46_B2_B04_MR	g3097320	BLASTN	531	5e-17	79	Glycine max gene for Bd 30K, complete cds
19470	GM_M46_B2_B05_MR	g4115365	BLASTX	120	1e-10	35	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
19471	GM_M46_B2_B08_MF	g1710663	BLASTX	152	9e-09	60	Putative DNA-directed RNA polymerase III 130 KD polypeptide (RNA polymerase III subunit 2) gi 1204209 gnl PID e223661 (Z69727) putative DNA-directed RNA polymerase III 130 kd subunit [Schizosaccharomyces pombe]
19472	GM_M46_B2_B08_MR	g1899025	BLASTX	171	2e-11	73	(U28215) hexokinase 2 [Arabidopsis thaliana] gi 3687232 (AC005169) hexokinase [Arabidopsis thaliana]
19473	GM_M46_B2_B09_MR	g4006828	BLASTX	164	3e-10	31	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
19474	GM_M46_B2_B10_MR	g3355474	BLASTX	195	4e-16	68	(AC004218) unknown protein [Arabidopsis thaliana]
19475	GM_M46_B2_C02_MR	g4063770	BLASTX	87	1e-10	29	(AB004906) transposase [Ipomoea purpurea]
19476	GM_M46_B2_C03_MR	g1174162	BLASTX	287	2e-32	96	(U44976) ubiquitin-conjugating enzyme [Arabidopsis thaliana]
19477	GM_M46_B2_C05_MF	g905361	BLASTX	205	8e-15	35	(U22103) gag-protease polyprotein [Glycine max]
19478	GM_M46_B2_C08_MR	g3097320	BLASTN	386	2e-10	71	Glycine max gene for Bd 30K, complete cds

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19479	GM_M46_B2_C09_MR	g507910	BLASTN	394	3e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19480	GM_M46_B2_D01_MR	g2213582	BLASTX	172	1e-11	43	(AC000348) T7N9.2 [Arabidopsis thaliana]
19481	GM_M46_B2_D04_MF	g507910	BLASTN	566	6e-19	79	Glycine max BSR-101 satellite SB92 genomic sequence.
19482	GM_M46_B2_D04_MR	g507910	BLASTN	562	9e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
19483	GM_M46_B2_D05_MR	g3269282	BLASTX	261	2e-20	38	(AL030978) putative protein [Arabidopsis thaliana]
19484	GM_M46_B2_D08_MF	g2961349	BLASTX	199	9e-14	45	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
19485	GM_M46_B2_D12_MR	g507910	BLASTN	340	9e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19486	GM_M46_B2_E07_MF	g3319359	BLASTN	367	1e-09	64	Arabidopsis thaliana BAC T7M24
19487	GM_M46_B2_E07_MR	g3746069	BLASTX	186	5e-15	47	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
19488	GM_M46_B2_E11_MR	g508826	BLASTN	471	3e-14	63	Drosophila melanogaster Oregon-R mitochondrial A+T region.
19489	GM_M46_B2_F02_MF	g3810596	BLASTX	141	2e-13	50	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19490	GM_M46_B2_F02_MR	g1480927	BLASTN	1896	4e-80	94	Glycine max cdc2 protein kinase ((cdc2(1)) nonprocessed pseudogene
19491	GM_M46_B2_F03_MR	g507910	BLASTN	404	1e-11	77	Glycine max BSR-101 satellite SB92 genomic sequence.
19492	GM_M46_B2_F08_MR	g507910	BLASTN	393	4e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19493	GM_M46_B2_G02_MF	g3935164	BLASTX	296	6e-24	44	(AC004557) F17L21.7 [Arabidopsis thaliana]
19494	GM_M46_B2_G04_MF	g310932	BLASTN	351	9e-10	75	Nicotiana tabacum ribosomal protein L17 mRNA, complete cds.
19495	GM_M46_B2_G07_MF	g507910	BLASTN	372	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19496	GM_M46_B2_G07_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19497	GM_M46_B2_G12_MR	g4092470	BLASTN	369	1e-09	64	Arabidopsis thaliana BAC T24G23 from chromosome IV near 21 cM, complete sequence [Arabidopsis thaliana]
19498	GM_M46_B2_H07_MF	g3777527	BLASTX	151	2e-17	44	(AF053008) gag-pol polyprotein [Glycine max]
19499	GM_M46_B2_H09_MR	g3645899	BLASTX	245	1e-26	43	(U68408) 5' end not determined experimentally [Zea mays]
19500	GM_M46_B2_H11_MF	g4063760	BLASTX	157	3e-09	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19501	GM_M46_B2_H12_MR	g3645899	BLASTX	232	2e-17	56	(U68408) 5' end not determined experimentally [Zea mays]
19502	GM_M47_A1_B08_MF	g2522230	BLASTX	189	4e-14	35	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
19503	GM_M47_A1_B10_MF	g1946371	BLASTX	230	2e-17	48	(U93215) regulatory protein Viviparous-1 isolog [Arabidopsis thaliana]
19504	GM_M47_A1_C03_MF	g2642165	BLASTX	195	4e-14	69	(AC003000) hypothetical protein [Arabidopsis thaliana]
19505	GM_M47_A1_C05_MF	g505129	BLASTN	411	1e-11	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
19506	GM_M47_A1_C08_MF	g507910	BLASTN	580	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19507	GM_M47_A1_D07_MF	g18495	BLASTN	390	1e-10	62	Cotton set 5A Lea gene for seed protein D-29
19508	GM_M47_A1_D11_MF	g2708743	BLASTX	214	3e-15	36	(AC003952) putative Tal-1-like reverse transcriptase [Arabidopsis thaliana]
19509	GM_M47_A1_G04_MF	g1769898	BLASTX	449	1e-41	64	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19510	GM_M47_A1_G09_MF	g3097320	BLASTN	416	8e-12	71	Glycine max gene for Bd 30K, complete cds
19511	GM_M47_A1_G11_MF	g18559	BLASTN	759	2e-27	73	G.max gene for catalase
19512	GM_M47_A1_G12_MF	g4063756	BLASTN	375	7e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19513	GM_M47_A1_H07_MF	g4063760	BLASTX	238	6e-18	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19514	GM_M47_A2_B02_MR	g507910	BLASTN	408	8e-12	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19515	GM_M47_A2_B04_MF	g77236	BLASTX	200	1e-14	39	pol polyprotein - mink cell focus-forming virus (fragment) >gi 50857 (X52622) integrase (409 AA) [Mus musculus]
19516	GM_M47_A2_B05_MF	g905361	BLASTX	354	5e-31	79	(U22103) gag-protease polyprotein [Glycine max]
19517	GM_M47_A2_B07_MR	g1931641	BLASTX	180	5e-12	72	(U95973) unknown protein [Arabidopsis thaliana]
19518	GM_M47_A2_B08_MF	g3377855	BLASTX	346	2e-34	63	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
19519	GM_M47_A2_B12_MR	g3645899	BLASTX	320	7e-28	55	(U68408) 5' end not determined experimentally [Zea mays]
19520	GM_M47_A2_C03_MF	g905361	BLASTX	628	1e-60	97	(U22103) gag-protease polyprotein [Glycine max]
19521	GM_M47_A2_C08_MR	g3426334	BLASTN	480	1e-14	60	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
19522	GM_M47_A2_C10_MR	g2564750	BLASTN	364	2e-09	63	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
19523	GM_M47_A2_C12_MF	g114734	BLASTX	198	4e-15	92	Auxin-induced protein AUX28 gi 81759 pir A28993 aux28 protein - soybean gi 169921 (J03919) auxin-regulated protein (Aux28) [Glycine max]
19524	GM_M47_A2_D01_MF	g100484	BLASTX	252	1e-19	46	hypothetical protein - garden snapdragon
19525	GM_M47_A2_D02_MR	g2443320	BLASTX	208	1e-14	36	(D85597) polyprotein [Oryza australiensis]
19526	GM_M47_A2_D04_MF	g1888357	BLASTX	99	2e-12	68	(X98130) alpha-mannosidase [Arabidopsis thaliana] gi 1890154 gnl PID e307744 (Y11767) alpha-mannosidase precursor [Arabidopsis thaliana]
19527	GM_M47_A2_D08_MF	g3777527	BLASTX	575	1e-53	89	(AF053008) gag-pol polyprotein [Glycine max]
19528	GM_M47_A2_D08_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19529	GM_M47_A2_D10_MR	g1167523	BLASTX	402	2e-35	54	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
19530	GM_M47_A2_D11_MF	g421954	BLASTX	294	2e-24	45	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19531	GM_M47_A2_D11_MR	g3810596	BLASTX	301	8e-25	38	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19532	GM_M47_A2_F04_MF	g3810596	BLASTX	157	2e-09	31	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19533	GM_M47_A2_F06_MF	g905361	BLASTX	188	6e-13	34	(U22103) gag-protease polyprotein [Glycine max]
19534	GM_M47_A2_F08_MF	g3777527	BLASTX	322	1e-26	65	(AF053008) gag-pol polyprotein [Glycine max]
19535	GM_M47_A2_F10_MR	g507910	BLASTN	583	1e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
19536	GM_M47_A2_G02_MF	g3319362	BLASTX	161	7e-10	33	(AF077408) contains similarity to reverse transcriptase (Pfam: rvt.hmm, score 19.29) [Arabidopsis thaliana]
19537	GM_M47_A2_G03_MF	g507910	BLASTN	541	8e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
19538	GM_M47_A2_G03_MR	g507910	BLASTN	536	1e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.
19539	GM_M47_A2_G06_MF	g3142328	BLASTN	990	7e-38	88	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19540	GM_M47_A2_G06_MR	g3645899	BLASTX	234	1e-17	43	(U68408) 5' end not determined experimentally [Zea mays]
19541	GM_M47_A2_G07_MR	g3184283	BLASTX	322	9e-29	77	(AC004136) putative TBP-binding protein [Arabidopsis thaliana]
19542	GM_M47_A2_G10_MR	g3492803	BLASTX	239	8e-18	47	(AJ002479) ENBP1 [Medicago truncatula]
19543	GM_M47_A2_G12_MF	g421954	BLASTX	193	2e-13	38	hypothetical protein 3 - potato transposon Tst1 gi 21433 (X52387) ORF3 [Solanum tuberosum]
19544	GM_M47_A2_H05_MR	g1272349	BLASTX	262	2e-21	51	(U51740) secreted glycoprotein 3 [Ipomoea trifida]
19545	GM_M47_A2_H10_MR	g4063760	BLASTX	409	3e-36	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19546	GM_M47_B2_A01_MF	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19547	GM_M47_B2_A02_MF	g507910	BLASTN	607	8e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
19548	GM_M47_B2_A10_MR	g2065531	BLASTX	418	3e-38	69	(U78526) endo-1,4-beta-glucanase [Lycopersicon esculentum]
19549	GM_M47_B2_B02_MF	g507910	BLASTN	376	2e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19550	GM_M47_B2_B02_MR	g507910	BLASTN	384	9e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19551	GM_M47_B2_B06_MR	g1769898	BLASTX	308	6e-26	46	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19552	GM_M47_B2_B11_MF	g2462134	BLASTX	203	8e-15	39	(Y13368) reverse transcriptase [Beta vulgaris]
19553	GM_M47_B2_C01_MF	g4063760	BLASTX	183	4e-12	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19554	GM_M47_B2_C01_MR	g629693	BLASTX	418	2e-38	55	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
19555	GM_M47_B2_C04_MR	g421955	BLASTX	323	3e-28	56	hypothetical protein 4 - potato transposon Tst1 gi 21434 (X52387) ORF4 [Solanum tuberosum]
19556	GM_M47_B2_C05_MR	g3097320	BLASTN	1173	4e-46	81	Glycine max gene for Bd 30K, complete cds
19557	GM_M47_B2_C12_MF	g507910	BLASTN	617	3e-21	82	Glycine max BSR-101 satellite SB92 genomic sequence.
19558	GM_M47_B2_C12_MR	g507910	BLASTN	616	3e-21	84	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19559	GM_M47_B2_D03_MR	g2129618	BLASTX	103	8e-12	37	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19560	GM_M47_B2_D06_MF	g3044184	BLASTN	348	1e-08	65	Plasmodium falciparum mature parasite-infected erythrocyte surface antigen gene, complete cds
19561	GM_M47_B2_D08_MR	g4063756	BLASTN	535	4e-17	66	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19562	GM_M47_B2_D10_MR	g3777527	BLASTX	591	2e-55	88	(AF053008) gag-pol polyprotein [Glycine max]
19563	GM_M47_B2_E01_MF	g18768	BLASTN	346	3e-09	74	Soybean Tgm6 transposable element 3' end
19564	GM_M47_B2_E04_MR	g439616	BLASTN	1576	2e-65	92	Soybean G protein alpha subunit mRNA, complete cds.
19565	GM_M47_B2_E05_MR	g3810595	BLASTX	159	2e-09	35	(AC005398) putative reverse-transcriptase [Arabidopsis thaliana]
19566	GM_M47_B2_E07_MR	g507910	BLASTN	385	9e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19567	GM_M47_B2_E08_MR	g3142328	BLASTN	1089	2e-42	79	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19568	GM_M47_B2_E09_MR	g3746069	BLASTX	208	1e-14	38	(AC005311) putative reverse transcriptase [Arabidopsis thaliana]
19569	GM_M47_B2_E12_MF	g4063760	BLASTX	333	4e-28	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19570	GM_M47_B2_F02_MR	g1144549	BLASTN	254	1e-08	69	Anopheles gambiae 12S ribosomal RNA, D-loop, and tRNA-Ile mitochondrial genes, partial sequence.
19571	GM_M47_B2_F04_MR	g13536	BLASTN	370	6e-10	63	Yeast (S. cerevisiae) mitochondrial genes for several tRNAs (Thr(2), Cys(2) and His). >gi 343930 gb K00537 YSCMTTGO1 Yeast (S.cerevisiae) mitochondrial cap-oxi1 region: Thr-2, Cys-2 and His-tRNA genes.
19572	GM_M47_B2_F08_MF	g3142328	BLASTN	689	3e-24	89	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19573	GM_M47_B2_F10_MF	g3777527	BLASTX	645	4e-61	96	(AF053008) gag-pol polyprotein [Glycine max]
19574	GM_M47_B2_F10_MR	g507910	BLASTN	579	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
19575	GM_M47_B2_G04_MF	g3046850	BLASTN	362	3e-09	80	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24G6, complete sequence [Arabidopsis thaliana]
19576	GM_M47_B2_G05_MF	g3688173	BLASTX	211	5e-15	33	(AL031804) putative protein [Arabidopsis thaliana]
19577	GM_M47_B2_G06_MR	g507910	BLASTN	386	8e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19578	GM_M47_B2_G08_MR	g2564750	BLASTN	355	5e-09	59	Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families
19579	GM_M47_B2_H03_MR	g18559	BLASTN	360	2e-11	72	G.max gene for catalase
19580	GM_M47_B2_H08_MF	g3777527	BLASTX	631	1e-59	96	(AF053008) gag-pol polyprotein [Glycine max]
19581	GM_M47_B2_H08_MR	g507910	BLASTN	373	3e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19582	GM_M47_B2_H09_MF	g2522228	BLASTX	292	5e-25	75	(AB007466) reverse transcriptase-like protein [Vicia faba]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19583	GM_M47_B2_H10_MR	g3355474	BLASTX	160	2e-10	65	(AC004218) unknown protein [Arabidopsis thaliana]
19584	GM_M47_B2_H11_MR	g3142328	BLASTN	990	7e-38	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19585	GM_M48_B1_C08_MF	g3777527	BLASTX	271	3e-21	68	(AF053008) gag-pol polyprotein [Glycine max]
19586	GM_M48_B1_C09_MF	g629693	BLASTX	301	5e-26	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
19587	GM_M48_B1_C09_MR	g4050011	BLASTN	535	4e-17	64	Pisum sativum peabody/Ty3-type retrotransposon gag-pol precursor (gag-pol) pseudogene, complete sequence
19588	GM_M48_B1_C10_MR	g3171875	BLASTN	447	4e-13	63	Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.1...
19589	GM_M48_B1_D03_MR	g4063760	BLASTX	170	1e-10	34	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19590	GM_M48_B1_D10_MR	g1931641	BLASTX	181	4e-14	70	(U95973) unknown protein [Arabidopsis thaliana]
19591	GM_M48_B1_D12_MF	g3097320	BLASTN	963	1e-36	78	Glycine max gene for Bd 30K, complete cds
19592	GM_M48_B1_D12_MR	g2129618	BLASTX	186	2e-12	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19593	GM_M48_B1_E11_MR	g507910	BLASTN	602	1e-20	83	Glycine max BSR-101 satellite SB92 genomic sequence.
19594	GM_M48_B1_F06_MR	g4063760	BLASTX	596	3e-56	75	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19595	GM_M48_B1_G01_MR	g1196896	BLASTN	386	1e-10	81	Glycine max acidic ribosomal protein P0 mRNA, complete cds
19596	GM_M48_B1_G07_MF	g130582	BLASTX	284	9e-23	51	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
19597	GM_M48_B1_G09_MF	g3097320	BLASTN	849	2e-31	74	Glycine max gene for Bd 30K, complete cds
19598	GM_M48_B1_G12_MF	g2588616	BLASTN	376	6e-10	64	Human BAC clone RG119P24 from 7q31, complete sequence [Homo sapiens]
19599	GM_M48_B1_G12_MR	g2244916	BLASTX	176	1e-14	31	(Z97339) hypothetical protein [Arabidopsis thaliana]
19600	GM_M48_B1_H02_MF	g322662	BLASTX	171	1e-19	73	S-receptor kinase-related protein - Chinese kale gi 17915 (Z18883) S-receptor kinase related protein [Brassica oleracea]
19601	GM_M48_B1_H04_MR	g4063760	BLASTX	565	7e-53	74	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19602	GM_M48_B1_H06_MR	g3097320	BLASTN	718	2e-25	75	Glycine max gene for Bd 30K, complete cds
19603	GM_M48_B1_H08_MR	g3810596	BLASTX	232	2e-17	38	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19604	GM_M48_B1_H09_MR	g4063760	BLASTX	482	6e-44	64	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19605	GM_M48_B1_H10_MF	g18559	BLASTN	924	7e-35	80	G.max gene for catalase
19606	GM_M48_B2_A01_MR	g3941524	BLASTX	213	1e-16	88	(AF062916) putative transcription factor [Arabidopsis thaliana]
19607	GM_M48_B2_A04_MR	g3860271	BLASTX	214	1e-15	31	(AC005824) putative selenium-binding protein [Arabidopsis thaliana]
19608	GM_M48_B2_A08_MF	g130582	BLASTX	152	1e-08	58	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
19609	GM_M48_B2_B03_MF	g3097320	BLASTN	706	6e-25	79	Glycine max gene for Bd 30K, complete cds
19610	GM_M48_B2_B05_MF	g4063760	BLASTX	142	2e-09	36	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19611	GM_M48_B2_B05_MR	g507910	BLASTN	418	3e-12	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19612	GM_M48_B2_B06_MR	g507910	BLASTN	516	1e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
19613	GM_M48_B2_B07_MF	g3097320	BLASTN	1067	3e-41	81	Glycine max gene for Bd 30K, complete cds
19614	GM_M48_B2_B08_MR	g1762671	BLASTN	365	1e-09	62	Elenchus japonica 18S ribosomal RNA gene, partial sequence
19615	GM_M48_B2_B09_MF	g507910	BLASTN	366	6e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19616	GM_M48_B2_B09_MR	g507910	BLASTN	381	1e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19617	GM_M48_B2_C01_MF	g400246	BLASTX	247	3e-20	84	S-ADENOSYLMETHIONINE SYNTHETASE 1 (METHIONINE ADENOSYLTRANSFERASE 1) (ADOMET SYNTHETASE 1) gi 169665 (M62758) S-adenosylmethionine synthetase [Petroselinum crispum]
19618	GM_M48_B2_C03_MR	g18559	BLASTN	368	1e-09	72	G.max gene for catalase
19619	GM_M48_B2_C07_MF	g3617837	BLASTX	256	6e-32	70	(AF035820) gibberellin action negative regulator SPY [Hordeum vulgare]
19620	GM_M48_B2_C10_MF	g4063760	BLASTX	557	5e-52	75	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19621	GM_M48_B2_D02_MR	g2522230	BLASTX	249	2e-20	34	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
19622	GM_M48_B2_D05_MF	g2764526	BLASTN	489	4e-15	65	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
19623	GM_M48_B2_D06_MR	g3695395	BLASTX	240	1e-18	41	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
19624	GM_M48_B2_D08_MR	g3337395	BLASTN	362	9e-10	64	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19625	GM_M48_B2_D12_MF	g3142328	BLASTN	1885	9e-79	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19626	GM_M48_B2_D12_MR	g2522230	BLASTX	185	8e-24	45	(AB007467) retrotransposon-like gene; the first amino acid was determined to be leucine [Vicia faba]
19627	GM_M48_B2_E10_MR	g2129618	BLASTX	210	5e-15	34	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19628	GM_M48_B2_E12_MR	g99730	BLASTX	246	7e-29	48	hypothetical protein 3 - Arabidopsis thaliana retrotransposon Ta1-2 (strain Kashmir) (fragment) gi 1345512 gnl PID e73215 (X53975) orf 3 [Arabidopsis thaliana]
19629	GM_M48_B2_F01_MF	g507910	BLASTN	387	7e-11	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19630	GM_M48_B2_F01_MR	g507910	BLASTN	368	5e-10	69	Glycine max BSR-101 satellite SB92 genomic sequence.
19631	GM_M48_B2_F08_MR	g3176795	BLASTN	400	1e-11	62	Homo sapiens allele 12 fragile site locus (FRA10B) minisatellite, 5' sequence
19632	GM_M48_B2_F10_MF	g4063760	BLASTX	427	4e-38	71	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19633	GM_M48_B2_F10_MR	g2995405	BLASTX	422	7e-38	54	(Y12432) polyprotein [Ananas comosus]
19634	GM_M48_B2_F11_MF	g4063760	BLASTX	160	1e-09	40	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19635	GM_M48_B2_G05_MR	g3176711	BLASTX	262	1e-20	48	(AC002392) bZIP-like protein [Arabidopsis thaliana]
19636	GM_M48_B2_G06_MR	g3885334	BLASTX	258	4e-22	66	(AC005623) putative argonaute protein [Arabidopsis thaliana]
19637	GM_M48_B2_G09_MF	g2586082	BLASTX	280	3e-22	50	(U72725) retrofit [Oryza longistaminata]
19638	GM_M48_B2_G10_MR	g4138290	BLASTX	200	3e-15	77	(AJ005841) thioredoxin M [Oryza sativa]
19639	GM_M48_B2_H02_MR	g3426334	BLASTN	436	1e-12	62	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
19640	GM_M48_B2_H04_MR	g4160362	BLASTN	391	6e-12	63	Saccharomyces cerevisiae complete mitochondrial genome
19641	GM_M48_B2_H09_MF	g3645899	BLASTX	169	1e-10	36	(U68408) 5' end not determined experimentally [Zea mays]
19642	GM_M48_B2_H10_MF	g2801676	BLASTN	751	8e-28	74	Glycine max telomere-associated sequence STAS5
19643	GM_M48_B2_H10_MR	g20749	BLASTN	809	2e-30	70	Pea PSU2 gene for U2 snRNA
19644	GM_M49_A2_A04_MR	g1666236	BLASTX	172	7e-12	29	(U76261) unknown [Hordeum vulgare]
19645	GM_M49_A2_A05_MR	g18559	BLASTN	686	2e-34	79	G.max gene for catalase
19646	GM_M49_A2_A05_T7	g3777527	BLASTX	712	2e-68	95	(AF053008) gag-pol polyprotein [Glycine max]
19647	GM_M49_A2_A07_MR	g3097320	BLASTN	1317	1e-52	84	Glycine max gene for Bd 30K, complete cds
19648	GM_M49_A2_A09_MR	g3702722	BLASTN	525	1e-16	66	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K12B20, complete sequence [Arabidopsis thaliana]
19649	GM_M49_A2_A12_MR	g3036785	BLASTN	354	6e-09	62	Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains histone genes H2A/l,H2B.1A,H4,H2A.1b,H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG island

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19650	GM_M49_A2_B01_MR	g507910	BLASTN	642	2e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
19651	GM_M49_A2_B03_MR	g3319345	BLASTX	221	3e-16	38	(AF077407) contains similarity to maize transposon MuDR (GB:M76978) [Arabidopsis thaliana]
19652	GM_M49_A2_B08_T7	g4063760	BLASTX	371	4e-32	67	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19653	GM_M49_A2_B11_T7	g3021343	BLASTN	961	2e-37	76	Cicer arietinum mRNA for hypothetical protein homologous to EST B23019
19654	GM_M49_A2_C01_MR	g2791937	BLASTX	345	1e-30	73	(AJ001200) reverse transcriptase [Alstroemeria aurea]
19655	GM_M49_A2_C04_MR	g3695395	BLASTX	128	7e-09	42	(AF096372) contains similarity to reverse transcriptase (Pfam: PF00078 rvt, E=4.3e-08) [Arabidopsis thaliana]
19656	GM_M49_A2_C05_MR	g2522227	BLASTX	180	5e-13	60	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
19657	GM_M49_A2_C05_T7	g1769899	BLASTX	213	1e-16	45	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19658	GM_M49_A2_C10_T7	g1769898	BLASTX	152	4e-09	54	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19659	GM_M49_A2_D03_T7	g2522228	BLASTX	270	1e-22	77	(AB007466) reverse transcriptase-like protein [Vicia faba]
19660	GM_M49_A2_D04_MR	g507910	BLASTN	404	1e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
19661	GM_M49_A2_D04_T7	g507910	BLASTN	624	1e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
19662	GM_M49_A2_D06_T7	g3142328	BLASTN	1229	9e-49	80	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19663	GM_M49_A2_D09_T7	g2511696	BLASTN	717	8e-26	83	Phaseolus vulgaris Moldavian encoding asparagine-specific endopeptidase precursor (clone cp6b)
19664	GM_M49_A2_D10_MR	g507910	BLASTN	349	4e-09	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19665	GM_M49_A2_E01_T7	g2443320	BLASTX	281	2e-22	45	(D85597) polyprotein [Oryza australiensis]
19666	GM_M49_A2_E02_MR	g507910	BLASTN	471	1e-14	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19667	GM_M49_A2_E06_MR	g507910	BLASTN	568	5e-19	82	Glycine max BSR-101 satellite SB92 genomic sequence.
19668	GM_M49_A2_E07_T7	g3097320	BLASTN	348	1e-08	64	Glycine max gene for Bd 30K, complete cds
19669	GM_M49_A2_E08_MR	g2995405	BLASTX	409	2e-36	59	(Y12432) polyprotein [Ananas comosus]
19670	GM_M49_A2_E11_MR	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19671	GM_M49_A2_E11_T7	g507910	BLASTN	384	9e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19672	GM_M49_A2_F01_MR	g3033389	BLASTX	221	3e-16	43	(AC004238) Cf-2.1-like protein [Arabidopsis thaliana]
19673	GM_M49_A2_F02_MR	g2388571	BLASTX	186	1e-23	70	(AC000098) Strong similarity to Arabidopsis peroxidase ATPEROX7A (gb X98321). [Arabidopsis thaliana] gi 2738254 (U97684) peroxidase precursor [Arabidopsis thaliana]
19674	GM_M49_A2_F02_T7	g100484	BLASTX	384	5e-34	54	hypothetical protein - garden snapdragon
19675	GM_M49_A2_F03_T7	g3142328	BLASTN	1060	4e-41	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19676	GM_M49_A2_F08_T7	g2997694	BLASTX	120	2e-11	38	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
19677	GM_M49_A2_F12_T7	g3645899	BLASTX	378	6e-33	52	(U68408) 5' end not determined experimentally [Zea mays]
19678	GM_M49_A2_G03_MR	g3142328	BLASTN	1173	3e-46	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19679	GM_M49_A2_G07_T7	g434060	BLASTN	531	4e-17	73	Soybean DNA for basic 7S globulin, complete cds
19680	GM_M49_A2_G09_T7	g2961349	BLASTX	171	7e-11	51	(AL022140) LTR retrotransposon like protein [Arabidopsis thaliana]
19681	GM_M49_A2_G11_T7	g2914703	BLASTX	159	3e-11	57	(AC003974) unknown protein [Arabidopsis thaliana]
19682	GM_M49_A2_G12_MR	g2760839	BLASTX	349	2e-30	62	(AC003105) putative receptor kinase [Arabidopsis thaliana]
19683	GM_M49_A2_H06_MR	g3777527	BLASTX	624	6e-59	86	(AF053008) gag-pol polyprotein [Glycine max]
19684	GM_M49_A2_H07_T7	g3367647	BLASTX	259	4e-26	56	(Y17298) enolase [Cunninghamella elegans]
19685	GM_M49_A2_H12_MR	g18695	BLASTN	500	8e-16	75	Soybean nodulin 22 gene
19686	GM_M49_B1_A04_T7	g3924609	BLASTX	301	3e-32	60	(AF069442) putative polyprotein of LTR transposon [Arabidopsis thaliana]
19687	GM_M49_B1_A05_T7	g18559	BLASTN	387	2e-10	67	G.max gene for catalase
19688	GM_M49_B1_A06_MR	g2951945	BLASTN	378	5e-10	61	Human Chromosome 16 BAC clone CIT987SK-A-589H1, complete sequence [Homo sapiens]
19689	GM_M49_B1_A10_MR	g507910	BLASTN	509	2e-16	80	Glycine max BSR-101 satellite SB92 genomic sequence.
19690	GM_M49_B1_B01_T7	g3522943	BLASTX	201	1e-22	58	(AC004411) putative p-glycoprotein [Arabidopsis thaliana]
19691	GM_M49_B1_B02_MR	g4063760	BLASTX	271	2e-21	55	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19692	GM_M49_B1_B02_T7	g507910	BLASTN	702	4e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
19693	GM_M49_B1_B06_MR	g4063760	BLASTX	208	1e-14	45	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19694	GM_M49_B1_B08_MR	g18559	BLASTN	351	7e-09	63	G.max gene for catalase
19695	GM_M49_B1_B10_MR	g18660	BLASTN	644	3e-22	76	G.max hsp22 gene for low MW heat shock protein
19696	GM_M49_B1_B12_T7	g2511697	BLASTX	292	1e-24	77	(Z99956) asparagine-specific endopeptidase precursor [Phaseolus vulgaris]
19697	GM_M49_B1_C02_T7	g2129746	BLASTX	216	5e-17	78	SUPERMAN protein - Arabidopsis thaliana gi 1079669 (U38946) SUPERMAN [Arabidopsis thaliana] gi 1585427 prf 2124420A SUPERMAN gene [Arabidopsis thaliana]
19698	GM_M49_B1_C07_MR	g3947733	BLASTX	163	2e-10	34	(AJ009719) NL25 [Solanum tuberosum]
19699	GM_M49_B1_C12_T7	g3142328	BLASTN	1171	4e-46	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19700	GM_M49_B1_D01_MR	g3142328	BLASTN	1122	7e-44	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19701	GM_M49_B1_D02_T7	g3142328	BLASTN	1156	2e-45	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19702	GM_M49_B1_D03_T7	g1666236	BLASTX	212	2e-16	30	(U76261) unknown [Hordeum vulgare]
19703	GM_M49_B1_D06_T7	g2522228	BLASTX	499	5e-47	67	(AB007466) reverse transcriptase-like protein [Vicia faba]
19704	GM_M49_B1_D12_MR	g3928116	BLASTN	388	2e-10	66	, complete sequence [Homo sapiens]
19705	GM_M49_B1_E03_MR	g507910	BLASTN	382	1e-10	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19706	GM_M49_B1_E11_MR	g158813	BLASTN	428	4e-13	67	Drosophila hydei Y chromosome lampbrush loop transcribed repeats.
19707	GM_M49_B1_E11_T7	g3645899	BLASTX	172	8e-25	56	(U68408) 5' end not determined experimentally [Zea mays]
19708	GM_M49_B1_F01_MR	g4063756	BLASTN	428	3e-12	71	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19709	GM_M49_B1_F01_T7	g507910	BLASTN	711	2e-25	87	Glycine max BSR-101 satellite SB92 genomic sequence.
19710	GM_M49_B1_F02_T7	g3142328	BLASTN	653	1e-22	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19711	GM_M49_B1_F03_T7	g1076509	BLASTX	183	7e-22	72	chloroplast RNA binding protein - kidney bean gi 558629 (X82030) chloroplast RNA binding protein [Phaseolus vulgaris]
19712	GM_M49_B1_F05_MR	g18660	BLASTN	590	9e-20	75	G.max hsp22 gene for low MW heat shock protein
19713	GM_M49_B1_F12_MR	g1769898	BLASTX	173	2e-14	48	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19714	GM_M49_B1_F12_T7	g2213582	BLASTX	137	9e-14	57	(AC000348) T7N9.2 [Arabidopsis thaliana]
19715	GM_M49_B1_G01_T7	g535454	BLASTX	102	1e-09	48	(U13940) cysteine proteinase [Alnus glutinosa]
19716	GM_M49_B1_G03_MR	g4063760	BLASTX	311	1e-25	60	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19717	GM_M49_B1_G09_MR	g2462058	BLASTX	118	4e-11	50	(Y13389) reverse transcriptase [Antirrhinum majus]
19718	GM_M49_B1_G09_T7	g2864621	BLASTX	188	3e-13	42	hypothetical protein [Arabidopsis thaliana]
19719	GM_M49_B1_G10_T7	g3002819	BLASTX	122	9e-24	74	(AF041852) RPB140 [Chloranthus spicatus]
19720	GM_M49_B1_G12_T7	g2864621	BLASTX	165	9e-11	40	hypothetical protein [Arabidopsis thaliana]
19721	GM_M49_B1_H04_MR	g3142328	BLASTN	1050	1e-40	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19722	GM_M49_B1_H05_T7	g99755	BLASTX	375	3e-35	54	RNA-directed DNA polymerase (EC 2.7.7.49) - Arabidopsis thaliana retrotransposon Ta1-1 (fragment) gi 16356 (X53973) reverse transcriptase [Arabidopsis thaliana]
19723	GM_M49_B1_H09_MR	g3645899	BLASTX	168	6e-15	44	(U68408) 5' end not determined experimentally [Zea mays]
19724	GM_M50_A1_A01_MR	g18559	BLASTN	753	4e-27	76	G.max gene for catalase
19725	GM_M50_A1_A02_MR	g3649752	BLASTN	350	9e-09	66	Plasmodium falciparum MAL3P3, complete sequence [Plasmodium falciparum]
19726	GM_M50_A1_A05_T7	g3334667	BLASTX	253	3e-20	41	(Y10493) putative cytochrome P450 [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19727	GM_M50_A1_A06_T7	g507910	BLASTN	365	7e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19728	GM_M50_A1_A09_MR	g4063760	BLASTX	274	5e-23	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19729	GM_M50_A1_B01_T7	g3777527	BLASTX	202	6e-14	34	(AF053008) gag-pol polyprotein [Glycine max]
19730	GM_M50_A1_B03_MR	g99922	BLASTX	496	1e-46	69	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
19731	GM_M50_A1_B04_T7	g1167523	BLASTX	373	3e-32	50	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
19732	GM_M50_A1_B06_MR	g2245044	BLASTX	336	5e-28	59	(Z97342) similarity to reverse transcriptase - Arabidopsis thaliana retrotransposon 2 (fragment) [Arabidopsis thaliana]
19733	GM_M50_A1_B10_MR	g4038056	BLASTX	286	3e-23	39	(AC005897) putative transposon [Arabidopsis thaliana]
19734	GM_M50_A1_B10_T7	g3097320	BLASTN	1186	1e-46	78	Glycine max gene for Bd 30K, complete cds
19735	GM_M50_A1_B12_T7	g507910	BLASTN	581	1e-19	83	Glycine max BSR-101 satellite SB92 genomic sequence.
19736	GM_M50_A1_C04_T7	g3097320	BLASTN	784	2e-28	73	Glycine max gene for Bd 30K, complete cds
19737	GM_M50_A1_C06_T7	g1769898	BLASTX	395	1e-35	58	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19738	GM_M50_A1_D04_MR	g18559	BLASTN	588	5e-25	80	G.max gene for catalase
19739	GM_M50_A1_E03_T7	g507910	BLASTN	447	1e-13	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19740	GM_M50_A1_E08_T7	g3386611	BLASTX	139	1e-13	53	(AC004665) unknown protein [Arabidopsis thaliana]
19741	GM_M50_A1_F01_T7	g3645899	BLASTX	208	7e-15	38	(U68408) 5' end not determined experimentally [Zea mays]
19742	GM_M50_A1_F05_MR	g4038056	BLASTX	217	7e-16	36	(AC005897) putative transposon [Arabidopsis thaliana]
19743	GM_M50_A1_F09_MR	g507910	BLASTN	358	1e-09	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19744	GM_M50_A1_F10_MR	g3777527	BLASTX	204	4e-14	42	(AF053008) gag-pol polyprotein [Glycine max]
19745	GM_M50_A1_G01_T7	g3142328	BLASTN	1281	4e-51	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19746	GM_M50_A1_G03_MR	g507910	BLASTN	352	3e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19747	GM_M50_A1_G06_MR	g3645899	BLASTX	154	1e-20	44	(U68408) 5' end not determined experimentally [Zea mays]
19748	GM_M50_A1_G08_MR	g2129618	BLASTX	176	2e-11	35	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19749	GM_M50_A1_G08_T7	g629693	BLASTX	149	3e-09	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
19750	GM_M50_A1_G09_T7	g2462058	BLASTX	259	1e-21	51	(Y13389) reverse transcriptase [Antirrhinum majus]
19751	GM_M50_A1_G11_T7	g1142701	BLASTN	1422	6e-58	87	Glycine max satellite STR120-A.3.
19752	GM_M50_A1_G12_MR	g99922	BLASTX	243	7e-20	58	hypothetical protein - soybean gi 930025 (X13528) ORF (334 AA); pid:e150225 [Glycine max]
19753	GM_M50_A1_H01_T7	g1167523	BLASTX	192	6e-13	36	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
19754	GM_M50_A1_H05_MR	g507910	BLASTN	490	1e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19755	GM_M50_A1_H09_MR	g507910	BLASTN	601	1e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19756	GM_M50_A1_H09_T7	g507910	BLASTN	579	1e-19	80	Glycine max BSR-101 satellite SB92 genomic sequence.
19757	GM_M50_A1_H10_MR	g505129	BLASTN	352	6e-09	66	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
19758	GM_M50_A1_H12_T7	g18559	BLASTN	895	2e-33	75	G.max gene for catalase
19759	GM_M50_A2_A01_MR	g3097320	BLASTN	458	1e-13	71	Glycine max gene for Bd 30K, complete cds
19760	GM_M50_A2_A08_MR	g3097320	BLASTN	381	3e-10	72	Glycine max gene for Bd 30K, complete cds
19761	GM_M50_A2_A10_T7	g905361	BLASTX	149	9e-09	83	(U22103) gag-protease polyprotein [Glycine max]
19762	GM_M50_A2_B05_T7	g531389	BLASTX	373	3e-32	47	(U12626) copia-like retrotransposon Hopscotch polyprotein [Zea mays]
19763	GM_M50_A2_B06_MR	g1167523	BLASTX	105	3e-12	40	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
19764	GM_M50_A2_C12_T7	g130582	BLASTX	267	6e-21	47	RETROVIRUS-RELATED POL POLYPROTEIN (PROTEASE ; REVERSE TRANSCRIPTASE ; ENDONUCLEASE) (TRANSPOSON TNT 1-94) gi 100342 pir S04273 hypothetical protein - common tobacco gi 20045 (X13777) ORF [Nicotiana tabacum]
19765	GM_M50_A2_D03_T7	g1769897	BLASTX	156	1e-09	60	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19766	GM_M50_A2_D07_MR	g4038056	BLASTX	185	3e-14	38	(AC005897) putative transposon [Arabidopsis thaliana]
19767	GM_M50_A2_D12_MR	g2262107	BLASTX	156	2e-17	96	(AC002343) Ser/Thr protein kinase isolog [Arabidopsis thaliana]
19768	GM_M50_A2_E11_T7	g3789709	BLASTN	374	7e-10	65	Homo sapiens clone UWGC:g1564a209 from 7p14-15, complete sequence [Homo sapiens]
19769	GM_M50_A2_E12_T7	g3777527	BLASTX	257	9e-20	40	(AF053008) gag-pol polyprotein [Glycine max]
19770	GM_M50_A2_F01_T7	g100484	BLASTX	395	3e-35	55	hypothetical protein - garden snapdragon
19771	GM_M50_A2_F04_T7	g2244915	BLASTX	239	3e-18	39	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
19772	GM_M50_A2_F06_T7	g3777526	BLASTN	607	2e-20	70	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
19773	GM_M50_A2_F12_MR	g2244915	BLASTX	183	3e-12	33	(Z97339) strong homology to reverse transcriptase [Arabidopsis thaliana]
19774	GM_M50_A2_G01_MR	g629693	BLASTX	161	3e-16	50	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
19775	GM_M50_A2_G02_MR	g2443320	BLASTX	153	9e-09	38	(D85597) polyprotein [Oryza australiensis]
19776	GM_M50_A2_G04_MR	g2995405	BLASTX	169	1e-10	40	(Y12432) polyprotein [Ananas comosus]
19777	GM_M50_A2_G04_T7	g3810596	BLASTX	293	6e-24	42	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19778	GM_M50_A2_G05_MR	g148071	BLASTX	148	8e-10	44	(M54881) thioredoxin [Escherichia coli]
19779	GM_M50_A2_G07_MR	g507910	BLASTN	498	7e-16	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19780	GM_M50_A2_G08_MR	g1217967	BLASTX	184	2e-17	52	(X96431) high affinity sulphate transporter [Hordeum vulgare]
19781	GM_M50_A2_G12_MR	g1769898	BLASTX	474	2e-44	63	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19782	GM_M50_A2_G12_T7	g100488	BLASTX	102	9e-10	50	TNP2 protein - garden snapdragon
19783	GM_M50_A2_H06_T7	g2462936	BLASTX	351	3e-31	53	(Y12321) open reading frame 2 [Brassica oleracea]
19784	GM_M50_A2_H07_T7	g18559	BLASTN	817	5e-30	72	G.max gene for catalase
19785	GM_M50_A2_H09_MR	g3426334	BLASTN	466	4e-14	60	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
19786	GM_M50_B1_A03_MR	g507910	BLASTN	491	1e-15	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19787	GM_M50_B1_A03_T7	g507910	BLASTN	439	3e-13	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19788	GM_M50_B1_A07_MR	g507910	BLASTN	360	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19789	GM_M50_B1_A07_T7	g507910	BLASTN	402	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19790	GM_M50_B1_A08_MR	g507910	BLASTN	359	1e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19791	GM_M50_B1_A08_T7	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19792	GM_M50_B1_A10_MR	g2129613	BLASTX	146	4e-10	58	homeotic protein BEL1 - Arabidopsis thaliana gi 1122533 (U39944) BELL1 [Arabidopsis thaliana]
19793	GM_M50_B1_A10_T7	g4115365	BLASTX	170	1e-10	36	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
19794	GM_M50_B1_B01_T7	g3142328	BLASTN	1482	3e-60	84	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19795	GM_M50_B1_B04_MR	g4140712	BLASTX	451	7e-45	55	(AF110183) putative integrase [Oryza sativa]
19796	GM_M50_B1_B05_T7	g2995405	BLASTX	396	4e-35	54	(Y12432) polyprotein [Ananas comosus]
19797	GM_M50_B1_B07_MR	g18559	BLASTN	983	2e-37	74	G.max gene for catalase
19798	GM_M50_B1_B08_MR	g507910	BLASTN	429	9e-13	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19799	GM_M50_B1_D04_T7	g2429543	BLASTX	188	1e-12	48	(AF025472) contains similarity to S. cerevisiae mitochondrial DNA repair and recombination protein PIF1 (NID:g5771350 [Caenorhabditis elegans]
19800	GM_M50_B1_D08_MR	g507910	BLASTN	391	5e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19801	GM_M50_B1_D08_T7	g507910	BLASTN	388	6e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19802	GM_M50_B1_E02_MR	g2335097	BLASTX	167	2e-10	36	(AC002339) putative receptor-like protein kinase [Arabidopsis thaliana]
19803	GM_M50_B1_E03_MR	g507910	BLASTN	459	4e-14	76	Glycine max BSR-101 satellite SB92 genomic sequence.
19804	GM_M50_B1_E06_T7	g505129	BLASTN	357	3e-09	63	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
19805	GM_M50_B1_E07_MR	g3777527	BLASTX	514	3e-47	85	(AF053008) gag-pol polyprotein [Glycine max]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19806	GM_M50_B1_E10_T7	g3386534	BLASTX	351	2e-33	57	(AF078934) mariner transposase [Glycine max]
19807	GM_M50_B1_E11_MR	g507910	BLASTN	371	4e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19808	GM_M50_B1_E11_T7	g507910	BLASTN	358	1e-09	71	Glycine max BSR-101 satellite SB92 genomic sequence.
19809	GM_M50_B1_E12_MR	g2245113	BLASTX	152	3e-09	71	(Z97343) glycerol-3-phosphate permease homolog [Arabidopsis thaliana]
19810	GM_M50_B1_E12_T7	g2245126	BLASTN	371	1e-09	65	Arabidopsis thaliana DNA chromosome 4, ESSA I contig fragment No. 9.
19811	GM_M50_B1_F01_MR	g4063760	BLASTX	255	9e-20	41	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19812	GM_M50_B1_F01_T7	g2995405	BLASTX	253	9e-20	44	(Y12432) polyprotein [Ananas comosus]
19813	GM_M50_B1_F08_MR	g180902	BLASTN	506	8e-17	63	Human variable number tandem repeat (VNTR) region, allele 14R2 3' to collagen type II (COL2A1) gene.
19814	GM_M50_B1_F09_T7	g2462134	BLASTX	247	1e-19	37	(Y13368) reverse transcriptase [Beta vulgaris]
19815	GM_M50_B1_F10_MR	g507910	BLASTN	647	1e-22	84	Glycine max BSR-101 satellite SB92 genomic sequence.
19816	GM_M50_B1_F10_T7	g507910	BLASTN	477	6e-15	78	Glycine max BSR-101 satellite SB92 genomic sequence.
19817	GM_M50_B1_F11_MR	g905361	BLASTX	220	2e-16	35	(U22103) gag-protease polyprotein [Glycine max]
19818	GM_M50_B1_F12_MR	g507910	BLASTN	588	6e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
19819	GM_M50_B1_G06_T7	g3283026	BLASTX	266	3e-21	41	putative transposase [Arabidopsis thaliana]
19820	GM_M50_B1_G07_T7	g3142379	BLASTX	284	6e-24	61	(AF053008) envelope-like [Glycine max]
19821	GM_M50_B1_G08_MR	g4153865	BLASTN	368	1e-09	62	Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence [Homo sapiens]
19822	GM_M50_B1_H02_MR	g2443320	BLASTX	170	1e-10	40	(D85597) polyprotein [Oryza australiensis]
19823	GM_M50_B1_H03_T7	g905361	BLASTX	439	2e-40	96	(U22103) gag-protease polyprotein [Glycine max]
19824	GM_M50_B1_H04_MR	g18559	BLASTN	399	5e-11	69	G.max gene for catalase
19825	GM_M50_B1_H05_T7	g3142328	BLASTN	752	4e-27	82	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19826	GM_M50_B1_H09_MR	g4063756	BLASTN	548	1e-17	65	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19827	GM_M50_B1_H10_T7	g3142328	BLASTN	981	2e-37	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19828	GM_M50_B2_A01_T7	g3645899	BLASTX	347	1e-29	50	(U68408) 5' end not determined experimentally [Zea mays]
19829	GM_M50_B2_A02_MR	g3688105	BLASTN	1921	1e-79	99	Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence [Homo sapiens]
19830	GM_M50_B2_A03_T7	g3176693	BLASTN	377	5e-10	63	Arabidopsis thaliana chromosome I BAC T27I1 genomic sequence, complete sequence [Arabidopsis thaliana]
19831	GM_M50_B2_A07_MR	g106323	BLASTX	533	1e-50	87	hypothetical protein (L1H 5' region) - human

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19832	GM_M50_B2_A09_MR	g1143359	BLASTN	818	3e-30	99	Human COL4A6 gene for a6(IV) collagen, exon 4
19833	GM_M50_B2_A11_MR	g3002473	BLASTN	947	1e-35	81	Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence [Homo sapiens]
19834	GM_M50_B2_B04_MR	g3927853	BLASTN	459	4e-15	73	Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angelman Syndrome region, complete sequence [Homo sapiens]
19835	GM_M50_B2_B06_MR	g3688105	BLASTN	1921	1e-79	99	Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence [Homo sapiens]
19836	GM_M50_B2_B11_MR	g106323	BLASTX	533	1e-50	87	hypothetical protein (L1H 5' region) - human
19837	GM_M50_B2_B12_T7	g4049353	BLASTX	141	4e-17	57	(AL034567) putative protein [Arabidopsis thaliana]
19838	GM_M50_B2_C01_MR	g1143359	BLASTN	818	3e-30	99	Human COL4A6 gene for a6(IV) collagen, exon 4
19839	GM_M50_B2_C03_MR	g3002473	BLASTN	947	1e-35	81	Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence [Homo sapiens]
19840	GM_M50_B2_C05_T7	g18695	BLASTN	348	8e-09	70	Soybean nodulin 22 gene
19841	GM_M50_B2_C08_MR	g3927853	BLASTN	459	4e-15	73	Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angelman Syndrome region, complete sequence [Homo sapiens]
19842	GM_M50_B2_C08_T7	g18559	BLASTN	656	1e-22	71	G.max gene for catalase
19843	GM_M50_B2_C10_MR	g3688105	BLASTN	1921	1e-79	99	Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence [Homo sapiens]
19844	GM_M50_B2_D02_T7	g507910	BLASTN	477	6e-15	77	Glycine max BSR-101 satellite SB92 genomic sequence.
19845	GM_M50_B2_D03_MR	g106323	BLASTX	533	1e-50	87	hypothetical protein (L1H 5' region) - human
19846	GM_M50_B2_D03_T7	g4092471	BLASTN	413	1e-11	68	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
19847	GM_M50_B2_D04_T7	g1769897	BLASTX	242	9e-37	65	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19848	GM_M50_B2_D05_MR	g1143359	BLASTN	818	3e-30	99	Human COL4A6 gene for a6(IV) collagen, exon 4
19849	GM_M50_B2_D07_MR	g3002473	BLASTN	947	1e-35	81	Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence [Homo sapiens]
19850	GM_M50_B2_D11_T7	g169974	BLASTN	415	8e-12	64	Glycine max vspA gene, complete cds.
19851	GM_M50_B2_E01_T7	g2464905	BLASTX	225	6e-18	58	(Z99708) minor allergen [Arabidopsis thaliana]
19852	GM_M50_B2_E02_MR	g3688105	BLASTN	1921	1e-79	99	Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence [Homo sapiens]
19853	GM_M50_B2_E07_MR	g106323	BLASTX	533	1e-50	87	hypothetical protein (L1H 5' region) - human
19854	GM_M50_B2_E09_MR	g1143359	BLASTN	818	3e-30	99	Human COL4A6 gene for a6(IV) collagen, exon 4

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19855	GM_M50_B2_E11_MR	g3002473	BLASTN	947	1e-35	81	Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence [Homo sapiens]
19856	GM_M50_B2_E11_T7	g2341043	BLASTX	208	5e-24	74	(AC000104) Strong similarity to Arabidopsis REV3C (gb X62461). [Arabidopsis thaliana]
19857	GM_M50_B2_F01_T7	g2995405	BLASTX	361	3e-31	50	(Y12432) polyprotein [Ananas comosus]
19858	GM_M50_B2_F04_MR	g3927853	BLASTN	459	4e-15	73	Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angelman Syndrome region, complete sequence [Homo sapiens]
19859	GM_M50_B2_F06_MR	g3688105	BLASTN	1921	1e-79	99	Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence [Homo sapiens]
19860	GM_M50_B2_F10_T7	g507910	BLASTN	455	6e-14	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19861	GM_M50_B2_F11_MR	g106323	BLASTX	533	1e-50	87	hypothetical protein (L1H 5' region) - human
19862	GM_M50_B2_G01_MR	g1143359	BLASTN	818	3e-30	99	Human COL4A6 gene for a6(IV) collagen, exon 4
19863	GM_M50_B2_G03_MR	g3002473	BLASTN	947	1e-35	81	Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence [Homo sapiens]
19864	GM_M50_B2_G08_MR	g3927853	BLASTN	459	4e-15	73	Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angelman Syndrome region, complete sequence [Homo sapiens]
19865	GM_M50_B2_G10_MR	g3688105	BLASTN	1921	1e-79	99	Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence [Homo sapiens]
19866	GM_M50_B2_G12_T7	g2058281	BLASTN	395	4e-11	75	A.thaliana mRNA for AtRanBP1a protein
19867	GM_M50_B2_H03_MR	g106323	BLASTX	533	1e-50	87	hypothetical protein (L1H 5' region) - human
19868	GM_M50_B2_H05_MR	g1143359	BLASTN	818	3e-30	99	Human COL4A6 gene for a6(IV) collagen, exon 4
19869	GM_M50_B2_H07_MR	g3002473	BLASTN	947	1e-35	81	Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H66), complete sequence [Homo sapiens]
19870	GM_M50_B2_H12_MR	g3927853	BLASTN	459	4e-15	73	Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angelman Syndrome region, complete sequence [Homo sapiens]
19871	SB_M01_A1_A12_MF	g1769898	BLASTX	111	4e-13	36	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19872	SB_M01_A1_E10_MF	g3142328	BLASTN	919	1e-34	76	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19873	SB_M01_A1_E12_MF	g507910	BLASTN	397	3e-11	74	Glycine max BSR-101 satellite SB92 genomic sequence.
19874	SB_M08_A1_A12_MF	g4049332	BLASTN	471	3e-14	75	Arabidopsis thaliana DNA chromosome 4, BAC clone F8B4 (ESSAII project)

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19875	SB_M08_A1_B03_MR	g3142328	BLASTN	445	4e-13	74	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19876	SB_M08_A1_B10_MR	g3777527	BLASTX	323	3e-35	87	(AF053008) gag-pol polyprotein [Glycine max]
19877	SB_M08_A1_B12_MF	g4092471	BLASTN	424	4e-12	72	Arabidopsis thaliana chromosome IV map near 21 cM, complete sequence [Arabidopsis thaliana]
19878	SB_M08_A1_C08_MR	g2828327	BLASTN	416	1e-12	66	Lycopersicon esculentum cv Red River unknown sequence PCR random amplified RAPD band 10
19879	SB_M08_A1_D04_MR	g507910	BLASTN	524	5e-17	80	Glycine max BSR-101 satellite SB92 genomic sequence.
19880	SB_M08_A1_D07_MF	g2464905	BLASTX	234	6e-19	58	(Z99708) minor allergen [Arabidopsis thaliana]
19881	SB_M08_A1_D12_MF	g2642431	BLASTX	192	7e-13	29	(AC002391) putative retrotransposon polyprotein [Arabidopsis thaliana]
19882	SB_M08_A1_E06_MF	g1769898	BLASTX	241	1e-18	47	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19883	SB_M08_A1_E06_MR	g2522227	BLASTX	234	6e-19	54	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
19884	SB_M08_A1_E12_MF	g18559	BLASTN	565	1e-18	69	G.max gene for catalase
19885	SB_M08_A1_F12_MR	g1575536	BLASTX	163	6e-10	68	(U65533) regulator of nonsense transcript stability [Homo sapiens]
19886	SB_M08_A1_G04_MF	g4063760	BLASTX	239	4e-18	50	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19887	SB_M08_A1_G04_MR	g507910	BLASTN	399	2e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19888	SB_M08_A1_G10_MF	g2996647	BLASTN	377	5e-10	61	Homo sapiens chromosome 16, cosmid clone 390H2 (LANL), complete sequence [Homo sapiens]
19889	SB_M08_A1_G12_MR	g3687234	BLASTX	228	7e-17	58	(AC005169) putative copia-like transposable element [Arabidopsis thaliana]
19890	SB_M08_A1_H08_MR	g507910	BLASTN	349	4e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19891	SB_M08_A1_H11_MR	g18559	BLASTN	750	6e-27	75	G.max gene for catalase
19892	SB_M08_A1_H12_MR	g4063760	BLASTX	180	9e-12	48	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19893	SB_M08_A2_A08_MF	g507910	BLASTN	368	5e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19894	SB_M08_A2_A10_MF	g507910	BLASTN	364	8e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19895	SB_M08_A2_B01_MF	g2864621	BLASTX	137	5e-17	39	hypothetical protein [Arabidopsis thaliana]
19896	SB_M08_A2_B08_MF	g3777527	BLASTX	641	9e-61	92	(AF053008) gag-pol polyprotein [Glycine max]
19897	SB_M08_A2_B10_MF	g18559	BLASTN	897	1e-33	78	G.max gene for catalase
19898	SB_M08_A2_B11_MF	g18559	BLASTN	943	1e-35	76	G.max gene for catalase
19899	SB_M08_A2_C07_MF	g3337395	BLASTN	420	6e-12	63	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence [Homo sapiens]
19900	SB_M08_A2_E02_MF	g407858	BLASTN	374	6e-10	65	P.falciparum (FCR3) cpn60 gene.
19901	SB_M08_A2_E11_MF	g507910	BLASTN	527	3e-17	78	Glycine max BSR-101 satellite SB92 genomic sequence.

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19902	SB_M08_A2_F03_MF	g2443320	BLASTX	145	3e-12	51	(D85597) polyprotein [Oryza australiensis]
19903	SB_M08_A2_G02_MF	g4063756	BLASTN	470	3e-14	70	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19904	SB_M08_A2_G08_MF	g3426334	BLASTN	352	6e-09	59	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
19905	SB_M08_A2_H05_MF	g3600062	BLASTN	367	1e-09	61	Arabidopsis thaliana BAC T25C13
19906	SB_M08_A2_H08_MF	g507910	BLASTN	651	8e-23	85	Glycine max BSR-101 satellite SB92 genomic sequence.
19907	SB_M08_B1_A04_MF	g507910	BLASTN	755	2e-27	92	Glycine max BSR-101 satellite SB92 genomic sequence.
19908	SB_M08_B1_A06_MF	g3702339	BLASTX	219	4e-17	54	(AC005397) unknown protein [Arabidopsis thaliana]
19909	SB_M08_B1_A11_MF	g3142379	BLASTX	216	4e-18	47	(AF053008) envelope-like [Glycine max]
19910	SB_M08_B1_B01_MF	g505129	BLASTN	358	3e-09	67	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
19911	SB_M08_B1_B09_MF	g2864621	BLASTX	95	7e-09	36	hypothetical protein [Arabidopsis thaliana]
19912	SB_M08_B1_C06_MF	g1142699	BLASTN	1107	1e-43	81	Glycine max satellite STR120-A.1.
19913	SB_M08_B1_C11_MF	g1666236	BLASTX	151	2e-09	27	(U76261) unknown [Hordeum vulgare]
19914	SB_M08_B1_D12_MF	g1431738	BLASTN	727	4e-26	92	Soybean (Glycine max) low MW heat shock protein gene (Gmhsp17.5-M).
19915	SB_M08_B1_E04_MF	g507910	BLASTN	358	1e-09	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19916	SB_M08_B1_F04_MF	g4063760	BLASTX	371	4e-32	59	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19917	SB_M08_B1_F12_MF	g905361	BLASTX	712	1e-69	95	(U22103) gag-protease polyprotein [Glycine max]
19918	SB_M08_B1_G01_MF	g1769897	BLASTX	225	4e-17	37	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19919	SB_M08_B1_G03_MF	g3777526	BLASTN	1328	4e-53	88	Glycine max env pseudogene, partial sequence; uncharacterized long terminal repeat, complete sequence; gag-pol polyprotein (pol) gene, complete cds; and envelope-like gene, partial cds
19920	SB_M08_B1_H05_MF	g632064	BLASTX	170	4e-12	37	hypothetical protein - wheat gi 530779 (X79130) Triticum sp. (pAWJL3) leucine rich repeat region mRNA [Triticum aestivum]
19921	SB_M08_B1_H07_MF	g3269286	BLASTX	154	1e-09	55	(AL030978) putative protein [Arabidopsis thaliana]
19922	SB_M08_B1_H10_MF	g3645899	BLASTX	211	4e-15	52	(U68408) 5' end not determined experimentally [Zea mays]
19923	SB_M08_B2_A07_MR	g4063756	BLASTN	375	7e-10	64	Arabidopsis thaliana chromosome II BAC T9F8 genomic sequence, complete sequence [Arabidopsis thaliana]
19924	SB_M08_B2_A09_MR	g3142328	BLASTN	421	5e-12	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19925	SB_M08_B2_B08_MR	g3142328	BLASTN	1829	3e-76	94	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
19926	SB_M08_B2_C09_MR	g2960057	BLASTN	380	4e-10	66	Homo sapiens DNA sequence from BAC 722E9 on chromosome 22q13.2-13.33. Contains ESTs

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19927	SB_M08_B2_D08_MR	g2252828	BLASTX	193	1e-14	37	(AF013293) No definition line found [Arabidopsis thaliana]
19928	SB_M08_B2_D10_MR	g2462058	BLASTX	238	2e-21	41	(Y13389) reverse transcriptase [Antirrhinum majus]
19929	SB_M08_B2_E08_MR	g4165018	BLASTX	155	1e-13	66	(D89053) Acyl-CoA synthetase 3 [Homo sapiens]
19930	SB_M08_B2_F07_MR	g2979574	BLASTN	356	5e-09	63	Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence [Homo sapiens]
19931	SB_M08_B2_G10_MR	g3845197	BLASTN	371	1e-09	62	Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence
19932	SB_M08_B2_H06_MR	g1091678	BLASTX	266	3e-21	37	activator-like transposable element [Pennisetum glaucum]
19933	SB_M08_B2_H08_MR	g3377848	BLASTX	264	6e-22	47	(AF076274) contains similarity to reverse transcriptases (Pfam: rvt.hmm, score: 12.22) [Arabidopsis thaliana]
19934	SB_M09_A1_A04_MR	g629693	BLASTX	458	1e-42	55	probable integrase - common tobacco (fragment) gi 530742 (X80830) integrase [Nicotiana tabacum]
19935	SB_M09_A1_A05_MR	g507910	BLASTN	614	4e-21	83	Glycine max BSR-101 satellite SB92 genomic sequence.
19936	SB_M09_A1_A05_T7	g507910	BLASTN	550	3e-18	79	Glycine max BSR-101 satellite SB92 genomic sequence.
19937	SB_M09_A1_A06_MR	g4063760	BLASTX	171	1e-13	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19938	SB_M09_A1_A08_MR	g2522228	BLASTX	516	8e-49	62	(AB007466) reverse transcriptase-like protein [Vicia faba]
19939	SB_M09_A1_A09_T7	g3777527	BLASTX	623	8e-59	86	(AF053008) gag-pol polyprotein [Glycine max]
19940	SB_M09_A1_A10_MR	g507910	BLASTN	605	1e-20	82	Glycine max BSR-101 satellite SB92 genomic sequence.
19941	SB_M09_A1_A10_T7	g4063760	BLASTX	226	1e-16	58	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19942	SB_M09_A1_A11_T7	g4063760	BLASTX	191	7e-13	66	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19943	SB_M09_A1_B06_T7	g4063760	BLASTX	366	1e-31	53	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19944	SB_M09_A1_B07_MR	g3264544	BLASTN	459	1e-13	63	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
19945	SB_M09_A1_B08_T7	g100484	BLASTX	314	2e-26	50	hypothetical protein - garden snapdragon
19946	SB_M09_A1_C04_MR	g3645899	BLASTX	271	2e-21	56	(U68408) 5' end not determined experimentally [Zea mays]
19947	SB_M09_A1_C06_T7	g2160782	BLASTX	500	4e-47	62	(AF001505) putative ammonium transporter OsAMT1p [Oryza sativa]
19948	SB_M09_A1_C07_T7	g507910	BLASTN	403	1e-11	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19949	SB_M09_A1_C09_MR	g2924341	BLASTN	497	1e-15	63	Saccharomyces cerevisiae mitochondrial Tyr-tRNA, Asn-tRNA and Met-tRNA genes
19950	SB_M09_A1_C11_MR	g4063760	BLASTX	175	3e-11	37	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19951	SB_M09_A1_C11_T7	g3869065	BLASTN	400	5e-11	63	Arabidopsis thaliana genomic DNA, chromosome 5, TAC clone: K24M7, complete sequence [Arabidopsis thaliana]
19952	SB_M09_A1_D02_MR	g507910	BLASTN	381	1e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
19953	SB_M09_A1_D04_T7	g18559	BLASTN	944	9e-36	72	G.max gene for catalase

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19954	SB_M09_A1_D07_MR	g3319372	BLASTX	274	9e-22	43	(AF077409) similar to reverse transcriptases (PFam: rvt.hmm, score: 60.13) [Arabidopsis thaliana]
19955	SB_M09_A1_D07_T7	g2522227	BLASTX	206	5e-16	54	(AB007466) retrotransposon-like gene; the first amino acid was determined to be glycine [Vicia faba]
19956	SB_M09_A1_D10_MR	g100484	BLASTX	329	5e-28	48	hypothetical protein - garden snapdragon
19957	SB_M09_A1_E03_MR	g2129618	BLASTX	168	1e-10	39	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
19958	SB_M09_A1_E07_MF	g3777527	BLASTX	692	3e-66	93	(AF053008) gag-pol polyprotein [Glycine max]
19959	SB_M09_A1_E08_MF	g3097320	BLASTN	634	1e-21	73	Glycine max gene for Bd 30K, complete cds
19960	SB_M09_A1_F03_MR	g3319366	BLASTX	122	6e-10	53	(AF077409) contains similarity to helicases [Arabidopsis thaliana]
19961	SB_M09_A1_F06_MF	g507910	BLASTN	373	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
19962	SB_M09_A1_F06_MR	g507910	BLASTN	373	3e-10	70	Glycine max BSR-101 satellite SB92 genomic sequence.
19963	SB_M09_A1_F07_MF	g905361	BLASTX	654	2e-63	96	(U22103) gag-protease polyprotein [Glycine max]
19964	SB_M09_A1_F08_MR	g2522228	BLASTX	328	7e-29	58	(AB007466) reverse transcriptase-like protein [Vicia faba]
19965	SB_M09_A1_F10_MR	g18559	BLASTN	387	2e-10	76	G.max gene for catalase
19966	SB_M09_A1_G01_MR	g3264544	BLASTN	471	3e-14	67	Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence [Homo sapiens]
19967	SB_M09_A1_G04_MR	g4115365	BLASTX	298	3e-24	61	(AC005957) reverse transcriptase-like protein [Arabidopsis thaliana]
19968	SB_M09_A1_G06_MF	g3777527	BLASTX	310	2e-25	45	(AF053008) gag-pol polyprotein [Glycine max]
19969	SB_M09_A1_G08_MR	g4063760	BLASTX	450	1e-40	56	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19970	SB_M09_A1_G11_MR	g905361	BLASTX	583	7e-56	84	(U22103) gag-protease polyprotein [Glycine max]
19971	SB_M09_A1_G12_MF	g507910	BLASTN	693	1e-24	86	Glycine max BSR-101 satellite SB92 genomic sequence.
19972	SB_M09_A1_H03_MF	g1658457	BLASTX	416	3e-38	78	(U75248) reverse transcriptase [Gossypium barbadense]
19973	SB_M09_A1_H05_MR	g3426334	BLASTN	488	4e-15	61	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
19974	SB_M09_A1_H07_MR	g4063760	BLASTX	174	8e-14	38	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19975	SB_M09_A1_H10_MR	g1666236	BLASTX	203	2e-15	31	(U76261) unknown [Hordeum vulgare]
19976	SB_M09_A1_H12_MR	g3810596	BLASTX	152	9e-16	44	(AC005398) reverse-transcriptase-like protein [Arabidopsis thaliana]
19977	SB_M09_A2_A01_MR	g3645899	BLASTX	159	1e-09	49	(U68408) 5' end not determined experimentally [Zea mays]
19978	SB_M09_A2_A03_MR	g3645899	BLASTX	163	5e-10	48	(U68408) 5' end not determined experimentally [Zea mays]
19979	SB_M09_A2_A04_MR	g2342681	BLASTX	384	9e-34	59	(AC000106) F7G19.9 [Arabidopsis thaliana]
19980	SB_M09_A2_A05_T7	g18559	BLASTN	805	2e-29	73	G.max gene for catalase
19981	SB_M09_A2_A07_MR	g1732513	BLASTX	192	2e-14	70	(U62743) snapdragon myb protein 305 homolog [Arabidopsis thaliana]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
19982	SB_M09_A2_A07_T7	g18559	BLASTN	896	1e-33	75	G.max gene for catalase
19983	SB_M09_A2_B01_T7	g4063760	BLASTX	178	1e-11	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19984	SB_M09_A2_B03_MR	g3080376	BLASTX	171	4e-11	41	(AL022580) putative protein [Arabidopsis thaliana]
19985	SB_M09_A2_B07_MR	g100484	BLASTX	354	9e-31	51	hypothetical protein - garden snapdragon
19986	SB_M09_A2_B07_T7	g18559	BLASTN	590	1e-19	78	G.max gene for catalase
19987	SB_M09_A2_C08_T7	g3097320	BLASTN	710	4e-25	77	Glycine max gene for Bd 30K, complete cds
19988	SB_M09_A2_D02_T7	g4063760	BLASTX	173	5e-11	52	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19989	SB_M09_A2_D12_MR	g4063760	BLASTX	257	6e-20	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19990	SB_M09_A2_E05_MR	g507910	BLASTN	366	6e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19991	SB_M09_A2_E07_MR	g3080353	BLASTX	165	3e-11	66	(AL022580) cytochrome P450 [Arabidopsis thaliana]
19992	SB_M09_A2_F01_MF	g2764526	BLASTN	380	4e-10	63	Pisum sativum genomic DNA encoding the complete Ty3/Gypsy-like retroelement Cyclops-2
19993	SB_M09_A2_F05_MR	g1769898	BLASTX	311	3e-26	68	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
19994	SB_M09_A2_F07_MR	g507910	BLASTN	400	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
19995	SB_M09_A2_G07_MF	g4063760	BLASTX	175	3e-11	46	(AC005561) putative POL3 protein [Arabidopsis thaliana]
19996	SB_M09_A2_G07_MR	g3777527	BLASTX	200	3e-21	64	(AF053008) gag-pol polyprotein [Glycine max]
19997	SB_M09_A2_G10_MR	g905361	BLASTX	337	4e-29	78	(U22103) gag-protease polyprotein [Glycine max]
19998	SB_M09_A2_H01_MF	g3452231	BLASTN	353	6e-09	65	Plasmodium falciparum merozoite surface protein 4, merozoite surface protein 5, merozoite surface protein 2, and adenylosuccinate lyase genes, complete cds
19999	SB_M09_A2_H06_MF	g507910	BLASTN	483	3e-15	80	Glycine max BSR-101 satellite SB92 genomic sequence.
20000	SB_M09_A2_H07_MR	g3980397	BLASTX	156	5e-10	53	(AC004561) putative protein phosphatase 2C [Arabidopsis thaliana]
20001	SB_M09_B2_A04_MF	g4063760	BLASTX	260	3e-20	51	(AC005561) putative POL3 protein [Arabidopsis thaliana]
20002	SB_M09_B2_A05_MF	g3953462	BLASTX	144	7e-09	27	(AC002328) F20N2.7 [Arabidopsis thaliana]
20003	SB_M09_B2_A09_MF	g3142328	BLASTN	951	4e-36	93	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
20004	SB_M09_B2_A10_MF	g505129	BLASTN	391	1e-10	64	Winged bean DNA, Kunitz chymotrypsin inhibitor-3 gene homologous region
20005	SB_M09_B2_A10_MR	g3142328	BLASTN	686	4e-24	77	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
20006	SB_M09_B2_A11_MF	g3077640	BLASTX	324	2e-28	59	(AJ223151) O-methyltransferase [Prunus dulcis]
20007	SB_M09_B2_A12_MF	g2852684	BLASTX	220	3e-16	40	(AF017751) resistance protein candidate [Lactuca sativa]

Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
20008	SB_M09_B2_A12_MR	g13767	BLASTN	339	3e-09	59	Torulopsis glabrata mitochondrial intergenic region ATPase 9 - cytochrome oxidase 2 genes gi 343955 gb M11876 YSLMTIG05 Yeast (T.glabrata) mitochondrial DNA between ATPase subunit 9 and cytochrome oxidase subunit 2 genes.
20009	SB_M09_B2_B04_MF	g1707007	BLASTX	153	4e-09	33	(U78721) hypothetical protein [Arabidopsis thaliana]
20010	SB_M09_B2_B04_MR	g905361	BLASTX	215	7e-16	31	(U22103) gag-protease polyprotein [Glycine max]
20011	SB_M09_B2_B07_MF	g2129618	BLASTX	225	1e-16	41	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
20012	SB_M09_B2_B08_MF	g1769898	BLASTX	179	5e-12	50	(Y08010) lectin receptor kinase [Arabidopsis thaliana]
20013	SB_M09_B2_C03_MR	g2497540	BLASTX	333	2e-29	55	PYRUVATE KINASE, CHLOROPLAST ISOZYME G
20014	SB_M09_B2_C06_MR	g3142328	BLASTN	827	2e-30	70	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
20015	SB_M09_B2_C07_MR	g507910	BLASTN	655	6e-23	86	Glycine max BSR-101 satellite SB92 genomic sequence.
20016	SB_M09_B2_C08_MF	g3122625	BLASTX	211	2e-26	89	PROBABLE 26S PROTEASE REGULATORY SUBUNIT S10B gi 2394434 (AF024493) strong similarity to the AAA family of ATPases [Caenorhabditis elegans]
20017	SB_M09_B2_C09_MR	g13096	BLASTN	369	1e-09	65	Leishmania tarentolae maxicircle DNA fragment
20018	SB_M09_B2_D02_MF	g1142703	BLASTN	288	4e-12	75	Glycine max satellite STR120-B.1.
20019	SB_M09_B2_D03_MR	g2541876	BLASTX	228	2e-17	43	(D26015) CND41, chloroplast nucleoid DNA binding protein [Nicotiana tabacum]
20020	SB_M09_B2_D07_MF	g3777527	BLASTX	598	4e-56	86	(AF053008) gag-pol polyprotein [Glycine max]
20021	SB_M09_B2_D07_MR	g576756	BLASTN	235	3e-11	62	Myrmecia pilosula HI87-133 mitochondrion cytochrome b gene, partial cds.
20022	SB_M09_B2_D12_MR	g100484	BLASTX	150	3e-18	42	hypothetical protein - garden snapdragon
20023	SB_M09_B2_E03_MR	g2443320	BLASTX	117	9e-12	42	(D85597) polyprotein [Oryza australiensis]
20024	SB_M09_B2_E04_MF	g100484	BLASTX	348	4e-30	53	hypothetical protein - garden snapdragon
20025	SB_M09_B2_E06_MR	g100484	BLASTX	332	2e-28	59	hypothetical protein - garden snapdragon
20026	SB_M09_B2_E07_MF	g1272349	BLASTX	238	9e-19	47	(U51740) secreted glycoprotein 3 [Ipomoea trifida]
20027	SB_M09_B2_E07_MR	g3777527	BLASTX	250	5e-19	42	(AF053008) gag-pol polyprotein [Glycine max]
20028	SB_M09_B2_E08_MR	g100484	BLASTX	335	1e-28	60	hypothetical protein - garden snapdragon
20029	SB_M09_B2_E12_MF	g4006831	BLASTX	104	6e-12	38	(AC005970) putative reverse transcriptase [Arabidopsis thaliana]
20030	SB_M09_B2_F03_MF	g507910	BLASTN	339	1e-08	68	Glycine max BSR-101 satellite SB92 genomic sequence.
20031	SB_M09_B2_F04_MF	g2129618	BLASTX	172	5e-11	36	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
20032	SB_M09_B2_F07_MR	g2982253	BLASTX	201	2e-15	78	(AF051209) CROC-1-like protein [Picea mariana]

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20033	SB_M09_B2_F11_MR	g3068704	BLASTX	304	4e-25	44	(AF049236) unknown [Arabidopsis thaliana]
20034	SB_M09_B2_G01_MR	g2522228	BLASTX	339	4e-30	49	(AB007466) reverse transcriptase-like protein [Vicia faba]
20035	SB_M09_B2_G03_MF	g2995405	BLASTX	334	2e-28	58	(Y12432) polyprotein [Ananas comosus]
20036	SB_M09_B2_G03_MR	g2129618	BLASTX	173	4e-11	42	hypothetical protein 1 - Arabidopsis thaliana retrotransposon Athila gi 806535 (X81801) Athila ORF 1 [Arabidopsis thaliana]
20037	SB_M09_B2_G04_MR	g2995405	BLASTX	397	6e-37	65	(Y12432) polyprotein [Ananas comosus]
20038	SB_M09_B2_G08_MR	g2244802	BLASTX	205	1e-15	31	(Z97336) retrovirus-related polyprotein homolog [Arabidopsis thaliana]
20039	SB_M09_B2_H01_MF	g603866	BLASTN	394	6e-11	71	N.tabacum mRNA for L-Glutamate:tRNA-Glu ligase
20040	SB_M09_B2_H04_MF	g507910	BLASTN	395	3e-11	75	Glycine max BSR-101 satellite SB92 genomic sequence.
20041	SB_M09_B2_H04_MR	g507910	BLASTN	395	3e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
20042	SB_M09_B2_H08_MR	g1313966	BLASTX	131	3e-11	44	(Z72425) major allergen Mal d 1 [Malus domestica]
20043	SB_M09_B2_H12_MR	g3645899	BLASTX	217	1e-15	41	(U68408) 5' end not determined experimentally [Zea mays]
20044	SB_M11_B1_A10_MF	g1167523	BLASTX	261	3e-20	49	(D83003) ORF(AA 1-1338) [Nicotiana tabacum]
20045	SB_M11_B1_B04_MF	g507910	BLASTN	398	2e-11	72	Glycine max BSR-101 satellite SB92 genomic sequence.
20046	SB_M11_B1_C08_MF	g507910	BLASTN	362	9e-10	75	Glycine max BSR-101 satellite SB92 genomic sequence.
20047	SB_M11_B1_D06_MF	g507910	BLASTN	377	2e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
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20049	SB_M11_B1_E06_MF	g3426334	BLASTN	585	2e-19	64	Pisum sativum pectin methylesterase (rcpme1) gene, complete cds
20050	SB_M11_B1_F11_MF	g2586082	BLASTX	218	4e-21	56	(U72725) retrofit [Oryza longistaminata]
20051	SB_M11_B2_C03_MR	g2462058	BLASTX	213	1e-16	55	(Y13389) reverse transcriptase [Antirrhinum majus]
20052	SB_M11_B2_C12_MR	g2288997	BLASTX	229	2e-21	77	(AC002335) hypothetical protein [Arabidopsis thaliana]
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20055	SB_M11_B2_E02_MR	g905361	BLASTX	156	2e-09	70	(U22103) gag-protease polyprotein [Glycine max]
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20060	SB_M11_B2_H02_MR	g507910	BLASTN	363	8e-10	72	Glycine max BSR-101 satellite SB92 genomic sequence.
20061	SB_M11_B2_H03_MR	g2623990	BLASTX	121	2e-11	64	(Y13156) ferrochelatase [Arabidopsis thaliana]
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Seq No.	CloneID	NCBI gi	Method	Score	P-value	%Ident	Description
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20065	SB_M12_B1_A03_MR	g507910	BLASTN	343	7e-09	74	Glycine max BSR-101 satellite SB92 genomic sequence.
20066	SB_M12_B1_A07_MR	g3142328	BLASTN	729	5e-26	81	Glycine max partial SIRE-1 sequence ribonuclease H and envelope-like genes, partial cds, and long terminal repeat, complete sequence
20067	SB_M12_B1_B08_MF	g2462936	BLASTX	347	7e-31	56	(Y12321) open reading frame 2 [Brassica oleracea]
20068	SB_M12_B1_B10_MR	g507910	BLASTN	374	3e-10	73	Glycine max BSR-101 satellite SB92 genomic sequence.
20069	SB_M12_B1_E03_MR	g2995405	BLASTX	431	7e-39	63	(Y12432) polyprotein [Ananas comosus]
20070	SB_M12_B1_E05_MR	g18559	BLASTN	601	3e-20	74	G.max gene for catalase
20071	SB_M12_B1_E07_MF	g3377855	BLASTX	294	2e-29	70	(AF076274) contains similarity to reverse trancriptase (Pfam: rvt.hmm, score: 96.80) and CCHC-type zinc fingers (Pfam: zf-CCHC.hmm, score: 14.43) [Arabidopsis thaliana]
20072	SB_M12_B1_F01_MR	g4063760	BLASTX	418	4e-37	57	(AC005561) putative POL3 protein [Arabidopsis thaliana]
20073	SB_M12_B1_F08_MF	g3650039	BLASTX	205	9e-15	52	(AC005396) putative En/Spm transposon protein, 5' partial [Arabidopsis thaliana]
20074	SB_M12_B1_F08_MR	g3097320	BLASTN	349	9e-09	61	Glycine max gene for Bd 30K, complete cds
20075	SB_M12_B1_F09_MF	g2522228	BLASTX	353	2e-31	66	(AB007466) reverse transcriptase-like protein [Vicia faba]
20076	SB_M12_B1_F09_MR	g3420042	BLASTN	355	5e-09	59	Arabidopsis thaliana chromosome II BAC T13E15 genomic sequence, complete sequence [Arabidopsis thaliana]
20077	SB_M12_B1_G04_MR	g2997694	BLASTX	175	1e-12	34	(AF053721) putative retrovirus-related polyprotein [Lithospermum erythrorhizon]
20078	SB_M12_B1_G08_MF	g3550435	BLASTN	412	1e-11	62	Hordeum vulgare Hotr1 gene
20079	SB_M12_B1_G08_MR	g4063760	BLASTX	230	5e-17	47	(AC005561) putative POL3 protein [Arabidopsis thaliana]
20080	SB_M12_B1_G11_MF	g507910	BLASTN	341	8e-09	72	Glycine max BSR-101 satellite SB92 genomic sequence.
20081	SB_M12_B1_H06_MR	g507910	BLASTN	386	8e-11	70	Glycine max BSR-101 satellite SB92 genomic sequence.
20082	SB_M12_B1_H09_MR	g4106406	BLASTN	397	9e-12	62	Sorghum bicolor centromere specific element pHind22, complete sequence

Table Headings

Seq no.

Provides the SEQ ID NO. for the listed sequences.

Clone ID

The clone ID number refers to the particular clone in the PhytoSeq database.

NCBI gi

Each sequence in the GenBank public database is arbitrarily assigned a unique NCBI gi (National Center for Biotechnology Information GenBank Identifier) number. In this table, the NCBI gi number which is associated (in the same row) with a given clone refers to the particular GenBank sequence which is used in the sequence comparison.

Method

The entry in the "Method" column of the table refers to the type of BLAST search that is used for the sequence comparison.

Score

Each entry in the "Score" column of the table refers to the BLAST score that is generated by sequence comparison of the designated clone with the designated GenBank sequence using the designated BLAST method.

P-Value

The entries in the P-Value column refer to the probability that such matches occur by chance.

%Ident

The entries in the "%Ident" column of the table refer to the percentage of identically matched nucleotides (or residues) that exist along the length of that portion of the sequences which is aligned by the BLAST comparison to generate the statistical scores presented.

Description

A description of the database entry referenced in the "NCBI gi" column. Sequences were analyzed by BLASTX against the non-redundant protein database maintained by NCBI, and a description of the top hit is provided.

We claim:

1. A substantially purified nucleic acid molecule, said nucleic acid molecule capable of specifically hybridizing to a second nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof.

2. The substantially purified nucleic acid molecule according to claim 1, wherein said nucleic acid molecule comprises a region having a single nucleotide polymorphism.

3. A transformed cell having a nucleic acid molecule which comprises:

(A) an exogenous promoter region which functions in said cell to cause the production of a mRNA molecule; which is linked to

(B) a structural nucleic acid molecule, wherein said structural nucleic acid molecule encodes a protein or fragment thereof selected from the group consisting of a *Glycine max* protein or fragment thereof in Table 1; which is linked to

(C) a 3' non-translated sequence that functions in said cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of said mRNA molecule.

4. The transformed plant according to claim 3, wherein said structural nucleic acid molecule is in the antisense orientation.

5. The transformed plant according to claim 3, wherein said plant is a dicot.

6. The transformed plant according to claim 3, wherein said plant is a monocot.

7. A transformed plant having a nucleic acid molecule which comprises:

(A) an exogenous promoter region which functions in a plant cell to cause the production of a mRNA molecule wherein said promoter nucleic acid molecule is selected from

the group consisting of SEQ ID NO:1 through SEQ ID NO:20082 or complements thereof or fragment of either; which is linked to

(B) a structural nucleic acid molecule encoding a protein or peptide; which is linked to

(C) a 3' non-translated sequence that functions in a plant cell to cause termination of transcription and addition of polyadenylated ribonucleotides to a 3' end of said mRNA molecule.

8. The transformed plant according to claim 7, wherein said structural nucleic acid molecule is in the antisense orientation.

9. The transformed plant according to claim 7, wherein said plant is a dicot.

10. The transformed plant according to claim 7, wherein said plant is a monocot.

11. A method for determining a genomic polymorphism in a plant that is predictive of a trait comprising the steps:

(A) incubating a marker nucleic acid molecule, under conditions permitting nucleic acid hybridization, and a complementary nucleic acid molecule obtained from said plant, said marker nucleic acid molecule having a nucleic acid sequence selected from the group consisting of SEQ ID NO: 1 through SEQ ID NO: 20082 or complements thereof;

(B) permitting hybridization between said marker nucleic acid molecule and said complementary nucleic acid molecule obtained from said plant; and

(C) detecting the presence of said polymorphism.

Abstract

The present invention is in the field of plant genetics. More specifically the invention relates to nucleic acid molecules and nucleic acid molecules that contain markers, in particular, single nucleotide polymorphism (SNP) and repetitive element markers. In addition, the present invention provides nucleic acid molecules having regulatory elements or encoding proteins or fragments thereof. The invention also relates to proteins and fragments of proteins so encoded and antibodies capable of binding the proteins. The invention also relates to methods of using the nucleic acid molecules, markers, repetitive elements and fragments of repetitive elements, regulatory elements, proteins and fragments of proteins.

<110> Byrum, Joseph R.
Kovalic, David K.

<120> Nucleic Acid Molecules And Other Molecules Associated With Plants

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ttcttcattc taaaaaggga ttaagagacc gagggtctct tgttgtgaaa gaattctaaa 360

cacacaggaa gggttgtcct tgtgtgttta gaacttgtaa aaggaattta caagatagtg 420

gaactctcaa gc 432

<210> 16
<211> 432
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 16

tatcaaccaa atacccacgt tntcaaactc aaagtatatt acaattacaa aacataaata 60

agaaagatct tcacatctat aaaaagactt aatgaacatt aacagaaata aaacctacca 120

gaacctgtaa gtgaaagaaa atatacagac ccatgtaaac tatagaacat agatctaacc 180

ttttaagtgg aaaataacat aaacgtagaa gtatgcaaat gaagatttac caaatgaatt 240

cagtaatagc aactttacct gaaagtgtaa actgttaatg cagcacccaa tccgccaaaa 300

caatgggacc atgatcctct ggaactctac catgttaata acttccaaaa tttcttccag 360

ttcacccaga aacatcacct ctttctgact atttgttgct ggccaatatt tcaacaagcc 420

gcttatcaca at 432

<210> 17
<211> 349
<212> DNA
<213> Glycine max

<400> 17

agcttctata aaggttctta tggactgctt gtctcatcat tccagtaata ccttcaccca 60

caatattgaa aagcaaggga gctaggggat ccccttgcct caaaccccta gaaggattaa 120

actccttaga agggctacca tttatcaaaa ttgatatcga tgctgagtgg aggcaagctg 180

atatccaaga tctccatttt ggacaaaaac ccattctgca cagcatgtaa tccagaaaag 240

accaagaaac tgaatcgtag gccttttcaa agtccacctt aagaatcatc acaggtttct 300

tatttctcct tgcttcctca accacttcat taaggatcag aataccatg 349

<210> 18
<211> 451
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 18

tntaaggccc tcaaatgact ggatggcaac accccactta aatgattatg aaagagggat 60

aaatatgtga gattcttgga caaattaaaa gaaggaagtg gacctgtaaa gttattggaa 120

gacaagtcta gataaacaag ttggctgagt tctgagaatg aactaggaag tgttccatta 180

aattggcagt aagctagatc aattgtagat aactgcttca tattggaaat tgcacctgga 240

agctttcctg agaaatttgt atagctaaga ttcatgtgat gaagagaacc atgttgtggg 300

aagtttggca aagaaccccc aagatcttgg ttgtctgaga tgtcaaggac cttcaacgtt 360

gatatttgga atatatcttt tggaaaagaa ccattcaagc cacaacttct taactctagt 420

gtgactaaat tggagaaatt acaaaggatt c 451

<210> 19

<211> 406
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 19

agcttgtcaa ggccctaagc atggacaagt gttgttcagt gttgagagtg gtagccttga 60

caagtgttgt ccgggttgct tctgtcaagt tgtctggggt ggacaccctt tttgatgcaa 120

gaggctccaa gaggattggg ctagagctgc tgaagaaggt cctaaggttc tcatgaactt 180

taggatagat ttttgagccc atgggccaag gttgggtcca attatctttg tacgtattag 240

attacgatgt cactatattt ggttcttgta attagggctc cataatgtag gtagggtacc 300

ctagaaatat aggatttttc agcccttgta ttttagggca cctagactag ttnttgtatt 360

aagggtagtt ttgtaatttc acatgcacta agtgaatatt taatgt 406

<210> 20
<211> 460
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 20

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cttttaacaa tttaactaag tccttatttg tgattttctt gatcttattt gttgacttgg 120

aacaatgtgt gctttcatca agtaaattct tttggcatca tcaaaacctg cacgattcac 180

atttatgtca ctcaacctct aggttttgag atcaaaagga aggaattaat ggtgtacaag 240

ttgaataagg ccttgtatgg tcttaaacaa gcacctagag cctggaatag aaggattgac 300

tcatttttca tttagaatga attcaccaag tacacaatgg aatatgatgt atatgtgaaa 360

aggaaaacta agggaatact tttgatttgc ctatatgctg atgatttgct tgtgactggc 420

agcaatagtg aagaaataga gaaattcaaa gttgagatga 460

<210> 21
<211> 407
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 21

atgatataag actttgaggc caaactatat ccaatatcan aatgaggaat cttttaacaa 60

tttaactaag tccttatttg tgattttctt gatcttattt ggtgacttgg aacaatgtgt 120

gctttcatca cgtaaattct tttggcctca tcagaacctg cacgattcac atttatgtca 180

ctcctcctct aggttgtgag atcacaagga gggatttaaa ggcgtacacg tcgaataaag 240

ccttgtatgg tcttagacca gcacctacag cctggaatat aaggattgac tcagtttaca 300

ttgacaatga cttcaccaac tacacagtgg aatatgatgt gtatgagaaa aggataacta 360

cgggaatact tttgatctgc ctatatgctt atgatttgct tgtgact 407

<210> 22
<211> 427
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 22

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ttccacaagg gaagctcttg ctgcagaact tgcacatgtg tttcacttct tgatcttctt 120

ccattggatt gatttttcaa gatcacacac acgcacggat cagcaaagaa agcaaaatta 180

accacacttt cttgatcacc accaacacaa gagaaatcga tcacaaggga aaaacagcaa 240

caccccagat cagcatcaca tcttgaaagt ggttggagag aagaataata ccgagaagaa 300

gaagaagaga aaccccatgt ctgaaaattg caaggtggtg agtgcaagat ctaacgcaga 360

aaacaagagg aaaagaaaag ggacaagaga acgtgtagta gtagcacaaa ctattatata 420

tactata 427

<210> 23
<211> 427
<212> DNA
<213> Glycine max

<400> 23

taaacattca atttcgagcg tctccatata ttacgcgact caatcagaca tctgagtaaa 60

aagttattgt cgtttgaatt ggctcagagg ttcaacattc aattttgagc atctcgatat 120

attacgggac tcaatcagac atccgagtaa aaagttattg tcgtttgaaa tggctcagag 180

cttcaacatt caatttcgag cgtctcgata tattacggga ctcaatcaga catccgagta 240

aaaagatatt gtcgtttgaa ttggctcaga ggttcaacat ataatttgga gcgtctcgat 300

atattatggg actaaatcag acatccgagt aaaaagttat tgtcgtgtga attggctcat 360

aggttgaaca ttcaatttcg agcgtctcga tatattatgg gactcaatca gacatccgag 420

taaaaag 427

<210> 24
<211> 397
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 24

agctttaagc caattcatac gacaataact ttntactcgg atgtctgatt gagtcccgta 60

atataacgaa acgctcgaaa ttgaatgttg aagctctaac cctattcaaa caacaataac 120

gttttactcg gatgtctgaa tgagtctcgt aatatatcga cacgctcgaa attgaatgtt 180

gaagctctaa gcctattcaa acaacaataa cgttttactc ggatgtccga ttgagtgacg 240

taatatatcg agacggtcga aattgaatgg tgaacctatg agccaattta aacgacaata 300

acttttttact cggatgtctg attgagtccc gtatatatcg agacgctcaa aatgaatgtt 360

gacctctgag ccattcaaga caatactttt actcgat 397

<210> 25
<211> 405
<212> DNA
<213> Glycine max

<400> 25

agcttcttag tttcagatga tccagatggg tttgtagcta cctcatgcac tcctctaatg 60

actatggcat catttctggc gctaaactgc tgggagttgg aggccatctt ctcaattaaa 120

tttctggctt cagcaggagt catgtctcca agggctccac cactggcagc atctatcata 180

cttctctcca tattactgag tccttcataa aaatattgga gaagaagctg ttctgaaatc 240

tgatggtggg ggcaactggc acatagtttc ttatatctct cccagtactc atacaggctc 300

tctccactga gttgtctaat acctgagata ttcttcctga tggctgtggt cctggaagca 360

gggaaatttt tttctaagaa tactctctta aggtcatccc agctc 405

<210> 26
<211> 312
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 26

agcttgtatg ggtgagttat aaattataat acctcagctt ggttcaaaag atcatgttta 60

ctccgtcgca cgttgagcaa gttttgcaca gcttgcccct ctatggacat cctcacccga 120

ctagctctta ctctggcctg aactcgaacc aatgcctgca tgcaccttaa tgtccncgct 180

gtctgcttcc tcacctgtct ccccccgaac aagtgcttga atcctcacca ctggcttcaa 240

tgccctcaaa gcccttcttg cctgcaatca ccacacaagt gatgtcgaaa tataatgttg 300

gtctaatggt aa 312

<210> 27
<211> 394
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 27

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tattaatatt gtcaagctaa aggcacaatt tttgttatgc taattgataa caatgataga 120

aatgatctta gatacaccaa gctgccttgg atatgatgtt tgattcgatg atgattgggt 180

agtcagagta aatgttagtt tagagaggaa gaattaacta agttaattat attaaagatt 240

aataatttga aatgagacta ttaaaacata tagataataa attgtcataa tgaaaagttt 300

acgatctgtt tggaatatga taaaatagga taagatatac cattatgata aactttaggt 360

ttatttaata tttgatgcac actanataat atta 394

<210> 28
<211> 340
<212> DNA
<213> Glycine max

<400> 28

agctttcagc tatgtatctc attagtaata ctttttcgtg ctgttggatg ggcaacaatt 60

gcctccttgg tggtgatagt aatcactgtg ctttgcaata ctccactcgc aaagttacag 120

cacaagtttc aaagcaaact tatggtgaca caagatgata gattgaaggc ttgttctgag 180

gctcttgtga atatgaaggt gttgaagttg tatgcgtggg aaaccaattt tagaagttct 240

atagagagat taaggaatga ggagctcaaa tggttgtctg cagtgcaatt aagaaaggca 300

tacaacacct ttctcttttg gcctctcctg agttggctct 340

<210> 29
<211> 376
<212> DNA
<213> Glycine max

<400> 29

ctgaatgctc tattcaatgg agttgacaag aataccttca gactgatcaa cacttgcaca 60

gtggccaaag atgcgtggga gatcctgaaa accactcatg aaggaacctc caaagtgaag 120

atgtccagat tgcaactatt ggccacaaaa ttcgaaaatc tgaagatgaa ggaggaagaa 180

tgtattcatg acttccacat gaacattctt gaaattgcca atgcttgcac tgccttggga 240

gagagaatga cagatgaaaa gctggtgaga aagatcctca catccttgcc taagagattt 300

gacatgaaag tcactgcaat agaggaggcc caagacattt gcaacatgag agtagatgaa 360

ctcattggtt cccttc 376

<210> 30
<211> 396
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 30

agcttcatgc ttaactatgt atggaaaaac ttcattactg ttgttcaaga catacaagtg 60

agcttgtaac aaatcttcta cacttggagt gatcacctgc agtcctcttg aacccttacc 120

acccactctg tcatcatgcc gacactcagg aagcccaaca gctttagcct tctctaagta 180

ttctgaacaa aattcaatgg cttcttctgc aatgtacctc tcaacaatag atgcttccgg 240

acgatataga ttctttgtat acccttttaa gatcttcatt tatcgctcaa ccgggtacat 300

ccaccgtaga taaacaggac cacagcattt gatttctctg accagatgca caatcaagtg 360

aatcatgatg tcaaagaaag cangggaaaa tacatc 396

<210> 31
<211> 403
<212> DNA
<213> Glycine max

<400> 31

agcttaacaa tccttttgat ctatttcaaa atatttctat ccctatcata taacttgcct 60

cactcatatc cttcatttta aagttacaag agagaaactt tttcgttgag cattttttcta 120

aattggaaat tgtgatgttg agcatttttc catcttaaat ctctctagta ctttattgat 180

atatgctttt tgagacaagc ttaacaatcc tatgatctat ttcagaatat ttctatccct 240

atcacaaaac ttgcctcacc catatccttc atttcaaagt tattagagag aaacttctta 300

gtctcatgaa gaagatcaag atcattagtt gcaagcaata tatcatcaat atacaggatt 360

agaaaaataa ccttactcct actgaccttc agatatatac att 403

<210> 32
<211> 387
<212> DNA
<213> Glycine max

<400> 32

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aaggcgccta ctctcagctc ttctactttg tcttccgctg catctacatg gtggaaaatc 120

actattaaag gacctcattg aagctcacag atccaacctg catagagacc ccacaggcaa 180

gcttccatca taaccactct atttgcccta ccagggatat ccaacttgga cactgcactc 240

gccaagtaca tacacgacat acatcattac aatgacacta tcaacatcca cagcatctaa 300

gtctgatgac actatgatca tctacctgat cccgtctcga tgtcattctc aacatcaaca 360

gtatctgatc tcaatgacat aatcaac 387

<210> 33
<211> 377
<212> DNA
<213> Glycine max

<400> 33

tgaaggatgt aagattctgt gattcttcaa tgtccaccac aatgtgatca aactttgatg 60

tcagtgttct gagcaccttc tcaatcacca gttgttcctt aatttgttct ccacagcact 120

tcatctaatt ggtgagtgtg agaatcttgg tgaaatactc agctactgat tcagtctcct 180

ccattgcaag aagctcatac tgtcttctca atgtctgaag ctttaccttc tttatctttt 240

ctccaaagat aatccaatat ttatttagat caagatatct aaatatatat tttagtaaag 300

taaaagatag atacaattgc tttaatatat tatattgtta ttcttattct cgaaagatgt 360

tattatcata atatatt 377

<210> 34
<211> 381
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 34

ngccgccacg gagttntccg actatgctct tgtgtgttgg aacaagctac aaaaggagag 60

agcaagaaat gaagagccaa tggttgatac atggacggag atgaaaaaga tcatgaggaa 120

gcggtatgtt ccggctagtt actcaaggga cttgaaattc aagctccaaa aactaaccca 180

aggcaacaag ggggttgagg agtatttcaa ggaaatggat gtgctcatga ttcaagcaaa 240

tattgaagaa gatgaggagg taactatggc tcgatttctt aatggtttga ctaatgatat 300

ccgcgatatt gttgagctgc aggagtttgt tgaaatggat gatttgcttc acaaagcaat 360

ccaagtggag caacaattaa a 381

<210> 35
<211> 324
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 35

agcttgaaat tgaacaacgg aagctctcga gaaaatcgag tggtcataaa ttttcacaca 60

gatgtccgat tcggggaaat aatatatcga gacgcacgaa attgaacaac ggaagctctc 120

gagaaatttg aatggtcata acatttcact cggatgttcg atccggggac ataatttatc 180

gagacgctcg aaattgaaca accgaagctc tcgacanatt agaatggtcg taacttttca 240

cgcgaatgtt cgattcgngg acataactca tctagacgct cgaaattgaa caacggaagc 300

tctcgagaaa tttgaatggt cata 324

<210> 36
<211> 439
<212> DNA
<213> Glycine max

<400> 36

gtctccacta agttgcctaa tgcctgaaat gtcttttctg atggcagagg tcctagatgc 60

agggaagaat ttctccaaga acaccctctt aaggtcatcc cagttgaaaa tggacctggg 120

agcaaggtag tatagccaat cttttgccac tccctccaga gaatgaggaa aagcctttag 180

aaagatatga tcttcttgaa catcacgggg cttcatggtg taacaaacaa tatggaactc 240

cttaagatgc ttataaggat cttcacctgc aagaccatga aacttgtgca gcaaatgtat 300

tagtccagcc ttgagaacat aaggaacacc ttcatcagga tattgaatgc acaagctttc 360

ataagtgaaa tcaggtgcag ccatctccct aagagtcctc tcacgaagtg gaggtagagc 420

catgttctca gtatgaaaa 439

<210> 37
<211> 455
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 37

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ttgtcattct tgtttagttg cttgtaaatc tgaaggtgac attccaggat gcgttgcctt 120

tgttgggctg atatcttcat ttaatcaaaa tgacagatca acaaagtatt ctttatttt 180

gcataaagga tatagatgtt tgaaatcttc atgaccatct gcacataaag aagaaatttc 240

ttgtttaaat tctccaactt ctggtgggac ttttgctaaa gaaaaaaagc ctaatcattt 300

cttaaaaagg cttgaaattt cttttaaatt tgatccctgt agaatgtaat tgaagtttac 360

tggcagtagt atagacatcc attcctatga ggagatctct gtcgggcagt ttacttccaa 420

tgaccttggt ccanatgata caatcaggga aaaac 455

<210> 38
<211> 318
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 38

cacccgacga agagactgac aaaaacttat tctcttcttt ttggacaaag tattgcaagc 60

tgggggcaag ttaattttct taccatcaaa ccttggatgc aactgtgaac gtatgcccat 120

attagctaaa tgttgacggg tattcaagcc atccttcgtc tctgcctgaa tgttaaggag 180

cagtccaatc acactggcac aaacattntt cttcacatgc ataacatcaa tacaatgtct 240

aacgtcagga tcagaccagt tcggaaaaca aagaatatag acctcttctt tcatatgcaa 300

ctcttacttt tatacttc 318

<210> 39
<211> 461
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 39

tgtggttntt agcgatactc accaaaattg tgtaacacaa gcntacatca agtttatcat 60

gtcctagaag atccagttga acaacatcaa acacaaaatg ttgagcaact ttttgaacaa 120

catcaaacac aagatgttga acaacctgtt gaacaacaac caaaaggtgt ggatgtaaca 180

ttgagaagat caactagaat aaagaaacct gtaattccta gtgattatca tgtgtattca 240

caagagtctc aatatgactt tggagttgaa aatgatcctg agtcattttt gcaagcaatt 300

aacagttgtg attctaagct atggtatgat gctatgaaag atgaattgga atctatggta 360

aataataaag tatgggatct tgtagagttt cctaatggga taaagcctat tggatgtaaa 420

tgggttttca naaccaagaa ggattcatta ggtaacattg a 461

<210> 40
<211> 441
<212> DNA
<213> Glycine max

<400> 40

actcagctaa ccatgatgga aagtactgac caaatagaat ctttttatct ttaggattag 60

aacatatgat caagccagca ttaatgtttg ggacgtgtat ggtgatcaag aatcatttca 120

tctcttaatt caatcatctt acaatatgat ttatcaacaa ttaacaacta tgataaaaac 180

taagaccatt tcaatataat taaacgtaaa atacttaatt attcacagta ataattaaga 240

ataaaactta atagattgat ttatttatta ctccatcctt gactttcttt ctagagaata 300

gtagctttta tgtatctgtc attacaaagt tcagaagatc atattaagta tgtttgatat 360

cacatatacc cttagatatt tctctatcta taatcaaatc ttacatgtaa atgatgtaat 420

taccatggag tggagagaga g 441

<210> 41
<211> 457
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 41

tgaagaaatn gctaaggaaa atgtgaaatt atgaagtgat cttttctttt atattatgag 60

tatgnggctt taagcaatga agagtcatcc tcaaatgaaa ggaatgttgg tggcataaac 120

tctgtaactg tccatgtgcc taatacatct gctatgacta ggtttgatca attaatgagc 180

cttatgcatg acaaggaaat aattccacca atgaaatcag aactagatgc ttatcttgag 240

aagaaaaata cttatattcc taataatgga aactcctctt ttattgcctt ggagtggtgg 300

aggaataaca acttcaaata taagatttta tcaaagatgg caagagatac actagttgtt 360

ccagtatcaa tcgttgcatc acaatctaca tttagggctg gaggtagagt aattgatgag 420

tatcgttcta gattgaatga agaatctatt gaagctc 457

<210> 42
<211> 461
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 42

gggagaacca agatgcactg gcccagatgt caaggagttc attatttttg tgaattgaga 60

aacgatcttt gattgtaata gaattcaagg ccctgtaatc cacacacatg cgtcaagttc 120

catccttctt tttcacgagt aacactggag aggagaatgg gcttcgactg tgttgcatta 180

aactggaatt gagtaattcc ataactgtcg ttcaatttcc gacttctgga agtatggata 240

tttgtagggt ctaacatatg ttttgccttc aaaaaaaatt atttgctgat taacagaaaa 300

tgagaaacga gcaactcatt atataaaggg aaataacgtt ttgaagatga tttaattatg 360

aaaaaaggac aaattaaccg gatatatttt tacctctctt ttcttctttg tggtttgagg 420

attttttttgg atggtggctn ttgtcgccct caccaacatt a 461

<210> 43
<211> 156
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 43

tcttggatgg ctactcggng tataattaga tagcagtaga tcctaaagac caagaaaaaa 60

atggctttac atgccctttc ggtgtcttta cttacagaag ggatgccatt gngttatgta 120

atggccttgc caccttccaa agatgtatgc tagcta 156

<210> 44
<211> 442
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 44

taataaatct atatatggtt taaaacaagc ctcctgtagt gtttccttaa gtttcatggg 60

ataatttctt catttgattt tgatgaanac cccatggatt aatgcatata ccacaaggta 120

agtgggaagt aaaatatgtt tcttgtttta tatgttgatg atattttact tgacaccaat 180

gatcgaggtt tgctacatga agtgaaacaa tttcaatcta agaattttga catgaaagat 240

atggatgatg catcttatgt catcgacatt aagattaata gagataaacc tcgaggtatt 300

ttgggtctat cacaggaaac ctatattaac aaaactctag agagatttcg gatganagat 360

tgttcacgaa gggttgctcc cattgtgaag ggtgataggt ttagtttgaa ccagtgccca 420

nagaatgact ttgagaggga ac 442

<210> 45
<211> 436

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 45

ntggaatatt attttcgggc gctcgagcga aacccattct tactccaagc ttttaataat 60

atggccggga tctgtcatta cgtgcgacta tctccactat agaaagaaaa aagaaaagaa 120

caagctaatc cacaaatact aatataataa atactagaaa taaaggcttt ctacatatac 180

atatatcgtc caaaacaacg attnttatca gctgtagcaa agaatgaaac ttcatagaag 240

tcaaaatatg aagaaatcaa tatgtctaga tacccccttt tctatggata aaagatctaa 300

ttgataaagg aagcatcgta aggatccatt aacgcggttn tgaaccgata caataaaaac 360

tgcttactta tctcatgata gaaaagtcag gaatccactt atgtaataca gtagaatccc 420

cgatattntg agcagc 436

<210> 46
<211> 220
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 46

tcgtcttatt canaaccnca accaattatg anatccncta tctcccactt cacacctcgg 60

aacgcaccgt tcttatagag agaggcgctn tcacatcntt cttaggctgg gagaggaaat 120

gttcccatnt tttatgatac tccggngaac agatatccag tggagatgac ggngtggngc 180

ctgtagctca gaggattaga gcacgtggct acgaaccacg 220

<210> 47
<211> 405
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 47

tatgctgcat acattgataa tagacctcct cagctgcaaa tcttatctca gtagaataat 60

tatgaccttt caagcaatag atactattct cctnggagga ataatacaaa tgtgagatgg 120

acaagtaact ccacaagaac aatagcctgt tcttcatttt tagaatgttg ctggtccaag 180

caagccatat gttccttctc caatacagca gcagttacaa taaagacaac aagcagtttc 240

aacctttctt ataagagtta gtgagacaaa tgaccttcca gaatatgcga tttctagaag 300

agacaagagc cttcattcat agtctgacaa atcagatggc gcagatgggt actcatatga 360

accaagctta gtcccaaaat tttgacaaat tgtttcacaa gctgt 405

<210> 48
<211> 259
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 48

gtaatattat agccgatgct ctntctcggc gtcatgcatt actttctatg cttgaaacan 60

naatgattgg tcttgaatgt ttgaanaaca tgtatgaaaa tgatgaaact nttggagaaa 120

ttttttaaaa ttatgatatt ttttcagaan atggtttctt tagacatgaa ggctttcttt 180

tcaaagaaaa cannatgtgt gtgcctaaat tntctactag aaatttgctt gttttgtgaa 240

gcacatgaag gaggttaat 259

<210> 49
<211> 338
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 49

acatctaact cagactaccg attcatgcca ataatatatc gagacgcttg anattgaaca 60

acggaagctc tcgagagatt caaatggtca taactnttca catggatgtc caattcaagt 120

gcataatatt ctgagatgct ctaaatttaa catggaagca caagggaaat tanaacggcc 180

ataacctata acaaggatgt ccgattcagg ccaataatat attgagacgc tcgatattga 240

acacttatgc tctcaagaga ttcanatngt catacattnt cactcggatg tccgattcag 300

acgcataata taccaacatg ctcgatatta aacatcac 338

<210> 50
<211> 446
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 50

tccnctcccn ctcttttaag ataaaagaaa ataatttatc aatttattga taatcatcat 60

aaagaattaa atattntaaa aaattaacaa ctaanagatt gagtgtttcg attggatatc 120

gagttggagt ttatattttc gttgctcatt tgacttctgc ttatttattc tttgactgtt 180

gtgtgaattg aggtgttgtt tatctaagat taattcttat taaatttctt ctgttggagg 240

attaagtaat taaaatcaat gaattntacc attttgaagt tagtaaagtg gaaattttta 300

tacactgatg aataatgaag aaaacaaatt tataatttat tatacactta cgtatattca 360

catgtctaac cgatgaattt aaatcagaga cgatattttc ttaattaaaa cattttanag 420

aaatgaaact tanaactgat taatca 446

<210> 51
<211> 239
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 51

atggtgtctt ggagcgtgct tgtgattntn tctttcgcca tgctgcacaa ctntcaggtg 60

ttcccttgag aatggtggag agaagcagaa ggcagttccc tcttagaana gcccgtgatg 120

ctgcagaaga catgctctct gggctactca nagccaaggg tgatggattc atgacattga 180

tcgaaaatgg taaatggatg tgtgacgagg cacctcacag tggaaatgaa tatgtaaac 239

<210> 52
<211> 458
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 52

tcaagaatta tggcctcatc aaactacttg tttcccgagg gattttctat aaatagacct 60

cccatcttta atggagtggg ttaccactac tggaaaaccc gcatgcaaat ctttatagag 120

gcaatagatt taaatatttg ggaagccata gaacaaggac cttatgttcc cactataatg 180

gccggaagtg caacaataga aaaacctaga gcagattgga ttgaggaaga aagaagatta 240

gtacaatata atttaaaggc caaaaatatt attacatctg ccctaggaat agatgaatac 300

tttagggttt caaattgtaa aagtgctaag gaaatgtggg atacactaca ggtaacacat 360

gaaggcacta cagatgttaa aagctctagg ataaacactn taactcgtga atatgaactg 420

ttcanaatga atgtaaatga aagtatacaa gacatgca 458

<210> 53
<211> 224
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 53

catctacaac agacctcctt aacctcagca gtatattcat ccacaacaga ataattatga 60

cctctccagc aacaggtaca atcccgagtg gagaatcatc ccaaccttag atggtcgaat 120

ccttcacaac aacagcagca acaacaacaa ccttaatttc anaatgctgc tggcccaagc 180

agaccatacg ttcctccacc aatccagcaa caacaacagc aaca 224

<210> 54
<211> 290
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 54

gtttaagtct tctaaactgc ctatctatat tccatagcct ataacaactt ccgtgtgccc 60

atcggcttgt gggtgacaag ccggtgacaa taacaattta atgcccaact tgctccacaa 120

agtcctccan anatggctta agaacttaga gtccctatca ctaacaatgc tccttggcat 180

accatggagt ctcacaatct ccttgaataa cacatcagcc acatgggaag catcatcaac 240

tttcttacat ggaatataat gagccattnt agaacaccta tcaacaacca 290

<210> 55
<211> 272
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 55

gctcttaact gcacaaggct cttaatatgt gaagagtatc cttgtgtaac cttcacncga 60

cgaagacact gacanagact tatcttcttc ttattggaca cagtatggca ggctggcggc 120

aagtaaatat tcatcccatc agaccttgga tgcaactgtg atcgtatgcc catatcagct 180

agatcttaac gggtattcaa gccatccttc gtcttgcctt gaatggtaag gagcgtacca 240

atcacactgt cacaaacatt gttctccaca tg 272

<210> 56
<211> 423
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 56

ttatgcaggg aagctaagtg tgaagtatgc aatcctgcat atgtttggcg ctgcaaactg 60

ggtacccacc aatcacactt ccactgttgc cacaggtttg ggtaaatttc tgtatgctgt 120

tggaaccaag tccaaattta attttggaaa ctatattttt gatcaaactg ttaagcattc 180

agaatctttt gctgtcaaat tacccattgc cttcccaact gtattgtgtg gcattatgtt 240

gagtcaacat cccaatatct taaacaacat tgactctgtg atgaagagag aatctcctct 300

atccctgcat tacaaactgt ntgaggggac acatgtccca gacattgtct cgacatcagg 360

gaaagctgct gcttcaggtg ctgtgtccaa ggatgctttt gatgctgaac tcaaggacac 420

atg 423

<210> 57
<211> 449
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 57

ntaatgtgtt ctcccttgta gaactactaa ctgcagtaac agttgcagtc catctatccg 60

gtagtgatga caatagaatc aattccttca cctcatcctc aaatttaatt tgcactgact 120

ccaactgggc aagaatagta ttaagttcat taatatgatt agttatagag ttagcttctc 180

ccatcttgag gttgaacaac cgacgcatca agtatacttt cttggctgca gatggcttct 240

cgtacatatc tganaacgcc ttcattaagt ctgcagtagt cttctcgttt atgatgttga 300

atgcgacgtt cttggctaat gtgaatctaa tcacgccaag agcttgtcga tctagcaagt 360

tccattcttc ttgcctcatg tcatctggct tatcccctga tcagggttga tacaacttct 420

tctgatatag ataatcctct atctgcatc 449

<210> 58
<211> 373
<212> DNA
<213> Glycine max

<400> 58

gttgtcgctg agaaactggt tcccagaaga ttttttgagt gattattgct gaaaacccta 60

gccctgcaac gagtcctacg gaagtagaca cggagatgga caagaaaata cggtgtattg 120

tgagtagctt tttgaaagac gcctctgtac ctgaagctga tgaagatgtc ccaacatcgt 180

ccaacccaaa tgtttctgtg cctgatgtct agatagatgt tctaacatct tccggcccaa 240

atgctgaagt actctctttc cccagcacag agagatcaac agaggaagat gatcaagcct 300

cagaggagac tcctgcacca agggcaccag aacctgctcc aggtaacctc attgaccttg 360

aagaagtaga atc 373

<210> 59
<211> 402
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 59

gctagagctt agctacacat acctctctaa tagctaagct cacctccttg agatgagaag 60

ctagagctta gctacacacc cnctataata gctaagctca cccncatgac ananaaaaca 120

tganaataca aaanaaagtc cttactacaa agactactca naatgccccg aaatacaagg 180

ctaaaaccct atactattag aatggccaaa atacaaggcc caaacgaaga anaaacctat 240

tctaatattt acaaagataa gcgggtcatg cttagcccat gggctcgaaa tctaccctaa 300

ggctcatgag aaccttangg ccttcctttg atctctagcc caatctactt ggagtcttct 360

acccaatgcc cttgcaggat aggattgcat cacatgtcat ga 402

<210> 60
<211> 219
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 60

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gattggtctt gaatgtttga aaagcatgta tgaaaatgat gaaactnttg gagaaatctt 120

tagaaattgt gagaaatttt cagagnatgg tttctttaga catgaaggct ttcttttcan 180

agaaaacaaa ttgtgtgtgc ctaaatgttc tactagaaa 219

<210> 61
<211> 353
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 61

cgacacataa ctcccaccgc atatagaata tcgggccttg tattggttag ataccttata 60

ctccccacaa gactcttgaa gaccgtggaa tctaccttct ctccttcatc aaactttgat 120

agcttcaagc caccttccat atgtgtgttc acgggattgc aatcaagcat attatatatc 180

ttcaacactt cttttgtgta gctttcttgt gagacacaga taccattctc ccgttgttca 240

cttncattcc caagtatatg acatgagtcc atatttgcat atcaattcac agacatgact 300

cttgagtctc aacaatttgg tattgcgata aataggcatc cctaaacaat aat 353

<210> 62
<211> 365
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 62

ctctacaatt gcatcacctc tcaatgatct ggtgaagaag aatgtggcat ttacctgtgg 60

tgaaaaaaag gagcaagcct ttgctttgct caaagaaaag cttactaagg ctncagttct 120

agctcttcct gactnttcta anactttnga gctagaatgt gatgcctctg gagtgggagt 180

tagagctgta ttngtacaag gtgggcactc tattgcttat tttagtgaan aacttcatag 240

tgccaccctc aactacccca cctatgataa agagctntat gccttaataa gagccctcca 300

nacttgnnga atataccttn gttccanggg aattgcattc atagtgatca tcaatcactt 360

aagta 365

<210> 63
<211> 301
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 63

agagacatga aagaccggat gagntttact gtgagatgga agatctaact tataagcaac 60

aacacccacc ttatntaaca cctggaaagg accataaaat cgangggaga gnttttcatt 120

aatccttnta gccaaggatc ttctcttgta gggtgcatct tcaagaacac ccaatcaccg 180

actgtgtatt ctatgtcctg acgaacgttt gtggcattng ctcgcatgat atcttgagac 240

ttcaacanga tttctcttat agtagccaat aattaatcta agcaannttg tagttattga 300

c 301

<210> 64
<211> 341
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 64

tctacacctg ttgcaagagt ctgtggtcta tgttcttcta cagatcacca tacagatctc 60

ggtccttctt tgtagcaatc tggagtcaat gagcaacctg aagcttatgc tgcatacatt 120

tataatagac ctcctcagca gcaaaaccaa caacagaaaa ataattatga cctttcaagc 180

aatagataca atctaggttg gaggaatcat ccaaatctga gatggacaag tccttcacaa 240

caacaacagc ttatcgcttc tttctagaat gctgctggtc caagcaagcc atatgtntct 300

tctncaatac agcaacaaca gtcacaaana agacaacaag c 341

<210> 65
<211> 488
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 65

atctccttct tcactacatc aagaatcacc gngttgagtc ttctctgtgg ctgtcttact 60

gggttagctc catcttctan atntattcga tgcatacatg tggatgggct aataccagga 120

atgtccgcca gggtccagcc tatagccttc ttatgcttct tgagaactga caacaacttc 180

tcctcttgct catcagcaag ggaggcagat ataatcactg gagaactctt gctatcatcc 240

aagtaagcgt attntaaatn tgatggcaga ggcttcaatt ctggtgtggt cggctggaca 300

gtggtagaag gagatggttt ctcagccttt acctcataaa gaaagtcaga ggtatgtgta 360

cttcctgaaa catggttagt cctatctgac tctatnaaat caatctcaag aggtanaaca 420

ccaccaccag gcatgcantc aatatcactc tcagaatcac tctcagcatc anattcagac 480

atatgatc 488

<210> 66
<211> 396
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 66

cacacatgta gtgaacatct atgataacct gcttcgtgta agcattgtgt tagctataat 60

ntatgaagaa ccacttctag ttctataatt gtacaacata ttagcatatg ccanactatg 120

tgtatcattt ggatcaccag aataagaata ttacctcaat aaaatctcct tttggcatta 180

gtgctctgca tgcatctcta ntcctttggt atggtgatat taaactagtg atgcaaataa 240

caccagcatc tgcaaagaag ttagccacct cacctgaana tntaaatcgt gatgtctaan 300

tattaataaa acaataaaat ataatcggaa gatatcaggg anagcattta gaaagcaaca 360

taagaaaaaa cagaataact caccaatcct tctaat 396

<210> 67
<211> 358
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 67

gtatgtgtat gcagaagatg ataggatgaa gctaacttac aataattcca tgtgctcctc 60

tatagtaact gcttgntata gtcctgaatc gctcctgtcc agctgtatcc cactaaacaa 120

aacacaacan atgaatccaa gcttggcatg catgtggcaa taatcatgaa tatgatcaag 180

tgaaatgatg atntcgctnt gattctcatt acccaacacc gacagaggtg aatgcagaaa 240

ttatggtaaa ttacaccana caaactanaa acacaataat atagaatcgg ggcattatan 300

atgaagtagt cgggtaaaga cattgattcg tgtcagtgaa gtgtgatact cacaatct 358

<210> 68
<211> 431
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 68

tatcgagacg ctcganatca tcaacggaag ctctcgatan attcgaatgg tcataacatt 60

tcactcggat gtccgattcn gngacataat atatcgagac actcgaaagt gaacaacgga 120

agctctcatg atattcgaat gctcataaca tttcacacgg atgtccgatt cggggacata 180

actcatctag acgctcgaaa ttgaacaacg gaagctctcg agagattcga atggtcataa 240

gaattcacac gaatgttcga ttcggngaca taatatatcg atacgctcga nnatgaacaa 300

ccgaagctct ctagaaattc gaatggtcat aacatttcac tcggatcggt cgattcgnga 360

cataatatat cgagacgctc ganattgaac aacggaagct ctcgacanat tcgaatggca 420

taactttcac a 431

<210> 69
<211> 173
<212> DNA
<213> Glycine max

<400> 69

tatattgaga cacacaattt cgtgctcctt ctcttcctct ccctccactc atgttctcct 60

tactttaagc tcttatccat gagcttctat ggtggtgagc ttcttcttga ctcatcttct 120

gctagaaggg catctccatc atctttcttc tttttattca ctgccttaaa cta 173

<210> 70
<211> 380
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 70

gctgaatata tagctgcagg aagttgatgt gctcanagtc tttggatgaa gcaataactn 60

taacactctg gagtanacct tgatcacatt cctctaaaat gtgacagcac aagtgcgatc 120

aatctaacan aaaaaatctt gtcatgcatt ctagaactaa acacatagaa ataaggcatc 180

attntctcaa agatcatatg ttaaaagttg attggtgcat tgagttcata gatagtgagc 240

atcaactaac agacgttntc actanaccac ttgctagaga tagattctnt ttcgttagaa 300

atgaactaga catattagat gcatctagta tagaatgaca ttctatttgc atagtgtgtg 360

atgcacattc ttactcatat 380

<210> 71
<211> 393
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 71

tcagctgaat cacttccctc ttcanacact agaatagata ttatatnngg tctttataac 60

acaagtcata cctaattcng attggtctga ctaaacaatg tanaagtatt tatactagtg 120

atttatgaaa aataaattca ttntanatnt gtgtttaatt ntaatttatt gctggtgtaa 180

ataattttac cccatcaact aattaanaat cttaatgtaa ttataagaat ttaattattt 240

agcacccaca atataatata taggaaccag tacaaaaaat tctttttaac attagttgnn 300

tttaacattn tatatatgtt ttgtaatgta tgctaataag ttgatataga aacactacaa 360

gaaaaacact taaacatgtt tgatatattt ttt 393

<210> 72
<211> 269
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 72

accatacaga acctttgcct tccatgcagc aacctggagc aattgagcaa cctgaagctt 60

atgttgcana tatttacaat agacctnctc aacctcaaca gcaaaatcaa ccacagcaga 120

acaattatga cctctctagc aacagataca accctagatg gaggaatcac cctaatctca 180

gatggtccag ccctcagcaa caacaacagg gggtacggaa agtaccccct tgaattgtat 240

attcaagaca tttgagaata aacaaacac 269

<210> 73
<211> 365
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 73

cactcacaca ccgcactctc caatccttag ctcanaccta tggtcctttg atgctacttc 60

actttggaaa aatgccagtt cttggtgtct caactgctga ngctgcacgt gagggtatga 120

aaacacatga cctcgttntc tccaacagac cacatcgtaa gatgtttgat atcctcttgt 180

atggttccaa agatgtggca tcttctccat atggcaacta ttggaggcag ataaggagta 240

tatgtgtctt gcatcttctc agtgccaaan aggttcaatc ttttggtgca gtgagagaag 300

aagaaatctc cataatgatg gagaagatan ngcagtgtgt cttcttgatg ctgtgaatta 360

tctga 365

<210> 74
<211> 192
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 74

caaccaaaga tatgaagatg tgagatgtnt ggttctctgc catcgaataa ttcatatgaa 60

gtnttctnta aaatgggtct tattaaagcc ctatctaaaa tgtagcatgc agtgttaacg 120

gcttcagccc ataagtattc tggaagagga gtatcattca ataaagntct agcaatctcg 180

tccaaagatc ta 192

<210> 75
<211> 487
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 75

atgtataata aaataggtaa tgtgatacat agaaggatga caagcaataa aatcgaacat 60

aagaaagtat tacaaaaagt acgaataata ttaagataac ctcacataat ggagaaacag 120

cattcttgat aacaattcac ttccatcaca agaaanaaga tctgataccg tggactgatc 180

aaacgcatat tnganaaaga tatagaatag ttatatcttt gattcagtgt atggccaaaa 240

attgacggta cagaatgtat gaagagagtt tagtctaatt aactaaacag aatataccaa 300

tattgtaaac tntagtatgg tgttcagcta gtacggataa ngaaacaata caaaatttga 360

tctaaataat atagctctta tgtcaaagca caatangatg atttttaaca aatgactgaa 420

tcaacacgca tatatttatc aatctccaca aagatagaga tcatataaac atctcttata 480

tttatat 487

<210> 76
<211> 384
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 76

taatcaagat aagtatgaaa agggttnttc ataaactaag tagcacatgg attnttctca 60

naacatgttt accaaagagt ttttactctc tggtaatcga ttaccagatt attgtaatcg 120

attaccagta gcaaaatgga tttgaaaaag ttttcaaact gaatttacaa cgttccaatt 180

tatttcaaaa agctgtaatc gattacaatg ttttggtaat agattaccag tgcctttgaa 240

tgttgaaatt caaattcaaa tgtgaagagt cacatccttt cacataaaag ctttgagtaa 300

tcgattacat tgatttggta atcgattacc agtgattgtt tctaaataaa tcaaaagatg 360

taactcttca aaatgggttt tgac 384

<210> 77
<211> 401
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 77

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cattaagaac tagctctttt cttcctctat tgcctttagt tgaatacacc tttgtttggt 120

tctctatttt gttcttaacc ctctcatgca acttctttac aaattttgac ctagattccc 180

cttctttatg tataaaagaa gtgtccagtg ggaggggaat gaggtctaac agtgttaggg 240

gattgaaccc atagacaacc tcaaaagggg actgcttggt ggttctatga acccccctgt 300

tgtaggcaaa ttctacatga ggaagatact catcccaaga cttatggttg cctttcagaa 360

gagcccttat aatggtggat taaaacctat tcactacctc t 401

<210> 78
<211> 453
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 78

tctttcctaa atcaaagtat aaatgattnt atattataag tataaaccta ttaaaaaatt 60

ccgttcaaaa taataagata attttacctg aaattttgaa ccactccact tgtttttaat 120

gagccaattc caatcttctg gagatacgta ttttggtcta tcattttctt taagataagc 180

ttgatgtaaa tgataaagct tattcttgta ttgagattga attttcttca ttgcatattc 240

tctttcctcg ccagataaac taaaagcatc cttatatcaa acgttttcac cagcaaaagt 300

aaaaattaaa tactatcaag atacattatc aaaccaattt gaagatataa ctaatattca 360

aatatataaa taaattagat ataattaacc taattatata ctaacattca tatgtcgcca 420

catttcatct acaccatcct tactaatttc act 453

<210> 79
<211> 442
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 79

tgttcttagt aagatcgatc agacgatgct tttgttcctt ggagagcaac ccgtcttggc 60

cccagaaagt gttgccaatg ctctagtgga agtgatgaac gatcctttct cacacttaat 120

cgcctgttga taaaattctg caccaaatat ccaaacacca ttaaataaac taaaattcaa 180

ataattaatt gtatggatgg attagtcaaa taaaaatttc tattagccaa gatattatag 240

gaatttgtca agtctatcac gtgagcagtg ggcttagtgt tcctttcatt aggagattca 300

tgaaaattnt gtcggccaca naattgtgag acttcttaat caattaaatt aaaaaaaacc 360

tagtaaaata aaagttgacc agcatanact aatagtggga atataattag tatttgaatg 420

ccaaaatcaa ccacatattt tt 442

<210> 80
<211> 479
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 80

ctattaggac tcttgcaact cagctcgtac atatagtttc aatccgaggt ccttcaagag 60

acctagtaaa agtatcagcc tattgttcat tggaaccaac aaagtcagtc atgatttccc 120

ctgacaacac ctttactctt gcaaagtgac aatctatcta tgtgtgttta gtttgttcat 180

ggaagaccat attagatgca atgtgaagag cggtttgatt gtcacaaata agcttagtgt 240

cctgagtgcc taagtcttgt aatttcgcat gtagctgcta ccatggcaca atgttaagct 300

ttgatgctga atctagcaac tatattttgc ttcttgtttc tccatgagat caaattccct 360

caaagcaaaa cacaataacc agaggtagat ctcccgtcca tggntatcga attgaaagat 420

tcgaattgtg aatcagaaaa gctatattac gaatcgtgaa tcgaatcata tatgaatcg 479

<210> 81
<211> 456
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 81

tgtcaaataa atcactgcat attgtgcagt ccctatcatc cttcagagga atgtagaaga 60

gagtaggctt gcaaacaagg ttccaatttg gataaaagtg taaaactact tattaattag 120

aattttatga atcattgttt ggaatattga agaaaaaaga caacctgaca accagctgcc 180

ctgaaggaac taaaatcatg gcatccaaca agaactctgc atgcttcctg catggatatc 240

atcaataact tgaatagctg caagattgag aatctagtaa gtataaggag ctgttaacta 300

acttgcatag ctggaagact aagctcctca ggtacatgcc atgctcgatc tttctcgaag 360

gttgacaaag gctctggccc agaaagcaac cgatagaagt atctgaatag tagttccaaa 420

taactatcaa ttactgcana tggtcataaa caaaac 456

<210> 82
<211> 454
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 82

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ttcatcagtg ggctttcctt ctgtgtccag catcttggga tgttcccagc ctttgatgac 120

agctttccag gttctgctat ccagtgattt gagaaaggcc accatccttg ctttccagta 180

ttcatagttg gtcccatcca gaattggtgg tctgttcact ggtccgcctt ctttctccat 240

gttcatcaga atttatctcc ctagatctca ctcagtgatt tcgagtgcct gctctgatac 300

caattgaaat tctgatactg nggacagatg tcgtacagga tgtcacgaca tcacgcttca 360

gaacatgcag attatatttg acagtgtgaa caaattaaac aagttaataa cacaagagaa 420

ttgtaaccca gttcggtgaa cctcactaca tctg 454

<210> 83
<211> 453
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 83

gttgaatgca ttaaaggtaa acaaaccaaa agcaagaaat tgtgtgcata tagagctaca 60

gacgtcttgg aattgagaca tacaaacatt tgtgggccat ttcatacact ttcatggaat 120

ggtcaacaat attttatatc attcatagac gattactcca gatatgcata cttgtttctt 180

atacatgaaa agtcacaatc tttggatgta ttcaaaacat ttaaagttga agttgaaaat 240

caactccaca aaagaataaa gtgtgtcaga tctaaccatg gtggtgaata ctatggcaga 300

tatgacggtt caggtgaaca acatccggng ccttttgcca ggtacctaga ggaatgtgga 360

atcgtcccac agtacaccat gtcggngtca cctagcatga atggtgtggc tgaaagatga 420

aatagaactc ttaacgatat ggtaagaagc atg 453

<210> 84
<211> 432
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 84

ntgagcaaat tcaaacgaac aataactttt actcggatgt cagattgagt cccgtaatat 60

atcgaaaagc tcgaaattga atgttgaagc tctaagcaaa ttcaaacgac aaaaactttt 120

tactcggatg tctgattgag tcccgtaata tatcgaaaag ctcgaatgtg aatgtagaag 180

ctctgagcat attcaaacga caataacttt ttactcggat gtctgattga gtcccgtaat 240

atatcgagat gctcgaaatg gaataccgaa gctctgagca aattcaaaca ataataactt 300

tntactcgga tgtccgattg agtcccgtaa tatatctgaa cgctcganat tgaatgtcga 360

agctctgagc aaattcaaac gacaataaca ttttactcgg atgtctgatt gagtcccgta 420

tatatcttga cg 432

<210> 85
<211> 368
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 85

tccaccggtt gtgattgcga gataatattc gtggagggag aataaggaat cgtatgaaga 60

cagtacaagt ggaggtttca atctcttctc cgtctctctg acttttggga attctatcgg 120

agtagtcgga tgaataattg aaagaatttc tgggaaccgc tagagatgtt gttatcgctg 180

gctgaagaca cgtgagcccg cttagaggta agggatgagt ttatcgcaaa tgggattaga 240

atgaacatgt gtanggatcc ttagagaact aaatttgggt taatttgcga tggttattga 300

aatataattt ctctttatga ttataaatat aatattaatg gggtctatgt accaatgatg 360

ttctgatg 368

<210> 86
<211> 449
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 86

tctataaaag gttcgttcct aatttctcta caattgcatc acctctcaat gagctggtga 60

agaagaatgt ggcatttacc tgnggtgaaa aacaagagca agcctttgct ttgctccaag 120

aaaagcttac taaggcacct gttctagctc ttcctgattt ttctaaaact tttgataata 180

ttagggactt gtatgcttta gatgaacatt tctctcccat ttacgaaagt tgtgggaaaa 240

aggcccaaaa tggattctat ttggctaagg ggtatttgtt caaagaggga aagctttgca 300

taccccaagg atccattagg aaattacttg ttaaagatag ccatgagggt gggctcatgg 360

gccactttgg gatagacaag acgctcgtct tactcaaaga anagttttat tggccccata 420

tgaagaaaaa tgtccttaag cattgcact 449

<210> 87
<211> 382
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 87

tcattgatca attctgaagt tcacaattgt cataagttca tgaaaggagc aaaatgttgg 60

atcaagtggc ctcagaataa ttaagaaggg gggttgaatt aattattaat gagcctttac 120

taatcaaaaa cttatccttc ttaatgttac tagattcaat taggctttta ctactaagtt 180

aagaaagtaa agaacagaaa tagaaactta atcaaatgta aaagcaataa ttaaagtgca 240

cagcggaaat taaagagtat agggaagaac aagacaaacg caagaattnt atactggttc 300

ggcaaaactc atgcctacat ccaatcccca agcaacctgc ggttcttgag atttctttca 360

accttgtaaa atcctttaca ag 382

<210> 88
<211> 399
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 88

nttggtctta gaattaatca tcaaaagtct catttcattg tgtctaagaa tattccgaga 60

aggaaaactc anaaatttgc tatattttgg gtttccaata tatactcatg atattggtaa 120

atatttgggt ttacctataa ttagtggaag agttaaaaaa aaccacttct cgtttattct 180

ggataaagta aatgatcgct gagctggttg gaaatcgaag cttctcaata gacttggtcg 240

ggttacactt tgcaaatatg tcctcaattt tatccttaca tatgtcatgc aaaacatgtg 300

gctccttcaa ggcatttgtg attcccttga tattgctact agacaattca tctgcggatc 360

aacttcatct cattgggtga gttggaagac tnatcattc 399

<210> 89
<211> 396
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 89

tcttggcaat cctcattcca gcgatcagtt tggttnttgc gtaagagttt gaacaacggc 60

tcacaaatgg cggtgagctg cgatatgaat ctggcaatat aattcaagcg tcccaggaaa 120

cctcggactt gcctctctgt acggngttct ggcatctcaa ggatagcctt caccttttcg 180

gggtctacct ctatcccttt ctggcttaca acgaaaccaa gcaatttccc tgatttgacc 240

ccaaaggtac acttagcggg gttcaacctt aattgatatt tcttaagcct ttcgaacaac 300

ttccgctggt tgacaaggtg ttcttcctcg gatttagatt tagcaattat gtcgtccacg 360

tagacctcga tctcttgatg catcatatca tggaac 396

<210> 90
<211> 391
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 90

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acattagacg tagctntact cttagtaaga atattagaac aacacagcaa acaaaacact 120

ttctatgcat tgagcaaatg tattcaaaaa ataattatgg attagaacta agttttcaca 180

aatcttaagc aagcatcagt aacatcttta cctgcagcac tagaaagaac ccaattgtca 240

tcataaggaa cttgccacac agcatagcca agtaacttat tttcccttgc ataagaaacc 300

ttcattntga caacctcaac atcatcataa cctatccaag tcgatccatt ggagaagtaa 360

ttaactacat aagtagcatt gtacttgaca t 391

<210> 91
<211> 463
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 91

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aatcccagtt taccagttgg ttgttgccgt taaccaacaa atcttatttt atgttctctn 120

taatatttct ttntaattga agatgcttct tttacccaca gaaattgtat atttttcatg 180

caagtataac agttaaatga atagtagtta gtttaattgt atttcgaatt ttttttttata 240

attaaattat aagtgatttt ttagtttcta tggaaaaaat taagttggtt aagtttttta 300

ttttaaaaat taactaaatt tattcattnt gtcaaattnt tacttaaaaa ttntcaaatt 360

tttaatttta tctacatatt taggagttta tgaataaatt gagttagaaa ataattntaa 420

aaattatang taactttatt agaaaaatta gtaaatatta atg 463

<210> 92
<211> 363
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 92

tattggaatc agccaattgc tcagtgactg ttcttaattc tgtcatcttg aaggtgtata 60

gttgttgctt caagcataac cgatttgcaa gagactttgt catatacaag gattccagtt 120

tcaaccacat tgaggttggt gtcctttctc ttgcaacttc tcttatagct ttatttccaa 180

ggcatagtat gattgcactt ctggctctat ccatcatttc ttatttctcc tttgaactta 240

gagattcaga catcctttct tcttctttaa gagcttctac acagccatgc tgaatcaaga 300

ttgcttncat cttgatcctc cataacccga agtcattttc cctgagaact ctcatatcat 360

act 363

<210> 93
<211> 418
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 93

tgattaccct ggtgacactn tacttccagg aatgaaaatt ggagtgaact tcaaaaccgg 60

tcaacatcga gctctaagat catggagatc ctttacggat cctactccag gtaatttttc 120

acttggtgtt gatactcgtg gccttcctca attagttatt acaaatgaga atactaatag 180

taatgacata gcttatagac cagggtcatg gaatggtctt agtatcacgg ngcttcctgg 240

agaaataact gaccaattaa caaaatccct ttttgttatg aatcaagatg aggtcttcta 300

tgagattcag ctcttgaata gttcaactaa actcatgaga agcagaatgc ttccagaagg 360

gtatcaagta cgttttatat ggtcagatga aaaaaaatat gggattctca aattccta 418

<210> 94
<211> 435
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 94

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ggngaaggaa tcaattgctt ccacgttatt ggcctaggat tactgatcaa gagttgcaac 120

aaatatcagg agagtatcca acattgtaat ctgtcctata aattattatg aatcactgac 180

aggatactta ctggttgata cacttattat tattttgata gctaatcttt accttagtat 240

ttccttaacc atgattcatg atatgttcaa gttcaaattc tacaatcgtg ccactctttg 300

aaaagatgct tagtgcaagt gatgctggtc gaattggtcg cttggtttta ccaaaagcat 360

gtgctgaagt aatttatctt aactcatctg ttgaactggc atttactgtt gtcattttat 420

attaactaac aattc 435

<210> 95
<211> 320
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 95

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actcctgtgt tagttttgct taacccaaga gaacccttg aggtgtattg tgatgcatca 120

aagatgggtt taggaggagt gttgatgcaa aatggacaag tagtggttta tgcttctaga 180

caactcaaga ctcatgagag gaattatcct acccatgatc tggagttagc tgctgtnagt 240

tttgctctta acgcgtggag gcattaccta ttcgactcca gtttgaagtg tttagcgatc 300

ataaaagcct taagtatttg 320

<210> 96
<211> 392
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 96

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tgttagacaa gtggcctcag atatcttaag aaggggggtt gaattaagat attacaaact 120

attttcccaa ttaaaattct actttgattt taatgcaagt tcaaagttcc cttaaagatt 180

aatttctaaa tgatgattca aaataaccaa actgaatgta aaagtaaagc aacaataaat 240

aaaagagttt aagggaagag agagtgcaaa ctcagtttta tactggttcg gccacaccct 300

tgtgcctacg tccagtcccc aagcaaccca cttgagagtt ccactaactt gcaaaaaccc 360

tttacaagtt ctgaaccaca caaggacaac cc 392

<210> 97
<211> 330
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 97

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gttttcttgg cctgaacact gccgcaacta cctctcccat gttgagtatg gcaggaaccg 120

ccactccaca tcccgcttgg aaattacacc aatgactgaa gaatcaataa gtgactcatt 180

gagagatgta gaagacattt cttttagatt ctccacagaa ggagactcca agcagaatgg 240

agagatggac actgcagcaa ggcagaagca aattatggaa gcaatcatgt gcagggtctc 300

ttccactggc aagtctaatg ccagttactt 330

<210> 98

<211> 416
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 98

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tgcatgaatg acaagcaatt catggggctc cggataagat ttgaaggtag aggatagatg 120

aacagcacta ggcaatcaat tcgtggggct ccagacttga tggtggatga tgcatgaatg 180

acaagaaatt catggggctt tggataatat ttgagggtgg aggatagacg aacagcgcta 240

ggcaatcaat tcgtggggct ccagactcga tggtggagga tgcatgaatg acaagcaatt 300

catggngctc cggataagat ttgttggcag gactgaatgg tccaccggtt tttttcccac 360

cctaaaggcg aacatgtttt atcaaggaan aataaatcat tcatgagagc actata 416

<210> 99
<211> 403
<212> DNA
<213> Glycine max

<400> 99

tagacggcaa tttcgagcgt ctccatatat tacgggactc aatcagacat ccgagtaaaa 60

agttattgtc gcttgaattg gcctacaggt tctacattca atatcgagcg tcccgatata 120

ttacgtcact gaatcggaca tccgagtaaa aagttattgt cgtttgaatt tgctctgagc 180

ttcaacattc aatttcgagc gtctcgatat attacgggac tcaatcagac atccgagtaa 240

aaagttattg tcgttggaat tggctcataa gttcaacatt caatttcgag cgtctcgata 300

tattacggga ctcaatcaga catcgcgaga aaaagttatt gtcgcttgaa ttggctaaag 360

gttcaacata taatttcgag cgtctcgata tatttcggga ctc 403

<210> 100
<211> 398
<212> DNA
<213> Glycine max

<400> 100

ctgatgcaac atttggagag gttaatgaaa caacgagatg atgcacttca tgagaggttg 60

gatcaaatgg agaatataga tcataatgga gaagaaagga ggagaagagg gaataatggt 120

gttcatagac aaaaccgaat tgatggtatt aaactcaaca ttcctccctt taaaggaaag 180

aatgatccgg aggcctactt gtagtgggag atgaaaatag agcatgtttt ctcatgcaac 240

aactatgagg aggaccaaaa ggtgaagctt gtcgccgcgg agttttccga ctatgctctt 300

gtgtggtgaa acaagctaca aaaggagaga gcaagaaatg aagagccaat ggttgataca 360

tgggcggaga tgaaaaggat catgaggaag cggtatgt 398

<210> 101
<211> 405
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 101

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aatttattgt tgtcagaatt tgcactgagc ttctgttttc aatttcgagt gtctcgatat 120

attacgagac tcaatcggac atctgagtta aaagctattg ctctttgtat ttgctacgag 180

cttccgattt caattacgag cgtctcgata cattatgggt ctcaatcgga catccgacta 240

aaaagttatt gtcgttagaa tttactcata gcctttattt taaattntca acgtgtcgat 300

atattacggg actcaatcgg acatccgagt aaaaagttat tatcatttga atttgctcag 360

agcttctgtt ttcaatttgg agtggtgtcg ataaatgtgg gactc 405

<210> 102
<211> 452
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 102

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ttttcataaa acttgatggt gagaatattc caatcaagca taacccactt gacccttttg 120

caccccattt ttagggcttg ctttgccacc acagagagca acattctccc aagccccttc 180

gtcttataac actccctcaa gaacaagttc tccatgtaaa accctcgctt ctctagaacg 240

agagagaagt tcggaaaaaa caagacaaac ccaacaatgg aaacaccttt gagggttntt 300

aaattgtagt ttctcgagat aactattact taatgggaat aataaatgaa taattaataa 360

ttatggacta aattataatt gggttaaatt ggaagcagtt ttagagaaaa ctattatttg 420

attggagtag tnggtataag ggtcaatact ca 452

<210> 103
<211> 298
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 103

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acctttgttt ggttctctta ttggttctta accctctcat gcaacttctt tacaaactct 120

gacctagatt ccccttcttt atgtataaaa gaagtgacta gtgtgaggtg aatgaggtct 180

aacggtgtta ggggatngaa cccatagaca acctcaaaag gggactgctt ggtggttcta 240

tgaaccaccc tgttgtaggc aaattctaca tgaggaagat actcatccca agacttat 298

<210> 104
<211> 428
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 104

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ctaagtcact ggcatctaga agtcctaatt ctctcgtaat ggtgtagaac gaatctttgt 120

gtagtggttc tgtgaagata tttgcgagtt gantttggt atctacaaat tctagaacac 180

agtcaccttt taggacatga tctctaagaa gatgatgcct aatttctatg tgctcggttc 240

tagagtggaa aactaggttc ttagatatat ttatggcgct tgtgttgtca cattntatgg 300

ngatgtggtc taatacaatc ctataatcag atagttgtta tttcatccac agaatctgtg 360

cacaacaact accagcagag atgtattctg cttcggttgt ggataatgct acaataattt 420

tgcttctt 428

<210> 105
<211> 273
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 105

ctgatcaaca catgcacagt ggccaaggat gcatgggaga atcctgaaac cactcatgaa 60

ggaacctcca aagtgaagat gtccagaatg caactattgg ctacaaaatt cgaanatctg 120

aagatgaagg aggaagagtg tattcatgac ttccacatga acattcttga aattgccaat 180

gcttgcactg ccttgtgaga aaggatgaca gactgaaagc tggtgagaaa gatcctcaga 240

tctttgccta agagaattga catganagtc act 273

<210> 106
<211> 335
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 106

tgtatggaga tctgagcact tcttctctct atgtcttcac aatcatctct taggcggaag 60

ttgcagaatc atcatgatga agatactata ttcngcacgt tatcgttgat attttggacc 120

cttaccttga ttgcattgct taaatatgta ttcatactat tgtgtgctga tgacaacggt 180

gaacgtatgc tgctgataac tttattctct tagataattg ttcttataca taggttacga 240

tctgtgtgag tgtgagctga gtatgatact tgtgtcatca ggtggaacat ttgcctttat 300

tcgctgctgt ggatgcatgc cacgcttaaa ttact 335

<210> 107
<211> 314
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 107

ggttgaatta agatatcaca tactntntct tnaataanaa atctattttg attntaaccc 60

anatcccaag aattctttca naatgaactc ctaaataatt atgcannata aacttactga 120

atagaagcaa taagcaataa ccaataaaag agtttaaggg aataaagaat gcanactcag 180

aattatactg gttcgcccac atccttgtgc ctaagtccag tccccaagca acccgcttga 240

gagtncacta tcttgcnaaa gcccttacag tctgaacaca caggacaccc ttctttggtc 300

agattgttac acaa 314

<210> 108
<211> 340
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 108

tgtgtcgtct gcatactgca atatgctgac tntgacttca tttctgccca cattgaaacc 60

ttgaaacagg ttnttatcca ttgcttcttt cnaccagcgc gttggtcctt ccacaagaat 120

gttaaacagg aacggngata gagggtctcc ttgtcttaag cctctntggn gaataaactc 180

aggtgtagga cttccgttaa ccaatatgga tatggaagca gactttatgc agccttcaat 240

ccaagttacc cacctgtcac anaaacccat cctcttcaac aaatatagta caaactccca 300

agatactgaa tcatangcca ttntataatc tactttgata 340

<210> 109
<211> 240
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 109

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aacatggaat tcaccacaat tcttattccc caagaacacc tcaacagaat ggtgttgtgg 120

aaaggaaaaa tatatcccta taagaaggtg caagaaccct tctaaatgaa acaaggttac 180

cgaagtactt ttgggcagat gttgtacata ctatntatta caccttgaac agagtactta 240

<210> 110
<211> 351
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 110

tgcacaagac tctttaatat tgaagagtat ccttgtggaa ccttcttccg acgaagacac 60

tgacaaaaac ttatcttctc cttcttggac aaggtatgtg caggctgggg caagtaaatt 120

ttcttcccat cagaccttgg atgcaattgt gatcgtatac ccatatcagc tagatcttga 180

tgggtattca agccatcctt cgtcttgcct tgaatgttaa ggagcgtncc aatcacattg 240

tcacaaacat ntttcttcac atgcataaca tcaatacaat gtctaacgtc aagatcacac 300

cagtacagaa gatcaaagaa natagacctc ttcttcatat gcaactctga c 351

<210> 111
<211> 317
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 111

atctagaggt atacctagga tctctatcag acactatgct agatggcaca ccatgtaata 60

tgacaatctc actaatatac agacaggtca actnttccaa ggaagatatg atattaatgg 120

gaataaagtg agcagacttg gtcagcctgt caacaataac ccacatagaa tcaaaacctc 180

ttggggttct aggtagtcct acgacaaaat ccatagaaat atatgtccat tgtcactggg 240

tatcttcaag gggtgtaact atcctgaagg gctctgatat cttatactta tgacagacta 300

aacatgcata cacaaac 317

<210> 112
<211> 314
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 112

gcttgaatcg atacacacat actgtaatcg attaccagag cagtatttca gattatattc 60

tcatcagtca canntctttt attggttctt gaatggccat canaggctta tatatatgtg 120

acttgagaca ncgaattgct aagagattnt cagaacanna aggtcttatc ctcttanaaa 180

gcanaatcgt ttcatcctct taanaattcc ttggccaaaa cacttgtgat tcaataagga 240

attagttgag tgctcaaatt gttcaatcta tctctttcaa gagagaatac ttcttctctt 300

cttctntatt ctga 314

<210> 113
<211> 451
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 113

tattgtagcc gatgctctgt ctcggcgtca tgcattactt tctatgcttg aaacannaat 60

gattggtctt gaatgtttga aaagcatgta tgataatgat gaaacttttg gagaaattct 120

taaaaattgt gaagaatttt cagacaatgg tttctttaga catgaacgct ttcttttcac 180

agaaaacaaa ttgtgtgtgc ctaaatgttc tactagaaat ttgcttgatc gtgaagcaca 240

tgangaggtt taatggtgca ttntgtggtc caaaagactc tatagacatt acangaacat 300

ttnntattgc ctcatatgaa aaaggatgtg cagacactct gtgaacatcg cattgtattg 360

taaaatgcaa gtctaatggt aagcctcatg gattgatact ccattgcaat accgagtatc 420

ttgattgtta tcatggattt gtttgggctg c 451

<210> 114
<211> 415
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 114

gagggactca tggtcactat gaatgacaaa ttccgtggga taaaggtagt ggtgccatgt 60

tcccacagcc cgtactaagg catacaactc cttatnataa gttgaatagt taagggtacg 120

accacttaac ttttcactaa aataagcaat tggatggcct tcttgcatca acacagcccc 180

aatcccaaca tttgaagcat cacactcaat ttcaaaagat ttttgaaagt ttggcaacgc 240

aagtatggng gcattacgta gcttttgctt aagaacattg aaagcttctt cttgtttctc 300

tccccatttg aaaccaacat tcttcttgag cacttcattg agaggtgctg ccaatgtgct 360

aaaatccttc acaaatcgtc tatanaaact tgctaagcca tgaaaactcc tcacc 415

<210> 115
<211> 369
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 115

tttctctaca atngcatcac ctctcaatga gctggtgaag aagaaatgtg gcattacctg 60

nggtgaagaa caagagcaag cctttgcttt gctcatagaa aagcttacta aggcacctgt 120

tctagctctt cctgactgtt ctaanacttt tgagctagaa tgtgatgcct ctggagtggg 180

agttggagct gtattgttac aaggtgggca ccctattgtc ttatttagtg aanaacttca 240

tagtgccacc ctcaactacc ccacctatga taaagagctt tatgccttaa taagagccct 300

ccaaactcgt gaacattacc gttgttcaag gaatatgcat tcatagtgat catcaatcac 360

ttaagtaca 369

<210> 116
<211> 273
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 116

ctatatgata tagtgtattc tctatattat gttcgtatgt ggaggaggct aaattatcat 60

tctaattctc ttatagttnt aattgtgtaa tcttgattgt ataaattatt aaatatataa 120

acatttgttc ttattttatt atactatata gattgtcttt acattattgt atatcattta 180

aatattatga ggatatgaaa ttataattta acctttataa aaatagatgt aacgcaacat 240

agagactgat gctactttga tattccaatt gat 273

<210> 117
<211> 353
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 117

gagatcatcc nctcaacaac attatgggtg atatctcana tggggtaaca tctagacact 60

ctcttaaaga tntatgcaat aatatggctt ttgtatccat gattgaacac taaaatataa 120

aagaagccat aatagatgat aattggatca ttgccatgca agaagaatta aaccaatttg 180

aaagaaataa tgtgtggaaa ttagtagaac aacctggaaa ttatcctatc atatgaacaa 240

aatgtgtttt tagaaataaa ttatatgaac atggtataat tattagaaat aaagccaggt 300

tagtagcaca aggggataat caagaagaac gaatagacta tgaagaaaca tat 353

<210> 118

<211> 345
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 118

cagtgtttat attgcggttc caatgtggcc agagggttac ccagaacatg gaacggttca 60

agcaatgatg gattggcaga ggagaacaat ggatatgatg tacaaggatg atgctggagc 120

actaaaaggc aagggtaatg aggaagatcc tctcaactat tcgacattct tctgcctagn 180

taatagggag ctgaacaaag aatgagagta tgtgccccca gaaagaccag atcctcatac 240

agattatatg agagcacaag tgtcccgacg ctttatgatt tatgttcatg ccaagatgat 300

gatacgcatg tctgttaatt aagtttacca catcttccaa gatac 345

<210> 119
<211> 459
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 119

ngcaagctnt ctaaatgttt ctttgcccag tctcaggtag agtacttagg acatttggtt 60

tcgcatcggn gagtggagcc cttagcatca aaggtcactg caattcagca atggccaatt 120

cctcgtacaa cgaaggccgt aaggagcttc ctgggccttg ctggctttta tcgcaggttc 180

attcagaatt atgccattgg tgtggcccca ttagtcaaag ccacgaccaa agaacccctg 240

cattggacat ctgagacaca tgaagccttt gacactttga aacatgcctt gtcaatagct 300

ccggtgttag ctttaccaga cttcaacctt cccttcacag tcgagacaga tgcgtcagga 360

gttggtatgg gtgccattct ttcacagcga ggccacccca tagcattttt cagcaaacct 420

tttagtgcca agtactctga tcataacata catgcgaga 459

<210> 120
<211> 328
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 120

atagcccgag gactagagta cttgcataag ggatgcaaca ctcgaanttt acattntgac 60

atanagccac aacattcttt nggatgagaa gttctgcctc aagatatctg attntgggct 120

agcaaagcct tgtcctagaa atgaaagtat tatttccagg tctgatgcca gaggaacatt 180

atggtatgta gctccagaaa atttggcaga atttcacaca natctgatgt aatcttccac 240

tttanattta aaccacctaa accttaatgg gtaaaattaa ttctattatg cattanatgc 300

atcttatctt tgacttgaac tctacaat 328

<210> 121
<211> 314
<212> DNA
<213> Glycine max

<400> 121

gacgaagcgt gttgtgaatg gcgtctcgcg tggctagcat ggtatcgaca gcatcattgc 60

gtgatgacca cttgatgtaa ttggagatgg ccggaggagg cttaccatat gtgacctcgt 120

atggagtgaa gtcggtgccg gagtgctgag acgtgttgta agaccattca gctagggcta 180

agaattaaac cagtatgccg ggttgtggtg aacgaaggaa cgaagatatt gctcaatcgt 240

accgctcatc acttcggttt gcccatcgga ctggtgatga tacgccgtac tcatgcgtat 300

cgtcgtccca ctga 314

<210> 122
<211> 393
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 122

cagctccatt gatatcattt atttaatgca atgcacatgt ttcgaataag atttcttgta 60

tcacaggaaa agatctaatc caagttgaat tacggatcat actgattgtg gtgcgaaaac 120

tggcttgaag tagccatctg ggtaatatcc aaaccacgaa gtttcctctg gtattaaaac 180

agtgtcgcgc tcacactgtt aatgtataaa ataagactac aaatatataa gctttcctca 240

tgaaatcaat tagcaatatt ctattcataa tatcacaata atacatttag aggacttacc 300

atgataagta ccanattctg caagctactc aatcttttct tgtaagaagc atttctctta 360

tctggtattt cattgccatg cactggaaga aat 393

<210> 123
<211> 416
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 123

ctgcacaagg ctcttaatat ttgaagagta tccttgagga accttcaccc gacgaagaca 60

ctaacaaaaa cttatcttct ccttcttgga caaagtatgg caggctgggg gcaagtaaat 120

tttcttccca tcagaccttg tatgcaactg tgatcgtata cccatatcag ctagatcttg 180

acgggtattc aagccatcct tcgtcttgcc ttgaatgtta aggagcgtcc caatgactct 240

atcacagaca tttttctcca catgcataac atcaatacaa tgtctaacgt caagatcaca 300

ccaatacgga agatcaaaga atatggacct cttcttccat atgcaactnt gactattatc 360

cttcttttga gtcttcccag atacagtatt cacgtgttca acccgataat atacct 416

<210> 124
<211> 234
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 124

tttgagcgtc tcgatatatg acgagactac atcatacatc ttagtaanaa gttatagtcg 60

tttgaatatg ctcagagctt caacattcaa ttacgagcat ctcgctatat tacgggactc 120

aatcagacat ccgagtaaac agtttgttgt ttgaattgtc tgagagcact cacattcaca 180

ttctagcgcc tcgatatata tatggactct atcacacatc cgagtataaa gtta 234

<210> 125
<211> 375
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 125

tttgagccgt cgacgaccng ngatccttag agtcacctga ggctgctgct tacatcaaca 60

cttcaggggc tgtactactt acatggattg atgggcctat gcagttgaaa gcctggagaa 120

agaggatgcc tatngttgtt gggatgaatt ctccagattt acctgggtaa actctatcag 180

agagaatcaa aaccttgagt attcaagagc tgagtctaag acttcaaaga gagaaagact 240

gtgtcatcaa gagaatcagg agtgaccatg gcagagaatt tgaaacagca ggttcactga 300

atttgcacat ctgaggcata ctcatgagtt tttgcagcat tacacaaaca gaatgggata 360

gtgagaggaa aacag 375

<210> 126
<211> 354
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 126

tagctacaca cacccatcta anaactaagc tcacctcctt gagaaacttc cttgagaagc 60

tagaagctag ctacacancc ctataatagc taagctcacc cncatgacaa anaaacatga 120

naatacanaa aanatcctac tacaaagact actcanaatg ccctgaaata caaggctaan 180

accctatact actagaatgg ccaaaataca aggcccagac gaagganata cctattctaa 240

tatntacaaa gataagcggg ctcatactta gcccatgggc tcgaaatcta ccctaaggct 300

catgagaacn ctanggtctt cctttggatc tctagcccaa tctacttgga gtct 354

<210> 127
<211> 420
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 127

agtacaataa gctntatgtt ctaaatctac tggaagatga catcccttgc catgcaccat 60

ctagaatggg gaaagactgg taggggtctt ataggctatt ctatacaccc acaaagcatc 120

atccaattta gcaaaccaat ctttactaga attctcttta tctttgtaaa tgagacttca 180

acttgaccat ttttttgagg gtggtaaggc gatgcaacct tctgtctgac attatagtgc 240

tccaatgcct tctgtagttg cacattgcaa aaatgggaac ccccattact gatgagaact 300

ctaggagttt ccaacccacg aaaaatattc ctcttcacaa accgaatgac tatttttgca 360

tcacctttct gtgtggcaat ggcttacacc cattttgata gaaactcttt aaatgacaca 420

<210> 128
<211> 390
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 128

agcttgtagg gttatagtct cacgattgtc acgtgctcat gcaacaattg ttagccgtgg 60

ctatacgaga catcttgcca aacaaagtca ggttcacgat aacttgcctg tgcttttttct 120

tacatgctat gtgtagcaaa gtgattgatc cagtaatgtt tgatgagttg gaaaacgaga 180

ccgcaattat actatgccag ttggagatgt attttccccc tgctttcttt gacatcatga 240

ttcacttgat tgtgcatctg gtcagagaaa tcaaatgtcg cggtcctgtt tatctacggc 300

ggatgtaccc ggctgagcga tacatgaaca tcttatnaga gtatacaaag aatctatatc 360

atccgaaagc atctattgtt gagaggtaca 390

<210> 129
<211> 349
<212> DNA
<213> Glycine max

<400> 129

aagcttctat agaatgttcg ttcctaattt ctctacaatt gcatcacctc tcaatgagct 60

ggtgaagaac gatgtggcat ttacctgagg tgaaaaacaa gagctagcct ttggtttgat 120

caaagaaaag cttactaagg cacatgttct aactcttctt gacttttcta aaacttttga 180

gctacaatga gatgcctttg gagcgggagt tggagctgta ttgatacaag gcgggcacct 240

tatttcttat attagtgaaa gacttcatag tgccaccctc aactacccca cctatgataa 300

agagctatat gccttaataa gagccctcca aacttgggaa cattacctt 349

<210> 130
<211> 455
<212> DNA
<213> Glycine max

<400> 130

ttataccatg gatgaataac agcggctcag ctacatcaaa aactaccaaa agaaacttag 60

agttgacaag tattgcagct tacaaagttc attggatact ggaacaaaca aaggctcgac 120

taaaggaaaa agagtcattt taccttcaac ctttgttggg agcccatgtt acatggatca 180

actttatttt gatggtatgg caatatgtgg tcatgttggt ttcctaaatc tttttataac 240

tctaacatgt tatccaaatt gtcctaaaat tcgtagatta ctttcacctt tgaatcttaa 300

accaacagac aggccagaca ttgtctcatg aattttcaga ttgaaatatg aacaaatgct 360

ttctgactta ccaaagcatc agctgctcag aaaagttgtt gttgcgcgta agtttagaat 420

gatctttgct gttgaacgta gaaatcaatt gatca 455

<210> 131
<211> 381
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 131

catcangaaa caatntcact ttaaaagtgg gtcccaattg gattcctaag tttcaactta 60

ccttttgga agtgacatca tggcagttag gtcccagctt tccatcgtgg attcagtcac 120

aaaacaaact tcaatatgtt ggactgtcta acacggngat tttagattct attcccactt 180

ggttctggga accacactct caggttttgt atttaaacct ctctcataat catatccatg 240

gtgagcttgt gactacaata aaaaatccaa tatctatcca aactgttgat ctaagcacac 300

atcacttatg tggtaaatac cctatctatc anatgatgtg tatgggttaa acctttcgac 360

caattcattc tctgaatcca t 381

<210> 132
<211> 420
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 132

gcttcttctt ggttctctcc ccattngaaa ccatcatttt tcttgagcac ttcattgaga 60

ggtgctgcca atgtgctaaa atccttcaca aatcgtctat aaaaacttgc taagccatga 120

aaactcctca cctcggacac agacttaggt gtaggccatt cttgaatagc cctaaccttc 180

tgctgatcaa cttgcactcc ttttgaactc acaacaaaac caagaaacac aacatggtta 240

gtacaaaaga tgcatttttc aagattggca tacaattgtt cttttctaag cacagtcaag 300

acagatttta aatgatcaat atgcaaatca agtgaagtgc tatagataag aatatcatca 360

aagtacacca caactacact ttctatgaac tctctcaaga tatggttcat taatctcatg 420

<210> 133
<211> 381
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 133

ttataagtgc gggtctggga gacgaangtc aagtggtcgc gatatgtgaa gatgatacgt 60

gctcatgcaa caattgttag ccatggctat acgagacatc ttgccaaaca aagttaggtt 120

agcgataact cgcatgtgct ntttcttcca tgctatatgt agcaaagtca ttgatcctat 180

caagtttgat gagttggaaa atgacgccgc aattatactg tgccagttgg agatgtattt 240

tccccctgct ntatttgaca tcatgattca cttgattgtg atctggacag agaaatcaaa 300

tgttgtggtc ctatttatct accgaggatg tacccggttg agcgatacat gaagatcgta 360

aaagggtata cgaagaatct a 381

<210> 134
<211> 447
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 134

ggaaggtttg tacatgacca aatctttagt taatcgtctt tacctanaac agtctttgta 60

tttgtttaag atgcatgaag atagatcact aggagaacaa ttggatttgt ttaataaact 120

gattctagat cttgaaaata tcgatgtcac tatatgatga tgaggatcaa gctttgttat 180

tgttgtgctc tttgcctaag ggttactcta atttcaaaga gactntattg tttggaagag 240

actttgtttc tcttgatgaa gtgcaggctg ctctgaattc aaaggaattg aatgaaagaa 300

aggaaaataa gtcctttaca agtggtgaag ggctgacagc aagaggcaag accttcatga 360

caaatagtaa atctgataag aagaagcana agccagaaaa ccagaagaat ggtgaaggaa 420

atgtcttcan aatcagaggt catcact 447

<210> 135

<211> 429
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 135

atgatttgga ttatcctcta nggcaatcag tattcagtat tttaaattcc ctctcaaaaa 60

attgcaggct tggtggcggt gccacaaagc tgccatatat tataagaggc ttagtagagg 120

tgcaatagtt acacaatgca gatggagggg gcgcatagcc aggaaagaac ttatgaaact 180

gaaaatggta tgttttacca tgattcttat acattaagta gatccttcag aaatagatga 240

caaaagatgt aacacgtcca tcctacaaaa cttatggcac aaaaagcaaa agatactatt 300

tgatcaattt ttaattgtaa aattgagttt caaattatag atatatacaa acaatattca 360

tatttttgt ttcattatta tcttcatgaa gggaaaaaca atagaagaac ttanaattct 420

cttctgatc 429

<210> 136
<211> 470
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 136

acactcttag gatttgccta gtttacattt cttgcttaca ttcataatag cttatttcct 60

ttaccttcca ttgtcaaacc gcctagatag ctttcctttt accaattagt tntttacctt 120

atctttcaca cctcttttag tgtttatttg gctagnttca accatagttt cttttacctt 180

ttgttntcaa acctccaaca agaaagaacc acaacttagg aaccaatatg agtcatcatt 240

catctagtgg taatggcaag ggtactagtc ataaagaccc tttatctaga atcttagatg 300

agttgagttc cctcacgtta tggaaagaan aacaagagag aaaagaanaa ggaagaataa 360

gagtggaaga aataaatcat gatgaaagaa agacaatatg agaggaagaa agaagaacaa 420

taatgaaaga aatgaanaga gaaaaacatg cctnctatag tagtcataac 470

<210> 137
<211> 451
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 137

ggcttctaca atctcccnct ntttgatgat gacaaccctg atatcaagaa acacatgcac 60

atacttttc ctagtcgatt actcacttaa ttctccatat tctacccctt tggttttgag 120

tttaagcttc acttgaaatt aagttaatta cttatgtgag ttcttgattt aatccctatt 180

tctctccccc tttggcatca acaaaaaacc aaagtgcgta acaaatataa aacatacaca 240

aataactaat catacacaag acattcattg aaaaatctaa accaatcatg aagcaagaaa 300

catgaataga tcaaatatat aaaaaccaca tagtcatata acataattca tatttgttca 360

gtcatactat gcaaataaaa gaaatactaa atgttcaaat gtcataataa tatagccaaa 420

tacacggcta gaaatcaaag tactaataat a 451

<210> 138
<211> 315
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 138

gcttcttatc caggcaattc ttgggggnga agctccttct tccttggctt attccctagn 60

ggatggtgcc tcccctatcc tcttctcctt tgccttccgc tgcatctcca tgatgaaaaa 120

tcaccattga aggacctcat tgaagatcaa agatccagcc tccatagaag ctccacaagc 180

aagcttccat caagttatga ccatttgaat ttctcgagat cttccgtggn tcaatttcgg 240

gcgtctccat atgtcatgtg cctgaatcgg acctccgtaa tataatttat gaccattcga 300

acttctctag agctt 315

<210> 139
<211> 432
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 139

agctntggag tttccaagtg ccaattcgtc ttcttcttta gtccagtctt cttctggctt 60

caatccatca gtgggctttc cttctgtgtc cagcatcttg ggatgttccc agcctttgat 120

gacagctttc caggttctgc tatccagtga tttgaggaag gccaccatcc ttgctttcca 180

gtattcatag ntggttccat ccagaattgg tggtctgttc actggtcctc cttctttctc 240

catgttcatc agaatttatc tccctaggtc tcactcagtg atttcgagtg cctgctctga 300

taccaattga aattctgata ccaatgccag atgtcgtaca ggatgtcacg acatcacgct 360

tcagaacatg cagattatct ctgagtggat gaacacgata aacaagtata taacacaaga 420

gaattgttta cc 432

<210> 140
<211> 442
<212> DNA
<213> Glycine max

<400> 140

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gcttatctac acacccccta taatagctaa gctcaccccc atgacaaaaa acatgaaaat 120

aacagagaaa agtccttatt acaaagacaa ctcaacatgc cccgaagtac aaggctaaaa 180

ccctatacta ctagaatggc caaaatacaa ggcctagacg aaggaataac ctattctaat 240

atttacaaag ataagcgggc tcatacttag cccatgggct cgaaatctac cctaaggctc 300

atgagaaccc taaggccttt ccttggatct ctagcccaat ctacttggag tcttctagcc 360

aatgcccttg cggggtaaga gtgcatcatt acttttcact cagatgtgcg attcaggcac 420

atcagatatc gagacgctcg aa 442

<210> 141
<211> 456
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 141

aacccatgga agctcctaat atctcccaca ctttgntggg tgggccattc ttggatggcc 60

ttgattttct caaggtccac ttggacccca tttctaccaa ctacaaaacc taagaagact 120

atattatcta cacaaaaggt acacttctct atatttgcat agagggtgtt tttcctaagg 180

actgaaagaa cttgcctgag atgttctaag tgatcatcta ggctcctact gtacactaaa 240

atatcatcaa aataaacaac tacaaatcta cctatgaaat ccattaagac atgatgcata 300

agcctcataa aggtgcttgg tgtgttagtg aagcccaaaa gcatcactat ccattcatac 360

acaccatact tggtcttgaa agcgcgttcc actcatcact ctttttcatc ctggattcgt 420

gataaccact tttaagatca tattttgaag agatat 456

<210> 142
<211> 193
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 142

atcagaccac ttccagngtg ctggaactac ttcacactga tttgatggng cctattctag 60

ttgaaagcct tggaggaaag aggtatgcct atgtcgatga ggatgatatc ttcagaatta 120

cctgagtcaa ctttatcaga gaaaaatcag acacctttga agctttaatt gagttgattc 180

ttatacttta aag 193

<210> 143
<211> 281
<212> DNA
<213> Glycine max

<400> 143

tcacacttac aaaggatata tgggtccatg agggacctcg ggctttctac agagggcttg 60

ttccatctct tcttggtatg attccttatg cagggattga tctcactgca tatgacacct 120

tgaaagatct atccaagaga tatattcttt atgacagtgg tatggtatta ctgcaaccac 180

attatctctt gaacttaatg gatttatttt accactctga aatttttagt gacacataac 240

acatgtaaac tcaacctttg aacttaaata tgtaattttt t 281

<210> 144
<211> 115
<212> DNA
<213> Glycine max

<400> 144

ctataaatct aagcttaaca tcagacccct ccaggtgtct gaactacttc acatttattt 60

gatggtgcct atgcaggttg aaagccttgg atgatagagg tatgcctatg ttgtt 115

<210> 145
<211> 405
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 145

agctncacgg cacgactgtt aggattaatg caatgattgc tgaactacaa gctctacagt 60

cgaatgagac ctggaggctc actcttcttc ctccacagaa aaccgccatt ggctgcaggt 120

ggatttacaa gatcaagtat cgcgctgatg gctcgattga aagatataaa gcacgtntag 180

tggcataggg ctacacgcag atggagggtc ttgattatct tgatacgttc tctcctgtag 240

catagttgac taccggtcgt cttcttcttg cccttgctgc cgtgaatcaa tggcatctgc 300

ggcaactgga cgttaataat gctttcctcc acagacaact tgatgaagaa gtttatatgc 360

aggttccacc gggattgacc gtttcacatc ctcaactggt atgtc 405

<210> 146
<211> 377
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 146

ggccgccacg gagttntccg actatgctct tgtgtggtgg aacaagctac aaaaggagag 60

agcaagaaat gaagagccaa tggttgatac atggacagag atgaaaaaga tcatgaggaa 120

gcggtatgtg ccggctagtt actcaaggga cttgaaattc aagctccaaa aactaaccca 180

aggcaacaag ggggttgagg agtatttcaa ggaaatggat gtgctcatga ttcaagcaaa 240

tattgaagaa gatgaggagg taactatggc tcgatttctt aatggtttga ctaatgatat 300

ccgtgatatt gttgagctgc aggagtttgt tgaaatggat gatttgcttc ccaaagcaat 360

ccaagtggag caacaat 377

<210> 147
<211> 451
<212> DNA
<213> Glycine max

<400> 147

atcctcttag tcacctgccg catgcaagct tgaaattgac aacggaagct ctccagaatc 60

tcatatggtg ataacttatc acacgaaagt ctgattcagg cgcatagtat atctagaccc 120

tcgaaattaa acaacgaaag ctatcgagaa actcatatgg tcataaattg tcacacggaa 180

gtccgattca tgcgcataat atatcgagaa ggttggattt gaaccaccaa tgctctcgag 240

aaattcagat ggtcataact tttcaaacag aagtccgata tatgcgcata atatatcgag 300

aacgttgaaa ttgaaccacg aatgctctcg agaaattcaa attgtcataa ctcgtcacac 360

gaaagtccga ttcaagcgca tactatatct acacgctctg aacttgacaa cgaaagctct 420

ccagaaattc atatggccat aacttgtcac a 451

<210> 148
<211> 361
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 148

agctttgata tggaaattaa gttganagta aatgatggta tgtataagac atcaatcagt 60

gtaatgaatg cagaaagttg tactgcgcct gagtgggtag catagacaag atggccattt 120

ggtaatctaa ccgtgatggg attaatttga tgatatgagt gaaagtttgt taaggaggag 180

gaaacgtgat cagtggctcc tgaatctaat atccaggagg tagagtttgc tttttcgtaa 240

gataggatta tacctgttgc atcgttattg gaacaagata aaatggaagc gacctgtggt 300

ttggtggatg ctgagtttcc agcagatggc tgttgtatta atgctagcca tgccttgtac 360

t 361

<210> 149
<211> 501
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 149

agtcacctgc ggcatgcaag cttctggttg ctgcgatgat cgaccagaac tgttccctga 60

actcatccaa gtcctcaaag gcttgagact cacagcagtt aaagctgaca tagccagtgt 120

tggtggcaga atcaaaagca tattggtgct ttgttctaag gatagagaag acagtgtttg 180

ccttgccact ctcaaacagt ccctcaaatc tgctgtcacc aaaattgctt catcatccat 240

ggcttctagn tgtcccgcta gaagtaagag gcagagattc ttcttgcctt ctcactgcct 300

acagttaatt atttattgca aanaatattt ttttccccac tattcattgc agtatggggc 360

aattatttgc tctattntca atatatatat atatatatat agactcccca ttaggaagat 420

aaaatcatga aatattagtt ctgtgcaacc aattaaggca tagttaaatt ganaggaaag 480

gacgcacagc atagtatgag t 501

<210> 150
<211> 412
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 150

agtctcacga ttgtcacgtg ctcatgcaac atttgttagc cgtggctata tgagacatct 60

tgccaaacaa agtcaggtta acgataactc gcctgtgctt tttcttccat gctatatgta 120

gcaaagtcat tgatccagtc atgtttgatg atttggaaaa tgaggccgca attatactgt 180

gccagttgga gatgtatttt ccccctgctt tctttgacat catgactcac ttgattgtgc 240

atctggtcag agaaatcaaa tgttgtggtc ctgtttatct acggtggatg tacccggttg 300

agcgatacat gaagatctta aaagggtata caaagaatct atatcgttca gaaacatcta 360

nttgtgagag gtacattgca gaagaagcca ttgaattttg ttcagaatac tt 412

<210> 151
<211> 483
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 151

gcttcacact tgataatgga gacacatgaa cagtgctatg taatgacatt catggtgctc 60

caaacaaagg tggagtatgg aggattgcct tgagggtccg cacttaggca atcatgaaac 120

tcaactccaa actcgaaagt ggaggacaca tgaacagccc taagcaataa cattcatgtg 180

gctccggaat aggatgagaa tggaggattg ccttgagggt cctctcttaa gcaatcatgg 240

aacacaactc caaactcgaa agtggaggac acatgaacag ccctaagcaa taacattcat 300

gtggctccga agcangatga gaatggagga ttgcctcgag ggtcctctct tatgaaatca 360

tgaaactcaa ctccacactc gaaagtggag aacacatgaa cagccctaag caataacatt 420

catgtggctc tggaacagga tgagaatgga ggaatgcctn gagggtccct cttaagctat 480

cat 483

<210> 152
<211> 479
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 152

agctngaaca cctattagta tttatatttc ttaaataata aatgtatgac atcaactcgt 60

cattggctcc caggttagtg gattaagcaa aatagaccaa tacaaactca cgggttaagt 120

cacctaaccc attgatccaa agtttacatt gtcacctcta cattagtgac tntttgttgc 180

ctttgtttcc tttaagcttt ntgtgtataa aaatatattt tttcttgtgt gaaatatttg 240

tttggaattc agttttaact atataataaa attgatggtt aagtttaata tatatttaaa 300

cagtcttgat catttgatta tgaggacttg gataaaatat atattcttca aagttttgtt 360

aatataactt ggtaaatata attctaattt tataaactat ganaaaatac aaaagttaga 420

tgaattcaag ctcaacacaa tagaacaagt accaacanat actatcatac atttgacat 479

<210> 153
<211> 313
<212> DNA
<213> Glycine max

<400> 153

tctcctacca ctgccttaca atagtcatca agcaatatgt tggcagcctt cacatctcta 60

tggattatct ttggatcaca ctgctcatga acgtatatta gctcccttgc tgctcctaag 120

gcaatttgct ttcttgtgcc ccagtccaac actggcttac ctgcaaatat ccatcactgg 180

tatatggatc agccactcaa cttacatagc acatgcatgt tcattctagt tctggttaca 240

taaacttctc tatatgcacc tttgagaaga acataagaag ttagaatcaa tttatgtacc 300

ttagttattg gag 313

<210> 154

<211> 402
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 154

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caaaaaanat aataatgacc cctgaagcta tcttggtgac agtgacaata agttgagcct 120

tgtgcagcaa aacttagtgt tgagtgaagg atgacttgtt gcttgtgaat tgacttaacc 180

agtttttgac agctttacct ttggcaatga agcagccatt gttcttccta tcaaccttca 240

acggactccc cattttgacc atcatcttct gaaccaacac tctcaccggc gactctcctc 300

tgacactgct atgctttccc aacccacana ccaccgtaaa ttccgcagga actccataat 360

tggaatcatt caaccttctt ccatctcctc aaccaaagca ca 402

<210> 155
<211> 436
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 155

tcttagatag caacttgttn tgtgctagta atgcatcttg agaggaaagc tccaggaagc 60

ttctttttgt gggaatatga gtccgatcac acaagatggc atgatcactt gcagccatgt 120

tctcaataag ctccatggct tcttctgggg tcttcaattt aatttttccc ccagcagaag 180

catcaaataa ctgcttggac tgtggcctta acccatctat aaaaatgttg aactgaattg 240

gttctgaaaa tccgtgagtc agtgttttcc gcagcaagct atggaatcgt tcaagtgctt 300

cgcttagaga ctcatccaga aactggtgaa atgaaaagat ggntgctttt ccttctactg 360

tcttagactc ggngaaatat ttcttcaaac atttctccac caattcatcc catgtcttga 420

gactgtntcc cttaaa 436

<210> 156
<211> 455
<212> DNA
<213> Glycine max

<400> 156

tctttgagaa aacttccttg agaagctaga gcttagctac actcaccccct ctaataacta 60

agctcacctc cttgagaagc cttcttgaga agattcctat agaagctaga gcttaggtac 120

acacacctct ctaatagcta agctcacctc cttgagatga aaagctagag cttagctaca 180

caacccctat aatagctaag ctcaccccca tgacaaaata catgaaaata caaaaaattc 240

cctactacaa agactactca aaatgtctcg aaatacaagg ctaaaaccct atactactag 300

aatggccaaa atacaaggcc caaacgaagg aaaaacctat tctaatattt acaaagataa 360

gcgggctcat atttagccca tgggctcaaa atctacccta aggctcatga gaaccctagg 420

gccttccctt ggatctctgg cccaatctac ttgga 455

<210> 157
<211> 285
<212> DNA
<213> Glycine max

<400> 157

gtataaccct tcagtttcaa tccagagtct ccatatatga ggaatgggtc tttagttctt 60

cttaagtact taagtatggt cttaactact ttccaatgtt cctcaccagg gtttgcgtga 120

tatcgactag ttacacctag tgcataagcg acatcaggac gtgtacaagt catggtgtac 180

atgatagctc ccactacact agcatatggt attctactca tgcgttctct ttcttcaaga 240

gttgttggac aatgttccct actaagagtt attgcaacgc ctaca 285

<210> 158
<211> 460
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 158

tactaaaaaa gcccattatt gtcgtatctt gctttcattg acaacctagn ttntgttggt 60

gaagctacaa tggatcaagt agaaatgatg tttgaattcc ttaattactt gtattagatc 120

tgggcaagta aacaacaagg acaagacgaa ggtgttcttt tataaaaaca taggcgatat 180

catgagaatt tagattaatg gcaagttggg ttttggtagg accaatgaca tcaacaagta 240

tttaggagtc aatatcaatc atgggagggt ttccaaaaaa tccttgcatg ggatcattga 300

caaagtctag aagtggctca gtgtttggaa aaagaggtca ttttccttta cgaggaggtt 360

gacattaact aaggcagctc tcaatgttct tccatcctac accataagcc atcgcacatc 420

ctttattcag ctngtgatga gttagacana atatgtcatg 460

<210> 159
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 159

tcaacattca atttcgagcg tctcgatata ttacgagcct caatcagaca tgcgagtaaa 60

aagttatggc cctttgtatt ggatcagagc ttcaacattc aatttcgagc gtctcgatat 120

gttacaggac ttcatcagac atcagagaaa aaagttatcg tccgttgagt tggctcagag 180

attcaacatt caatttcgag cgtctcgata tgttacggga ctcaatcaga catccgagaa 240

aaaagttatt gtcgattgaa ttggctcaga gcttcaacat tcaatttcga gcgtctcgat 300

atgttacggg actcaatcat acatccgagt aaaaagttat tgtcgtttga ataggctcag 360

agcttcancg ttcaatttcg agcgtctcga tatgtacggg actcaatc 408

<210> 160
<211> 388
<212> DNA
<213> Glycine max

<400> 160

aattctatca atagaccttc aatctttaat ggagagggtt accactactg gaaaacccga 60

atgcaaattc ttatcgaggc aattgatcta aatatctggg aagccattga aatagggcct 120

tatataccca ccacagtaga aagagtttca atagatggta gttcatcaag tgaaagcata 180

accatagaaa aacctagaga tagatggtct gaagaggata gaaaacgagt acaatacaac 240

ctaaaagcca aaaacataat aacatctgcc ctaggaatgg atgaatattt cagagtttca 300

aattgcaaga gtgctaagga aatgtgggac actcttcgat taacacatga aggaactaca 360

gatgttataa gatctaggat aaatgcac 388

<210> 161
<211> 392
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 161

gtgttggatc gcatgcagaa gagcctcgag cttgaggatt ggcacatgga gccttctaga 60

atgacacttt acaggtttgg caacacgtct tctaactcgg tctggtatga gttggcatat 120

tgtgaggcca acgggaggat taagaaaggt gatagggttt ggcaaatggc gttcgggtcc 180

gggttcaagt gtaacactgc tgtgtgggtt gctttgaata cgatcgaacc agggtccatc 240

aagagtccgt ggagggatga gatacataat tttcctgtca aggctgatcc acttccttgt 300

gagagaacaa atgaatgaat aatccaatca tgcacatttg ggtttgggaa tttctganga 360

aagtatgtgg tctgaattga ttattagtat ta 392

<210> 162
<211> 324
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 162

accacttcca ggcgtgctgg aactacttca catggacttg atggngccta tgcaagttga 60

aagccttgga ggaaagaggt atgcctatgt tgttgtggat gatntctcca gatttacctg 120

tgtcaacttt atcagagaaa aatcagacac ctttgaagta ttcaaggagt tgagtctaac 180

acttcanaga gaaaaagact gtggcagaga gtttgaaaac agcaggttta ctgaattctg 240

cacatctgaa tgcatcactc atgagttttc tgcagccatt acaccacaac agaatggcct 300

agttgagagg aaaaacaaga cttt 324

<210> 163
<211> 393
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 163

cagcttgtgc ctttcatgtc tggaatatga atgtttatat agattcaaag aaccttatgt 60

gctttgctga tggcttattc ccgttccaag gcttcaatgg tgtcttgtct tttacagact 120

tagttggaca tctgttgagt atgtaaacag cagtgtagac tgcttcagcc cagaatgtgt 180

taggtagtcc cttctccttg agccatcgat ctaagccatt ntccataaat tgcgcaattc 240

tttctctctg acacttcatt ttgttgagga gaatatgtga ctataagttg tcgctcaatg 300

cctncatcct cacaaaatct ttcaaactcg cgagaggtgt actctttgcc gtgatcactt 360

cttagtactt ttatctcgtt tccactttga ttt 393

<210> 164
<211> 461
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 164

tataaggctn tgagtgggaa atgatagtga gactcaactt gtataccaac cttgtgctac 60

aacaattgta gcaagaccta gtatccataa tgagagaaga atttttgttt aaaaccttgc 120

atcttgtatg aaagatgttc tctctttagg tttgggttag gtcacaagat taacttgttg 180

gatcgagtgg cctcagaaca attaagaagg gggggttaaa ttaattattc ttaaaccttt 240

actaattaaa aattactctt ttaaggcttt tactanattg ttaagagaat gaggactaga 300

agagaaactt aacagaaagt aaaagcagaa attaaatgca caacggatag taaaagagta 360

gggaagaagg aaacaaacac acaagagttn ttatactggt tcggcaacaa cccgtgccta 420

catccagtcc ccaagcgacc tgcggtcctt gagattcttt c 461

<210> 165
<211> 431
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 165

gagtttggag tgcacatttg aattacaaag atgtggagag ccatgaaaga agcaaagcaa 60

ctagtggaag ggaatgagag ggaacaatat gccaaagtat ttgattatgc acatgaattg 120

ttgaggagca atcctggatc aacagttaag atcaacacag tgccaagtcc agaaggtcca 180

ccataatttc agaggctatg tatttgtctt cctggctgta agaagtggtt tgttgctgga 240

tgtagaccat tcataggtct agatggatgt ttcctaaaga gtgcatttgg aggaaacttg 300

ctctctactg ttgggcttga tggcaataac cacatctttg ttattgctta tgctgtggtg 360

gacattgaga acaaagacaa ttggaaatgg tttctaactt ctgtacatga agatncttgg 420

gattatatac a 431

<210> 166
<211> 406
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 166

actttataca agaatgaagc tctgttacca cttgttagac aagtggcctc agatatctta 60

agaaggggggg gttgaattaa gatattccaa actacttccc caattaaaaa tctatttcac 120

tttttattca agttataaat tcccttaata atgaacttct taaatattga ttcaaataaa 180

acaatttgaa tatgaatata aaacaataat aaacaaagga gattaaggga agagaaagtg 240

caaactcaga tttatactgg ttcggccaca cccttgtgcc tacgtccagt ccccaagcaa 300

cccgcttgag agtntcacta tcttgtaaat tccttttaca agttctaaac acacaaggac 360

aatccttcct ttatgtttag aattccttta caacaagaga cccacg 406

<210> 167
<211> 462
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 167

ctcagcttgc agaatgtact ctacttaatt ttgaagattg tttcaaggaa gcatatatat 60

attcatcagg aaaacatcat agtggaagga aattgcagtg ttgtgatcca gaagatcctt 120

ccacccaagc ataaagatcc tgggagtgta acgattcctt gttcaattgg ggaagtcaat 180

gtgggaaaaa ctcttattga cctgngagcc agtatcaatt tgatgccact ctccatgtgc 240

aaaagattgg gagagttgga aataatgccc actcgaatga ctttacaatt agctgaccgc 300

tccattacca ggccatatgg agtaattgaa gatgttttgg ttagagtaaa acattntatc 360

tttccggcat actttgtggt aatggatatc tttgaagcta ctgacatccc tgtaatattg 420

ggaaggccat tcatgttgac cgcaagctgc atagttgata tg 462

<210> 168
<211> 442
<212> DNA
<213> Glycine max

<400> 168

tctcacagat aggacatgca tgatgccttt tcacactata tccacttaaa tttccatatg 60

ctggaaaatc attaatagta caaaacacca ttgcgtgtaa tgtgaatgtc tgctgcacat 120

ttgcatccca cacatctact ccttcttccc acaatatttt caagtcttcg attaatggtg 180

taagatacac atcaatatca ttccctggct gccttggacc cgtgatcatc atacacagga 240

taatgtattt acacaaaatg cacaactagg ggggaagctt gtaaatcatc agtaaaacag 300

gccacgaact atggttgctg cttaagttac cataaggatt cattccatca gaagcaagag 360

caacccttag gttccttggc tcgtccctaa actctggata caaacaatca attgtcttcc 420

attatggaga atcggtagga tg 442

<210> 169
<211> 262
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 169

tactcagctt gctgattaca tctnccccct tctcaagcaa attcttcttg atatcatcaa 60

aatcttcatg atcccgactc gttggtggag gatgcatgaa tgacaatcaa ttcatggcgc 120

ttcgaataaa agtggagaat ggaggatatg cgaatagcgc taggcaatca atttgcggtc 180

tcccgactcg ctggtggagg atgaatgaat gacaatctac tcatggggct ccgaataaaa 240

gttggaaatg gaggatttga ga 262

<210> 170
<211> 405
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 170

actcggatgt ctgattgagt cccgtaatat atcgagacgc tcgaaattga atgttgaacc 60

tctgagccaa ttcaaacgac aacaactttt tactcggatg tctgattgag tcccgcaata 120

tatcgagacg ctcggaattg aatgttgaag ctttgagcaa attcaaacga caataacttt 180

ttactcggat gtctgattga gtcccgtaat atatcgagac gctcanaatt gaatgttgaa 240

gctctgatcc aattcaaacg acaataactt tttactcgga taattgattg agtcccgtaa 300

tataactaga cgctcgaaat tgaatgttga agctctaagc caattcaaac gacaataact 360

ttttactcgg atgtctgatt gagttccgtc atatatcgag acgct 405

<210> 171
<211> 395
<212> DNA
<213> Glycine max

<400> 171

cgagcgtctc gttatattat aggactcagt cagacatccg agtaaaaagt tattgacgtt 60

tgaatttgct cagagcttca acattcaatt tcgagcgtgt tgctatatta cggtactata 120

tcagacatcc gaataaaaag ttattgtcgc ttgaatttgc tcagagcttc aacattcaat 180

ttcgagcgtc tccatatatt acgggactca atcagacatc cgagtaaaaa gttattgtcg 240

tttgaatttg ctcaaagctt caacattcaa attcgagcgt ctcgctatat tataggactc 300

agtcagacat ccgagaaaaa agttattgac gttggaattt gctcagagct tcaacattca 360

atttcgagcg tgtcgctata ttacgggact atatc 395

<210> 172
<211> 447
<212> DNA
<213> Glycine max

<400> 172

agatttgtgt tgattatata tcccttaata tgttggcggt gccagacaaa ttcccaattc 60

cagtgattga gttactgggt gagttaggga aggctgttgt tttttctaaa cttgatttga 120

aatctgggta cagattttaa agatgccctc atacagaggt tccaaccagc atccatggta 180

aactcatttg aatccttgtt aacactcaaa caagatcaag ctgttcacga attcatgaca 240

cagtttgaga aatatgcaag gtctgtgaag gggttagatg agcagtattt gatgggaatt 300

ttcatcaatg ggctaaaaga agagatttct gctgaattat ggttgtatga gcccaagacc 360

ttgtcagaag caatgaacaa ggcaggaaat taagaagaaa tagaataact gatttattat 420

tgattataaa gaaataagac aaacaat 447

<210> 173
<211> 333
<212> DNA
<213> Glycine max

<400> 173

gaggcagcat tatgcacaat ttctaaaaac tcttttattt tttatctaaa tggcaatcaa 60

actgaagtga acctttatgc ctggacacca cctaaactgt ttacatttgc ttgatgttat 120

tatatggatt gtttcactct ccaggctgag gagaggcact gtgagaatct aggtcgactt 180

ttgtgcactg ctaagctggt tgcaaagcaa gaaggtcctg atgatggctt caggattgta 240

attaatgatg gacgagacgg gggtaagcat tcttctccat gtcattgtag taacattggc 300

caatcagatt ttatttgatt cataggttct tgc 333

<210> 174
<211> 392
<212> DNA
<213> Glycine max

<400> 174

aacagaacaa ttatgacctc tctagcaaca gataaaccct ggatggagga atcaccctaa 60

tctcagatgg tctagccctc aacaacaaca acagcagcct gctccttcct tccaaaatgc 120

tgctggccca agtagaccat acattcctcc accaatccaa caacaacaat agccccagaa 180

atagccaaca gttgaggctc ctctgcaacc ttccctcgaa gaacttgtga ggaaatgacc 240

atgcagaaca tgcagtttca acaagagacc agagcctcca ttcagagctt aaccaatcag 300

atgggacaat tgacaacaca attaaatcaa caacagtccc agaattctga aaagctgcgt 360

tctcaatctg tcccaaatcc caaaaatgtc ag 392

<210> 175
<211> 448
<212> DNA
<213> Glycine max

<400> 175

cctgcacgca tgcaagctat acttcactgc ttcaagtagc gcatgattgt cttccatagg 60

aaaaactttt tctaaaggtt actattacac caagaagata ctgtaccaga tgggaatgga 120

gtatgaaaag attcatgcta gcccaaatga ttgtgtggaa gaaatgtctt ccaagattat 180

tttgatgatg ccaaagaatc aagagtcaag catgttccaa agaatcaaga gtcaagccag 240

tttcaagaat catgatcaag atttatgatt cgagaataat catgatcaag attcaggtac 300

tgcatctaga ctcaagattc aagaatcagg agaagactca atcaagataa gtattacaag 360

aatttttca caacattgaa tagtagaata atttttctaa aagaaaaatc ttttaccaaa 420

gagttttact ctcaggtaat cgattacc 448

<210> 176
<211> 467
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 176

tgtcagcgtg tccaagaccg ccacctctgt cattgtcctt gctgcatgtc gaatttggaa 60

atgcactcgt gccttagatt tgaaaataca cttcacgctt tagatctaaa aatgcactac 120

acctcagatt cataatgcat ggccttgcac acaacagatt tgtcgcgaca atctcccaga 180

gaaagtccca atcggccttc ttgttgtgca tcttgtcgtg attgatggta atgccaacga 240

cattggcgca agagtgggtt gtgatggtgc acatgggcct accgacaccg taacccacgt 300

cgaggattct gttgtcgggc ttggcctcga cactgtcaag gaggagtgtg gaagacgtcg 360

gtgatggagc tgctagaggt ataagtaaat cggttatttc atcactttca tgacccaacc 420

cacaaaagga accttattnt atttatnttg gctctcctaa ttaatca 467

<210> 177
<211> 422
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 177

agcttaacga aaggcatgcc aagtaggngg aattcctaaa gctatttcct tatgttatca 60

aacataaaaa gggaaaaggt aatattgtag ccgatactct ttctcagcgt catgcattac 120

tttctatgct tgaaacaaaa ttgattggtc ttgaatgttc gaaaagcatg tatgatatgg 180

aagcaatgtc ttccaaggtt antttgatga tgccaaagaa tcaagagtta agcaaagttt 240

caagcaaaga ttcaagattc aagaatcaag tttcaagttt caagattcaa gattcaagat 300

ttaagaatca agattcaaga aaaatcaaga tcaagattca agaatcaaga gaagactcaa 360

tcaagataag tactaaaaag tttttcacaa cattgagtag cacatgaagt tttctcataa 420

tc 422

<210> 178
<211> 476
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 178

actcctctta tgtggagtgg tgatggttgt ttattccttt tcattgngat agttgtatgg 60

attctggaac acaggataaa tgatgagttc aggggtccac ctaggcagca aattataacc 120

atgttgtggt caattattta tttcattatc ttactattgt acctagcata atagttgcac 180

acctttttgca tattcaagct ataaacgaaa actacaacta gaagtagctt tgctgtgggc 240

catggaaaac aacattggca gcacctgttt gtttgttagc atcatatata cacaaggagg 300

ttatcatttg tcagtcatgg tattggaaag attccaggat catcatccat aaggcattnt 360

gtagtcaaga tatttgtgat gatagcttct cggttctcac aacatgaatt tgctatattc 420

aggaattctg ttctgaagta tttatggaat atttgtttca gaaatttcta agatta 476

<210> 179
<211> 385
<212> DNA
<213> Glycine max

<400> 179

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gaaatctgaa tcaatcagaa gtggagctca tgaagtctct gcaggagcaa ttgtggcatg 120

ctgctaatgc ctatgaatct ttgctgaggc aaaaggctat agtgaaatgg ttaaaggaag 180

gggacaaaaa ttcagcttac ttccacaagc tgataaatca tagaagaaga cataatgcca 240

ttcaaggatt gatcattgat ggggaatggg ttcacgaccc tagtagggtc aaaactgagg 300

ctttcaatca tttcaaagat agaatttctg agcaagaatt taatagacca accctggatg 360

gtgtgcagct acctttcatt ggtca 385

<210> 180
<211> 425
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 180

agcttgctta agaccgtata ttgatttctt taatttgcac accatgtgtt ccttcccttc 60

aactgagaat ctcattggnt ggtccatata aacatcctcc tctaaatctt cattcaaaaa 120

ggcagntttc acatccatct gatgtagctc caagtcataa tgggctacta atgtcatgat 180

aattctgaaa gaatcctttc atgagatggg tgaaaacttc tctttataat caatgccatc 240

tttctgagta aatcccttat caacaagtct agccttgtaa cgttcaaggg tgccatgaga 300

gtcatgttta gtcttgaaga cccacttaca accaactctc ttacaaccct ttggtaattc 360

tacaaggtcc caaacaccat tatgttccat ggaatctatc ttttctttca tggcatttaa 420

ccact 425

<210> 181
<211> 350
<212> DNA
<213> Glycine max

<400> 181

cagctgtaga cactggctct ccccacaagt acttgggcat actcttgcct ttcaacatgc 60

ctcctaccat attcaatatg gttctgtgtt ttctttctgc agctccatta tgttgaggtg 120

tgcttggagg agtcacttca tgaattatgc cttcttgatc acaaaattct tgaaattctg 180

cagaaacata ttcaccacca ccatttgttc tcaatatctt gatcaatgag ccactttgcc 240

tttctgccat atttttgaac tttcaaagac ttcaaagaca tcactcttcc ttcttattac 300

ggaaacccat actttcctag tccattcatc aataacggat atgaagtatc 350

<210> 182
<211> 221
<212> DNA
<213> Glycine max

<400> 182

tctctacatt gcatcacctt ttaatgagct ggtgaagaaa atgtggcatt tacctggggt 60

gaaaaacaag agcaagcctt tgctttgctc ataaaaaagc ctactaaggc acctgttcta 120

gctcttcctg acttttctaa aacttttgag ctagaatatg atgtctctgg agtgtgagtt 180

gggagctgta tttgttacac aggtggcgcc accctatttg c 221

<210> 183
<211> 455
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 183

taccctgatg aggatgtccc atatgttctt aatactggac tgatccatnt gcttccaaag 60

tttcatggcc ttgcaggtga agacccacac aagcatctga aagaattcca tattgtctgc 120

tccaccatga aaccaccaga tgtccaggag gatcacatat ttctgaaggt ctttcctcat 180

tctttagagg gagtggcaaa tgactggcta tattaccttg ctccaaggtc catcacgagc 240

tgggatgacc tcaagagagt attcttagaa aaacaatttc cctgcttcca ggaccacagc 300

catcagaaaa gatatttcat gcattagaca actcagttga gagagcctat atgaatactg 360

ngagagaatt aaaaaattat gtgttagttg ccctcaccac cagatttcat agcaacttct 420

cctccaaata ttttatgaag gactcagcaa catgg 455

<210> 184
<211> 419
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 184

cttgngaaca ttaccttgtt tccaaggaat ttgtcattca tagtgatcat gaatcactta 60

agtacattag agggcaaaac aagttaaaca aaaggcatgc aaaatgggta gagtacctag 120

agcaattttc atatgttatc aaatacaaaa agggaaaaac aaacgtggta gttgatccct 180

tctcttggag acacatattg ttttactccc taagagctca nattntagga tttgataaca 240

ttagggactt gtatgcttta gatgaatatt tctctcccat ttatgagagt tgtgggcaaa 300

aggccccaga nggattctaa ttggctgagg ggtatttgtt canagaggga aaactttgca 360

taccccaagg atccatcagg aaattacttg tgaaagagag ccatgaatgt gggctcatg 419

<210> 185
<211> 261
<212> DNA
<213> Glycine max

<400> 185

ctcacgctgt ttcatgtaaa cctcttcttc ttatcaccat tcacgaacgc cgttttcaca 60

tccatttgat gcagctcaag atcaaaatga gctactaatg cccaaattac tcgaagagag 120

tctttcttat atacagggga aaaggtctct ctgtaatcga ttccttctct ttgagtgaat 180

cctttagcaa caagtcttgc cttatgtctc tcaatgttgg cttctgagtc tttctttggt 240

ttgaagaccc atctacattc g 261

<210> 186
<211> 354
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 186

ctcagctcgt cttaccatcc acaatcttac ggtcagaccg aggtggcaaa tcggatagta 60

taacaatact tgagggcctt cgtccatcgc aagccagcgt tgtggggacg atttctgttg 120

tgggcagaat ggtcgtataa tacttcgtgc cattcgagta cgggattaac tccgtttgaa 180

atcaccttcg ccgaaaacca ccagctatcc ctgaatacat angtggaaca tcacaggtgt 240

cataccctaa tttcgtccgg ggaccatccg tttgttggga tgcgaccctc gtttgaccac 300

ttcgaggtac ttggcaccca tcgttaggca atctgtgaag tttcgtgaca tgct 354

<210> 187
<211> 416
<212> DNA
<213> Glycine max

<400> 187

gtgtgattcc tttctttttc ttatcattct cctcatgttg attcagtctc attagttcca 60

tttcgtgttc ctataacttt ccaaataaag ttgcaagaga catgttagaa agatcccttg 120

attctgtaat agttgttacc tttggttgtc attccctact taaacatctt agaactttat 180

taataagatc ctcattggga aatatctttc ctaatgatgc aagatgattt actatgtgtg 240

tgaatctctt ttgcatatca tgtatagttt catttggatt cattctaaac aattcatatt 300

catgggttaa ggtatttatt ctagaacctt ttacatctat tgttccttca tgggttactt 360

gtaaggtatc ccacatatct tttgcactct tgcaatttga tactctaaag tattca 416

<210> 188
<211> 471
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 188

agctntgcat ggatgccaca cgtgaatctt ctgtatcatc catcatttct ttcattcaca 60

accccaacaa gatgtagtac actagagtta tgggcaaagc aatcagcatc ccaaaaataa 120

cactgcattg ggttaaagaa gaagctccat tggttaggat taaaagagaa agtaattgaa 180

tgaaaaggaa aaaggaatgg aggggagaga aagttctaat tgagccatat aagaattaga 240

tttgaatact cacgctgtgc tgagaatatc aggatgtaca ttatattcct tagcaaagac 300

aaatgggaca attccttggg gaagagctgc ctatattttt ttgacattca gttgccaaac 360

aaacaggaca agcaaacaaa caaacatgtc aactgcagtt tcaaatcctt ggtgtacaat 420

cacaaacatg atcattngaa tcctcactac tagtactaag atcttcaatt t 471

<210> 189
<211> 412
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 189

cttgacagct ctatggacca tgctatcatt cttcctgcta gcttagtatt tcttagcacc 60

ttcttgatgg ggtgatcctt cttgacgatg atctaagggc tctggaagta cggcttgagg 120

cgttgagcag aggttatgag tgctagcgcc actttctcga tcatttggta tctctttcca 180

acatcatgaa ggatgtgact gacaaagtag atgggtgttt ggtactttcc atcttcttgg 240

acaagggttg aactaatggc tttttctgcc actgaaaggt ataggaatag ggatgctcca 300

ngcttangtc aacttataac aggtggtgtt gcaatagttn tctttatagc tagganagct 360

tgcttacagg cttcgtttca caagaacgac tcggttttcc tgagtagctt at 412

<210> 190
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 190

agcttgcttc tacactaaga agcactctat attgagtgaa tcaccaaaga gagaacaacc 60

accaaaattg aggaccgttt tgtaattntg taatttacaa tttacttacc ttcatttctt 120

tcaagttttg taacaaaaag gcctttcatt ggaagtgtgt tgggagcctc caataagtta 180

ccaaacttcc atttgtgtgt aataattcta ggcaattttt ccttaagata gtgagtgttt 240

tgttgggaac cttgaatgtg gtcatccaaa cactcttang atttgcctag tttacatttc 300

ttgcttactt tcatagctta tttcctttac cttccctttt aaaaccacct agatagtttt 360

ccttttacca attagttntt ttaccttatc tttcacacct cttttagt 408

<210> 191
<211> 463
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 191

gctttgatca aagtgttcga gggggagcaa gcaaagatag aggataactt tcttcttggg 60

aagtttgagc tttttgggtt cactacatcg ccaagaggag ttccacaaat caatgtttta 120

tttgatgttg acgttgatgg catcgtagaa ttcattgcta gagataaaat catgaggatg 180

aaaaaaagga tcatgatcga caacaagtac tggaggttga gtccctaaga gatgaggaga 240

atagtgagat atgcaaagag gtataaggca tangatgtgg aggtaagggc aaacggaagg 300

ccagaacttg cttgagaatt gtgcttttga aatgatggac aaagtgaaga atcttaagaa 360

attagtaccc atagcaacaa tgttattntt tttagtttca ttaacaattc agtaaaaaaa 420

aataccgtgc gctaacttga aatgcccnct gcacacatgg ata 463

<210> 192
<211> 383
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 192

agcttagccc tagaggggat ggacctttc atgttttgga gaggatcaat aacaatgcct 60

ataagttggg cctcctagaa gagtatgcag ttagcaccac ttttaacatt tctgatttaa 120

ttacttttcc aggtggagct aatattgagg aggaggaact aacaaatttg agatcaaatc 180

ctcttcaagg gggaggggat gatgcaatcc tccctaggaa gggccagtca ctagagacat 240

gagcaagagg ctccaagagg attgggctag agctggtgaa gaaggcccta nggttctcat 300

gagcctcatg gtagatttct gagcccatgg gacaaggttg ggtctaatta tctttgtaca 360

tattaaacta ngatgtcatt ata 383

<210> 193
<211> 472
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 193

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gtggccttaa gcaagctttt attgctagtg gaagtgagga ttcacaggta tgaatcttca 120

atcatcattg atcaaaatgg gaaaatattc gccagtgtaa ttttttataa tttgcaaatt 180

gaaagccttg atgtttatat gtctctgtta aatgtgtttt atttgctaag tttttatagc 240

tgtctcaata atttgttaaa ataagttcaa catgcacttg atgcatgcta tcgaggatca 300

ctaaaatatt ggcataaaag acccatgaaa tggttctttg tggtctgatn tactggactt 360

gaatgaattg aactacacat cgctataatg ttcaagagtt cctggcttct gcaatattat 420

tctagtttat cttgataaaa ctaggaacat ctcgattgat aatgctggaa gt 472

<210> 194
<211> 410
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 194

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taaaatctag taacatcata atttaaactc actgcaacgg ataaatgaca atcaccatac 120

tcaagagcct catggataat gataagatct tcactaccct aatctaagaa aattagacga 180

taaaacaatn tatgtttggt gattacatag tggcactaat atgtaaatgc aaaaatgctg 240

acctggccat gttcattgaa agtatcgagt ccaacaattc caaggtcaag atctccagat 300

aacaattttc ttgtgatgta tttgggcctc taaaaccaaa ctttgagttt ggatagctgc 360

aataatgcaa gagaattggt ttatggtcat gtagagatat agtacattga 410

<210> 195
<211> 331
<212> DNA
<213> Glycine max

<400> 195

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agagttatga ccatttgaat tactggcgag cttccgttga tcaatttcga gcatctccaa 120

acattatgcg ccttaatcgg acatccgagt gaaaagttat gaccatttga agttctcgag 180

agcttccgtt gttcaatttc gagagtctcg atatattatg tccgtgaatc tgacattcat 240

gagaaaagtt atgaccactt gaatactcga gagctttcgt tgtcgcattt cgagcgcctc 300

cgtatattat tcgcattaat cggactttct a 331

<210> 196
<211> 300
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 196

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aggagacatg ctttacttgc tatgcttgaa actaagttgg ttggtctcga gtctttgaaa 120

gacatgtatg tgcatgatgt ggactttgct gaaatttttg ctgcatgtga aaagttttct 180

gaaaatggtt actataggca taatggattc ttggttaaag caaataaatt gtgtgtgcct 240

aagtgttcca ttagagagtt gcttgtgagt gaatcacatg aggnggggtt gatgggacac 300

<210> 197
<211> 461
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 197

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gcaagttgaa agccttggag gaaagaggta tgcctatgtt gttgtggatg atttctccag 120

atttacctga gtcaacttta tcagagagaa atcagacacc tttgaagtat tcaaggagtt 180

gagtctaaga cttcaaagag aaaaagactg tgtcatcaag agaatcatga gtgaccatgg 240

cagagagttt gataacagca ggtttactga attctgcaca tctgaaggca tcactcatga 300

gttctctaca gccattacac cacaacaaaa tggcatagtt gaaagggaca acaggactnt 360

gcaagaagct gctanggtca tgcttcatgc caaagaactt ccctataatc tctgggctga 420

agccatgaac acagcatgct tcatccacaa cagagtcaca c 461

<210> 198
<211> 402
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 198

tatccncata agagtgcaga acagctggcg agtcagcatt gattatagga ggctaatcca 60

ggtaaccaaa anagatcatt ttcccctgcc attcattgat canatgcttg agcgcttggc 120

aagtatgtct cattacaatn nttttatggt tnttctggtt atttacaaat tcatattgct 180

cctgaggatc aagaaaacac cacattcacc tatccctttg gcatttttgc ctataggagg 240

atgccctntg gcctatgcaa cgcctctggt accttccaac ggtgtatgct tagcattntc 300

aatgattntt tagagagttg catagatgtg tntatggatg attntactgt ttatggatcc 360

tcttntngat gcatgttgga tagtctagat agagttctta at 402

<210> 199
<211> 446
<212> DNA

<213> Glycine max

<400> 199

agcttatgct gcaaacatct acaatagacc ttctcaacct caacaacaaa atcaggcaca 60

acagaataac tatgacctct ccagcaacag gtacaatccc ggatggagga atcatcccaa 120

ccttagatgg tcgaatccgt cacaacaaca accttatttt caaaatgttg ttggcccaag 180

cagaccatat gttcctccac cattccagca acaacaacaa caacaacatc cccagaaaca 240

gcaaacagtt gaggcccctc cgcaaccttc ccttgaagaa cttgtgaggc aaatgactat 300

gcaaaacatg cagttttaac aagagaccag agcctccatt cagagcttaa ctaatcagat 360

gggatagttg gctacacagt taaatcaaca acagtcccag aattctgata gataccttct 420

aatctgtcag aatcccaaaa tgtgag 446

<210> 200
<211> 465
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 200

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gctgtccaag tttcatggtc ttgcaggtga agatcctcat aagcatctta agaagttcca 120

tattgtctgt tccaccatga agccccctga tgtccacgaa gatcatatct ttctaaaggc 180

ttttcctcat tctctggagg gagtggcaaa agattggctg tactaccttg ctcccaggtc 240

cattaccagc tgggatgacc ttaagagggt gttcttgggg aaattcttcc ctacatctag 300

gaccactgcc atcaganaag acatttcagg catcangcaa cttagtggag agagcttgta 360

tgagtattgn gaaagattca agaaattgtg tgcaagttgt ccccaccacc agaattttga 420

gcaactcttt ctgcaatatt tctatgangg acttancaac atgga 465

<210> 201
<211> 409
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 201

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tttcagctta accgacttca aagggtaggc tttccattga acgagttgtg ggacaagttc 120

aataacaatg acaagtanga aagaccaatg acttgcaaag gaatagttcc actaattctg 180

ttgtgtgaaa ggtcaagggt attgtaaatt tggcaattcc caacaccagg atgtatgctt 240

ccttccaaca cattatttga caagtcaagt tgaaacaaaa gactaaggtt gccaatggat 300

aatggaattt ctcctgacag tttgctcaca tttaaattca atgactgcat cttttggaac 360

atgacaaaag aagcaggaat agtcccagta atctgatggc caccaatat 409

<210> 202
<211> 393
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 202

ctattacgga cactatagat actcagctag aattgaacac ggaagctctc aagaaattca 60

nattgtctta tactttcaca cggaacaccg attcaagctc ataatatatc gagactctcg 120

aaattgaaca acgaaagctc tcgagaaatt caaatggtga aaacttttca gacgaaagtc 180

ggattcagac gcataatata tcgagaagct tgaaattgat caacggaagc tctcgagaaa 240

ttcaaatggt cataacttgt cacacggaag tccgattcag gcgcataata tatagagacg 300

ctggaaattg aacaacgaaa gctctcgaca aattcaaatg gtcataacta ttcacacgga 360

agtctgattc aggcgcatac tatatcgaga ctc 393

<210> 203
<211> 406
<212> DNA
<213> Glycine max

<400> 203

ggctgcagct tctcgatata ttatgcgcca gaatcggacc tcagtgtgat aagttatgac 60

cattttgaat tttcgagagc ttccattgtt caatttcaag cttctcgata aattatacgt 120

ctgaatcgga ctttcgtgtg ataagttatg accatttgaa ttcctcgaga gcttccattg 180

ttcaatttca aacttctcga tatattatac gtctgaatcg gactttcgtg tgataagtta 240

tgaccatttg aatttctcga gagcatccat tgtttaattt caagcttccc gatatattat 300

gcacatgcat cagactactg tgtgaaatgt tatgaccatt ttaatttctc gagagcttcc 360

gttgttcaat ttcgagcgtc tcgatatatt atgcgcctga atcgga 406

<210> 204
<211> 328
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 204

tctacttcat aacccccttga actacttcac attgatctat ctggtccctc tagaacaatg 60

agtttgggtg gtaattacta tggcttagtt atagtagatg attactcaag gctcatatgg 120

actttgtttt aaccaaaaat gaagcttttg gtggctttta aaaacttgcc aaggtgattc 180

ataatgaaca aggtctcaac attgtttcac ttagaagtga tcatagaggt gaatntcaaa 240

atgagtcttt tgaaaactnt tgtggagaaa atggaattca ccataatttn tcttgcccaa 300

gaacacccca acagaatggt tttgtgga 328

<210> 205
<211> 455
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 205

agcttctcac atctgactct ctagttccaa cgtggtgttt tctcttgatg cacttcctcc 60

gatcaccttg accaatggaa tctccttccc tcttaggtgc tttgttcgcc tatctttgat 120

cctcaaaggc aatgttccat atgtcaagtt cttcttcact tgtacgtcat ccaatttgat 180

cacacgagat ggatcatgga tatactcacg aagttgagac acatgaaaga caatgtgaag 240

gttagaaaga gacaggggta atgcaatttg gtatgcccac agtaccgact ttttttagaa 300

tttggaaagg acagataaaa tgaggtatga gttattgnga tttcaatgct cgaccaactc 360

cagtccacaa agtgactctc aagaatacat gatcactaac ctcgaactcc aagtctttcc 420

tccttcttgt cctgatagct ttctacctac tctga 455

<210> 206
<211> 422

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 206

tcacacttga taatggagaa cacatgatca gcgctaggca atgacattca tggtactccg 60

aacaaaggtg gagtatggag gattgccttg agggtccgca cttangcaat catgaaactc 120

agctccaaac tcgaaagtgg aggacacatg aacagcccta agcaataaca ttcatgtggc 180

tccagaaaag gatgagaatg gaggattgcc ttgagggtcc tctcttangc aatcatgaaa 240

cacaactcca aactcaaaag cggaggacac atgaacagcc ctaagcaata acattcatgt 300

ggctccggan aaggacaaga atggaggaat gccttgaggg tcttctctta agcaatcatg 360

gaacacagct ccagactcga aaatggagga cacatgaaca gccctaaagc ataacattca 420

tg 422

<210> 207
<211> 397
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 207

ngtanggtta aagtctcacg atagtcacgt gctcatgcaa cagttgttag ccatggctat 60

acgagacatc ttgccaaaca aagtcaggtt agcgataact cacctgtgct ttttcttcca 120

tgctatatgt agcaaagtca ttgatcctgt caagtttgat gagttggaaa atgaggccgc 180

aattatacta tgccagttgg agatgtattt tccccctgct ttctttgaca tcatgattca 240

cttgattgtg catctggtca gagaaatcaa atgttgtggt cctgtttatc tatggtggat 300

gtacccgatt gagcgataaa ttgcanaaga agccattgaa tttttttcag aatacttaga 360

gaatngctaa acctgtggcc ttctgagtct cgcatga 397

<210> 208
<211> 427
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 208

ggtagagtcc ctntgtgtct ctagcttcac acacatgtag nggaacatct atgnaaacct 60

gcaacgtgta agcattgcgt tagctataat ttatgaagaa ccacttctag ttctataatt 120

gtacaacata ttagcatatg ccaaactatg tgtatcattt ggatcaccaa aataagaata 180

ttacctcaat aaaatctcct tttggcatta gtgctctgca tgcatctcta ntcctttggt 240

atggtgatat taaactagtg atgcaaataa caccagcatc tgcaaagagt ttagccacct 300

cacctganaa ttntatatcg tgatgtctaa ttattaataa aacaataaaa tataatcgga 360

agatatcagg gaaagcattt agaaagcaac ataagaaaaa acagataaac tcaccaatcc 420

ttctaat 427

<210> 209
<211> 422
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 209

agcttgtaac ttatataata tatacatttt attgtaatta tattttaaca catcagaatg 60

gtgcgcccat aacccacagg tcccaggatc gaaacctggt tctgataaag agtggcttcc 120

gatctatcac atatatatat attttatgcg taaaacatat atcattacgc aatgacattt 180

gagtataata aaaaatagtt ctgcagggcc taacatttca gtgcttatat taatttagtt 240

accatttaaa ttttattatt gagtcaactt tttaacgtat attcatattt tctctttggt 300

aattntattt taatttgctt aagtaaacat atttttttatg gataataatg gcttccagtt 360

tcttagtgaa ccacatctga aaaattatac ttgaacaaga agatgtgttc actatgtcat 420

ag 422

<210> 210
<211> 357
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 210

tagatactca agcccattca aatgaaagga attcataatt aaaaagttga gaagggttca 60

cngaagagaa tntcaaaatg actctgaatt gttttgtgaa caaaatggca ttaatcgtaa 120

cttttccgct ccaagaacac cacaacaaaa tgggattgtg gggaggaaaa aaaagtccct 180

tgaggaactt gttagtgttt agctctactg agctntaaaa gattggctaa gatcttgtta 240

aaacataagc acttagacaa tgaatgaaag ctggagttgc tgcacatgat gtccaacgct 300

atgtcaagga ataagatncg gctgcacaat gcacaaggca agataaaatg tcaaatg 357

<210> 211
<211> 384
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 211

agcttgtctt ctctagcctc tnttgngctt ttctacattt ccttagtgac aagtcatctg 60

cctagaagtt tcttgtcttg acctggttgt tgtgtctttc tcatctgcca tgcacttcca 120

tgtttaattt cgagtgtctc ggtatattat gcgcctaaat tggacatccg agtaaaaagt 180

tatggccatt tgagtttgcc tagaactttt gtgttcaatt ntgagcatct tgatatatta 240

ttggcctgaa tcggatatcc aagtcaaaag taatggccat ttgaattttc cttctgcttc 300

catatataat tntgagcgtc tcgatatgct atgcacccga atcggatatt cgagtgaaaa 360

gttatgacca tttgaatttc ttga 384

<210> 212
<211> 344
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 212

tctggtggga catcttgact tgctntccaa tctgacattc accacanatt ctgccttctt 60

ctattttcag aatgagaatg cctctaacaa caccttttgtc aatgattttc ttcatgcctc 120

ttaagtgcag atgtccaaat ctttgatgcc atattctgac ttcatcttct ttggaggata 180

gacatgtgga ggagtaactg gtttcttgag gtgtccatag gtagcagttg tcctttgatc 240

tgctgccctt cattagaact tcactcttct catttgtcac caagcattct gactttgtga 300

agtttacatt gaatccttca tcacacagct gactgatgct gatc 344

<210> 213

<211> 355
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 213

ttgaattgct ttntggcctt ctggngtctc cctgcctcca attaagactc gatccgggtt 60

gaaaagatct tggattgcag ttccctcagc aaggaattca cggtttgaaa ggatttggaa 120

cttgattccc tttccattgt gagtcaaaat cttctctatg gcctcagcag ttttcacagg 180

gacagtggat ttctccacca caatcttgtc actcttgnag acatcagcaa tcatgcgtgc 240

tgcactcttc cagtaagtca aatctgcaac cttgtcggct tcaagaccac gagttnttgn 300

cggcgtgtng acggagacga acactatgtc agcctcatag acatgtttct caaca 355

<210> 214
<211> 311
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 214

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aaagttatga ccattagaat ttctcgagag cttccgttgt tcaatttcaa gagtctagat 120

gagttatgta cgcgaatcga acatctgtgt gaaaagttat gaccattcaa atatcttgag 180

tgcttccgtt gtgcaatttc gagcatcttg atatattatg tcccacattt ggacattcgt 240

gtgaaaaggt atgaccattc gaatttctcg agagcttcca ttgtttaatt tcgagagtct 300

agatgagtta t 311

<210> 215
<211> 415
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 215

gtatatgaca tgtcccactt gtactttntt tttttatcta atttgcatcc cacaaaatta 60

gaatctctgg atcttgattc atccactgat ttacctttct catttaagtc aaggtaggtt 120

gatgtagcca taagaatgga cgcttctttg cattnttcca taccaaattt ttttattagt 180

tctatgcagt atttattttg accgaggaag gttccatgtt tcattttctt gacttggagt 240

cctagaaaga aatttaattc tcccatcata gatgtctcaa attctttttt gcatacaaca 300

tgaaaatccc ttgcataagg tttcattagt atagccaaat ataatatcat caacatatat 360

ntgaacaatt aacaaatcat tgtttacttt cataatntaa caaagtttgt caact 415

<210> 216
<211> 305
<212> DNA
<213> Glycine max

<400> 216

tatagatact cagcctcatt ggagcttgag gcctaggatc ttcttatcaa tggattctct 60

tgcttcttgg aagatgaatg gaagcggaat ggagaaaggg agagagagag gagacgccac 120

ttcaaagaga agatgagtct agaagaagct caccaccata ggaggccatg gataagagct 180

tggaggaaga aggagatgaa tgaagggaga gggagagaag agcacgaaca tttgtgctct 240

acatgagctt tgagatctga agtttaatat tcaaatgatc aaagttgaaa aaaatgcaca 300

cacat 305

<210> 217
<211> 396
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 217

ntatcanatg gatgtaaaga gttcattctt atatggctnt attcaagagg aagtatatgt 60

agatcaacct cctagatttg agaattcaga caagcctaat catgttttta aattaaaaaa 120

aaggctttat atggcttaaa gcaagcccct agagcttggt atgagcgtct gagtaagttc 180

cttttagaaa aggatttctc tagaggcaag gtagatacta ccctttttcat aaatagaaaa 240

tcacatgaca ttntactggt tcaaatttat gttgatgata ttcattttag atctactaat 300

gaattattat gcaaggaatt ctctcatgac atgcaaagtg agtttgaatt gtcaatgatg 360

ggagaactct aattgtttct tggatacaaa ttaaac 396

<210> 218

<211> 325
<212> DNA
<213> Glycine max

<400> 218

agtgtttctt ttgcaagaag aagggacaca tgaaaaagaa ttgccccggg ttccacaaat 60

ggcttgagaa gaaaggtgaa tcaatctcat tagtatgtta tgaatctaat atgggtagtg 120

gtaatattaa cacctggtgg attgattctg gatctactat tcatattgca aattctttac 180

agggtatgca aaacctaagg aaaccagtgg gaagtgagca aagcatttta tcaggcaata 240

agctaggctc acatgtggag gccattggaa cttgcatttt gactttaagt agtggcttta 300

ttttaaaatt agaaaggact tttta 325

<210> 219
<211> 289
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 219

gcttatcttt ggttntacaa ccaaagtcca tgtgaacctt gagtaatcat ctactataac 60

taagccatag taatttccac ctaaactcag ttctagaggg accaaataaa tcaatgtgaa 120

aaagttcaag gggttttgaa gtagaaacaa catttttact ttgaaaggag tttttaactt 180

gctttccttt nttacaagct tcacacaatt tatttttctc aaacttaagt tntggaagac 240

caattactaa gtctttccta actagatgat taagatgatg catatttat 289

<210> 220
<211> 460
<212> DNA
<213> Glycine max

<400> 220

aagcacctga gctgcagcta tgctgctata ttacaataga ccttctttac ctcagcagca 60

aaatcaacca caacagcaca attatgacct cttcagcaac agatacaacc ctggatggag 120

gaatcaccct aatctcagat ggtctagccc tcagcaacaa caacagtagc ctgctccttc 180

cttccaaaat gttgctagcc caagcaaacc atacattcct ccaccaatcc aacaacagca 240

acagccccag aaacagccaa cagttgagac ccctccacaa ccttccctca gaagaacttg 300

tgaggcaaat gactatgcag aacatgcagt gtcaacaaga gaccagagcc ttcattcaga 360

gcttaaccaa tcagatggga caattggcta cacaattgaa tcaacaacag tgccaaaatt 420

ctgacaagct gccttcttaa gctgtccaaa atcccaaaaa 460

<210> 221
<211> 449
<212> DNA
<213> Glycine max

<400> 221

agcttgtcat ggtatatata tgtttcctaa tagtctactc tgtgttatat aatacttagt 60

taaatatatt gtgtatacta aaagcaaatg cttaacatta tacgtctttc gtactcaagg 120

atataccaac attgaagggc ggactgtctt gatgtagcga ttttaacagc gatgacacta 180

tctttgttct atatattaac tgtcatggag atggagctgt ctttgtaaac aatctttgtc 240

attatcagct gaaagatgaa catgttgttc gataggaaaa taatgaaata ccttatataa 300

atgtattgta aagttttaag aataaactgc tcaaattgcc agcagtttgt cgtagaatag 360

tagtgcaaat tcatgatgta aatgtattag aatacagaat aaacctatgg tgccgttatt 420

aattgttatg agaacatctt gggtcttgc 449

<210> 222
<211> 447
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 222

tgtaggcctt gaatcttctt catcaatgga gtcctttgct tcttgaagat aaattggaag 60

cggaatggag aaggaggaaa ggtgattaga gatgccactt caaggagaag atgagtcaag 120

aacaagttca ccgccatatg aagatatgga tataagagct taaaggtacg agaagatgag 180

tggagggaga gggagagaaa gggcacgaca tttatgcctc agatgaggta tgaaatgtga 240

agtgtaattt ctcanatgat caaagttaaa aatatgcaca cacaaggcct ctatttatag 300

tttaagtgtc atacaaaatt ggaggaaaat ctgaatttct attcaaattt cacttgaatt 360

tgaatttgtg gagccaaatt tggagccaaa atttcactaa ttaggattgc atcatccctt 420

ccnctctgaa aatgaattga cctcaaa 447

<210> 223
<211> 440
<212> DNA
<213> Glycine max

<400> 223

tcatcaagga tcttgttgaa atcatccaat tgttcagtgg ttgtttttta ctctgtcatc 60

ttgaaggtgt acagtttttg cttcaagcat agccaatttg caagggactt tgtcatatac 120

aatgactcca gtttcaacca cattgaggtt gttgtctttt ctcttgcaac ttctcttaaa 180

gctttatctc caaagcatag aatgattgca ctgctggctc tatcaatcat ctctgatttc 240

tcctttgagc ttagagattc agacatcctt tcttctcctt taagagcttc tgcacagcca 300

tgttgaatca agattgcttc catcttgact ctccataacc cgaagtcatt gtcccctgaa 360

aacttctcaa tatcgtatta tgatgatccc atctttcttg gtcttgatct tgtccccata 420

gacggcgcca cttgttgatt 440

<210> 224
<211> 407
<212> DNA
<213> Glycine max

<400> 224

cgcatgataa atactgggac agtctcaaac cctgatgtat cagtttcaga tccgtggagc 60

caatgcgcag tgggacaagt agagtcgcta aaatcattgg tcagactcct acctatgtgt 120

gcctcgggcg tcttgatgat ggcgtcccaa ggctcattct ctaccctgca agcaactacc 180

ttggaccgaa agctatttgg caatttcaag atgcctgcag ggtccttcaa tcttatcatg 240

atattgacct tatcaataga cattcccttg tatgaccgca taatggtacc tctactagcc 300

aaatacaggg gcttgccgaa tggattctgt agtaaaactc caattgggat tggattgctg 360

tttgtatgcg cagctaaagg aacatcagct gtagttgaaa ctattag 407

<210> 225
<211> 410
<212> DNA
<213> Glycine max

<400> 225

ctatattttc agtagatgaa tatgaatccg cggccacctc atgtactcct ctaaggacaa 60

tagcatcatt tgttgcactg aattgttagg agttggaagc catcttctca atcaaactcc 120

tagcctcagc acgggtcata tcaccaagag ctcccccact agcagcatta atcatactcc 180

tctccatgtt gctaagtccc tcatagaaat attgaggaag gagttgctca gaaatctggc 240

ggtgagggca gcttgcacac aatttcttga atctttacca gtactcatac gagctctctc 300

cactaagatg cctaatgcct gaaatgtctt ttctgatggc agtggtccta catgcaagga 360

ataatttctg caagaacact cttaacgtcg tccaagctga aaatggacct 410

<210> 226
<211> 442
<212> DNA
<213> Glycine max

<400> 226

agcatttaca atgattaaga tatactcttt caagtttttt ggccataaat tagtctggga 60

tctcaatcaa gtctcgagac tcttgaaggt caatggtctt taaactcacg aggttctgta 120

aaaaaaataa aaatacatca cattgaccat aaatcattaa aataaaattc ttagtataca 180

ttgaagctca tcatcctagg tgtggctctt gtgattgtga atgagtttca ttcgagtaag 240

caaaagacta gttaccactt tgtcttacga ttctctaccc tacctttgca aatagaaaga 300

aaaatgtagt atgtatattc acaatcatac ctgaacccca tcccagagct ttttgagctt 360

gctacgaggc atggaaatct ctacaagtcg ttcagcgcag aagttatacg gcaaagactc 420

aagacaacat tcatgccaat ga 442

<210> 227
<211> 384
<212> DNA
<213> Glycine max

<400> 227

tggatctgac tgccctgctt tatgtgatat acataattgg gtataaagac gactagggcg 60

cagtaactga cgtttgtttt tatatccaaa ttgtataacc tgtgataaat catttaaagc 120

cattggtcct ttattattca ttatatgatc aattctttta ccacttctag attgtgagta 180

tcaatgatta ttcatgatca caaagcatat gccaaactca gatgatagta tatcaaatta 240

ctatacttct gatcatgagg gcgagccctg gtgcatcggt aaagatgtgc ctcggtgact 300

tgttggtcat gggttcaaat ccagaaacag cctctttgca tatgcatggg taatgctgcg 360

tacaacatcc ctaccccata cctt 384

<210> 228
<211> 436
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 228

taagctcctt caactgcaca atgctcttaa tatttgaaga gtgtccttgt ggaaccttca 60

cccgacgaag acactgacaa aaacttatct tctccttctt ggacaaagta tggcgggctg 120

ggggtaagta aattatcttc ccatcagacc ttggatgcaa atgtgattgt atacccatat 180

cagctaaatc ttgacaggta ttcaagccat ccttcatctt gccttgaatg ttcatgagcg 240

ttccaaccac actgatacaa acatttttct ccacatgcat aacatcaata caatgtctaa 300

cgtcaagatt acacctgttc ggaagatcaa agataatgga ccttttcttg catatgcaac 360

tctgactttt atccttcttt tgagtacttc caaatgcagt atntaagtga tgaacccgct 420

gatatacctg ctcacc 436

<210> 229
<211> 432
<212> DNA
<213> Glycine max

<400> 229

agcttatgag catgagggtt agccttttct tgactataaa aataacgttg tttagttccc 60

ttgcttactc ccataatacc aggagccttg tgcatatcgc tttttataca taagctaatg 120

agtttctgtt gtaacaaaag tgtttgcact acactatttg tcactacatt cgcggtacgg 180

gctaaggctg attcatttat gcaggttgtc attggtcaag ctgctgtgca caggtgtaat 240

gcaactgtca acttccttga tgaaacaaga ccttcatatc ctgcaactgt aaataatggt 300

gacttgcaca agctatctgt tgatgtagct ggcaatttgc ttggcaccaa taatgttaat 360

attgacaaga cacctatcat ggccgctgaa gactatgcat tctatcaaga ggtcatacct 420

ggctacttca tc 432

<210> 230
<211> 428
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 230

ntccactcct ttggaagatc attatttgct tgagtttcat agtcttgaga atcctcattg 60

ctttcatctc ttttcctttt agaatccctt tcatgattat gtatctcttc taagaaatct 120

gaaacatcat ctaacacatt ctttcttgga gaaataacat tagactcatc aaaggaaaca 180

tgaatggatt cttcaatatt catagttctc ttattgtata ttctatatgc tttactatgc 240

aaggaataac caaggaagat tccttcattt gccttggcat caaactttcc taagttttct 300

tttccattat ttaatacaaa acatttgcaa ccaaagacat gtaaatgtga aatgtttggt 360

tttctaccat tgaataattc gtaagggagt ttctttaaga tgggtcttat taaagcctta 420

tttaagat 428

<210> 231
<211> 422
<212> DNA
<213> Glycine max

<400> 231

agcttcaaca ttcaatgtca agcgtctcga tatattacgg gactcaatca tacatccgag 60

taaatagtta ttgtcgtttg aattggctca gagcttcaac attcaatttc gagggtctcg 120

atatattacg ggactcaatc cgacatccga gaaaaaaatt attgtcgttt gaattggctc 180

agaggttcaa cattcaatta tgagcgtctc gatatgttac gggactcaat cagacatccg 240

agtaaaaagc tattgtcatt cgaattggct cagagattca acattcaatt tcgagggtct 300

cgatatatta cgggactcaa tcagacatcc gagtaaatag ttattgtcgt ttgaactggc 360

tcagaggttc aacattcaat ttcgagcgtc tcgttatatt acgggactca atcagacatc 420

cg 422

<210> 232

<211> 429
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 232

tcaagaatcn gatntcacag aatcaagatt caagaatgat ctttttttcaa gattcaatca 60

agcttcatga atcaagattc aagagcaatc aagatcaaga ttcaggaatc aagaaaagac 120

tcaatcaaga taagtactaa aagtttttcg taacattgag tggcacaaga atttttcaca 180

aaatctttaa cgagagagtt ctactttctg gtaatcgatt accgagagcc aacattggtt 240

ttcaaaactg atttacaaag cttgtaatcg attaccatga gcatgtaatc gattaccaat 300

attgtaaaat gttagatttc aaatctcaag agtcacaact agtgataaaa cattgtcaaa 360

tcattgtaaa cttgtctaat cgattacaca atacttgtaa tcgattacca gagtttctaa 420

acggtttga 429

<210> 233
<211> 469
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 233

ctaagctctg ctgcaatatt acaatagacc tcctcaacct cagcagctaa atcaaccacg 60

gtagagcaat tatgacctct ccagcaacag atacaaccct ggatggagga atcaccctaa 120

cctcagatgg tccagccctc agcaacaaca gcagcagcct gctccttcct tccaaaatgc 180

tactggccca agcagaccat acattccttc accaatctca caacagcaac aacctcagaa 240

acaaccaaca gttgaggccc ctccataacc ttccctcgaa gaacttgtga ggcaaatgac 300

tatgcagaac atgcagtttc agcaagagac cagagcctcc attcagagct taaccaatca 360

gatgggacaa tnggctaccc aattgaatca acaacagtcc cagaattctg aatagctggc 420

cttctcaagc tgtccaaaat cccaaatatg tcagtgccat atcattgag 469

<210> 234
<211> 414
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 234

ttctacaatc tcgagccttc anataaccct cctcaccttc ttccgcatca ttatcatcag 60

tatgaggacg aatattacat tcttctctat gccaaatttc agattgatct atccggtttt 120

cctcattggg ctccacctca atgctatcct tttctgagct agcatggacc accttatctt 180

ctgcacgtgc ctttgtctta taaaccattt cagactcatt aaaaataaca tcatgactta 240

taatgcatct tttgtgtcct ggctctaaac accacaatct gtacccctta aaaccctgag 300

gatatcctat aaacatacac ttgatagctc taggttccaa tgtgtcttgc cttatgtgag 360

cataagcaac acatccaaac accctacgtc tatcattatt tggaggatgc cctg 414

<210> 235
<211> 425
<212> DNA
<213> Glycine max

<400> 235

atactgcatt gttgactaat tgttgttgtt gttatttaca tctattttca gactcccaat 60

ttgcagattg agttttgggg ctgctttctt gctgaacaat gtttgttgga ctatgattgt 120

ataatatcct tgtcttctat cgcggctgcg tctgttatat ttcttttcaa acttattctg 180

gctctgaatg catacttaag gaaatattat gttatggata atgatataca catctcttta 240

atggaacgat attacccgtg tttcaacgca tgtgttctca tgtgatgaat tgatgattaa 300

ctgttcgcca atataataaa attattgctc tttactctaa tatatatagg taacgactta 360

atgttgaaga ttagagaagg tgtatccctt ctactccatc accattaact atcagctacc 420

ttctt 425

<210> 236
<211> 438
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 236

agctcgtagc ctattcgaac aacaataact nttcactcgg aagtctgatt gagtcctgta 60

atatatcttg acgctcgaat agtaagaccg aagctcgtag cagattcgaa cgacaataac 120

atgtcactcg gaagtcctat tgagtcccgt aatatatcga gacgctcgaa ttttaaaacc 180

gaagctcgta gcaaattcga acgacaataa catttcactc ggaagtccta ttgagtcccg 240

taatatatcg agacgctcga attttaaaac cgaagctctg agcatattcg aacgacaata 300

acatttcact cggaagtccg attgagtccc gtaatatatc gagacgctcg aaatttaaaa 360

ccgaagctcg tagctaattc gaacgacaat aacatttcac tcggaagtgt gagtgagtcc 420

cgtaatatat cgagacgc 438

<210> 237
<211> 392
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 237

gcattacatt attactcatg cttctaacca tgtctaatat tgttngattt ctgcgttctg 60

ccacaccatt ttgatctgga gaaccaagca tcttgtattg tgcaacactc ccatgttctt 120

gaagaaactt cgcaaatgaa cctggtgctt gtccatcctc tgtgtatcta ccataggact 180

ccccaccttt atgtgatctc acgatcttaa tatgttttcc acattgtgtc acatctgcat 240

ccttaaaaac tttaaaggca tctaaagctt cattcttaga atgaagtaag taaagacaca 300

tatatcgtga ataatcgttt ataaaggata tgaatactct ctgactagtg gcattcatgt 360

ctgggcaaag tatgtctgta tgtatgattt ct 392

<210> 238
<211> 424
<212> DNA
<213> Glycine max

<400> 238

agctttaaaa gtacccattt accaacctca tagtctactt cacgccattt agtatcatca 60

gtgcgtttca tcgtagcttg cgcttctaat agcttctgac gaatgcaaag aaaaacttcc 120

tcacagtgct tcagagtatc atccaccgca tctagtttgg aggagctagt gatatagtct 180

ggaaaagaga aaggtttccg cccaaacgtt atctcatacg gcgtagagcc cgtgcctgcg 240

ttccatgaag tattatgcga taattcgacc cagggaagga atctgcccca agtccccgac 300

cggcggtgca ccatagcccg caaatattgc tctattactc tgttcatgac ttcactctga 360

ccatcactct gtggatggta ggctgaactc attctaagcc ttgtaccact caattaaaaa 420

agct 424

<210> 239
<211> 376
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 239

taagtcacct gcggcatgca agcttctaaa ctttatacaa gaatgaagct ctgataccac 60

ttcttggaca agttgcctca gatatcttaa gaaggggggg ttgaattaag atatcacaga 120

ctattcccca attaaaaatt ctacttttaa tttaatccaa caacccaaga ttccttttaa 180

acaagaactc ctagataata atgcaaatta atcttactaa atagaaataa taagcaataa 240

acaataaagg agtctaaggg aagagaaaat gcaaactcag atntatactg gttcggccac 300

acccttgtgc ctacgtccag tccccaagca acccgctaga gaggttcact atcttgcaaa 360

atccctttac aagttc 376

<210> 240
<211> 441
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 240

ccaacgctct gatcaagctc tcccataatc tanangtaaa tctacgatct ctatcagata 60

ctatgctaga ttgcacacca tgtaacctga caacctcact tatatacgag gaggtcaact 120

tttccatgga aaatctgata ttaatgggaa tgaattgagc aaacttattc aatctatcaa 180

caataaccca tatagaatct aaacctctaa gggttctatg tagtcctacc acaaaattca 240

tggaaatgct gtcccacttc cactatggta tctctaaagg ttgcaactta cctgaaggtc 300

tctgatgtta tatcttatcc ttctgacaga ctangcatgc atacacaaac tcactaacct 360

ctctctttat gtatagccac caaaacatcg tctttaaatc atgatacatc tgtggagcac 420

catcatcaat gctcaaatta c 441

<210> 241
<211> 471
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 241

tgtaacaata ttntattgaa agtgagagta ttaatagaag ataaaaagtt atcgattata 60

aatttataga taaaattgaa aaacaactat gtagcttcta atttataagt tatatgacat 120

attttaagtt agtagcatta gcatgtggtt gtaggttttt aaaatatgtt aaaattccat 180

tttagtctca caaatttaaa atatcttgtt ctggtctatt gtttctagaa ataatatagc 240

taacaaaaaa aatactttta aataatcata ttttagtttt taattaatta tgaactctta 300

taatttttta aaaaataaat tttattaaaa tataaataaa ttatgtaaat aatggaataa 360

ttaaaatgaa cagtataata ttaaaattat ttctaaataa aaatagtatt atattatagg 420

agacaatata ttagagttct taataagtac tttagtcata taatctatcc a 471

<210> 242
<211> 451
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 242

agcttcacac aatnntattt tttttatcaa acttgagttn tggaaaacca attactaaga 60

ctttcctaac tagatgattt aaatgatgca tgttaatatg tgcagcccta tgatgccaca 120

atcatgaatc atctatctta ctcaccaagc aacttagctc atgaaaagat acatgttcaa 180

cattcaacat atagatatta cctattctct tactgatctg gacaacttta ccggatatgg 240

cttcacttat aagacatcaa tttctattga actctatttt gaacccttta tcacaaagtt 300

gactaatgct tagaagttat gctttagtcc atccacatat aacacattct taatctgagt 360

tntatgttga ttccctatat catgagaaat catatttttc cttttgtggt nngtctcaac 420

atgaccatag tttggacttg tcacacgtca t 451

<210> 243
<211> 379
<212> DNA
<213> Glycine max

<400> 243

agtcaactga cgctgccgct tcattgttca atttgagcgt ctagatatat catgcgcctg 60

aatctgacat tccagcgaga aggatgacca tttctattac tcgagagctc ttgtggttca 120

atttccaccg tctccttgag ggaggtgctt gacctccacg tccgagtgaa aaaggatgac 180

cattcttatt tttcgagagc ttccgttgtt ttatttccag cggctctata tccgatgcgc 240

ctgaattgga catccgagtg aaaatttata atcattaaga tttctcgaga gcttccgcac 300

tttcaattcg agcgtctcga tatattatgc acctgaatcg gacactcgag tgataaatta 360

tgaccatttt aatttctct 379

<210> 244
<211> 313
<212> DNA
<213> Glycine max

<400> 244

tattcaacaa tgacaaatca cataacataa ttttaagatt ctgagcctca ctagtagcag 60

tatctaaagc aataatttct gcttccatgg tagaatgtga aataatagtt tgttcagcag 120

atttccatga tattacacca ccagctaaag taaagacata atcacttgtc gattatgttt 180

catcagaatc aaaaatccaa tttgcatcac taaacccctc aattacttcc taatctacca 240

actacatatg ctatgacatg cctatagaga gttgtcaatt gcatcaaaga accactaatt 300

tgataatatt gtg 313

<210> 245
<211> 471
<212> DNA
<213> Glycine max

<400> 245

ggaaattaaa caatggaagc actcgagata ttcaaatggt cataacttat cacacggagg 60

tctgattcat gcgcataata tatcgagacg ctcgaaattg aacaacgaat gctctcgaga 120

aattcaattg gtcataactt gtcacacgga agtccaattc tggcgcatca catatcgaga 180

cgctgtaaat tgaacaccgg aagctctcga gaaattcata tggtcataac ttatcacaca 240

gaggtttgat ttaggcgcat aatatatcga gacgctcgaa attgaacaac gaatgctctc 300

gagaaattca aatggtcata acttatcaca cggaggtctg attcaggcgc ataatatatc 360

gagacgctcg aaattgaaca acgaatgctc tcgagaaatt caaatggtca taacttgtca 420

cacggatgtc caattctagc gcatcacata tcgagacgct gtaattgaac a 471

<210> 246
<211> 410
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 246

agctntagct tccaactcaa caggtaggtg acaagaattg ccatagacca attggaaagg 60

agtaagtctt gtaggagcta tgtatgttgt tctgcatgcc cacaaagctt catctagctt 120

ttgggaccaa tccttccttg attgagcaac tgtttttttct aatattttct taactttcct 180

attagaaact tcagcttgcc catgtggtaa ggcgaagcta ccttgggttt gacactgtag 240

tgttggagga ctttggtgag ttatacatta caaaaatgag atcctccgtc acttattagt 300

accctgggtg tgccaaacct tgagaagata ttatttctta ggaagcaaat aacaattttt 360

gcatttgcat gntgtaccac tactgattca acccattttc ttacatagtc 410

<210> 247
<211> 359
<212> DNA
<213> Glycine max

<400> 247

tcggacatcc gtgtgaaaag ttacgaccgt aaggatatgt ccagagctat catagttgaa 60

tttcgagcgt ctagacatag tatgcgcccg aatcggacat ccgtgtgaaa agttatgacg 120

atatgaatat ctcaagagct ttcgatggtg agtttcgagt gtatcgatat attataatac 180

ctgaatcgga cctccgtgtg aaaagttatg actatatgca tttatcgaga gtttccgatg 240

tatagtttcg agcgtatcga tatattataa gcctgaatcg gacatccgtg tgaaaagtta 300

tgaccattag aatttctcag gagctttcgt tgtgcagttt cgagcgtctc gatatatga 359

<210> 248
<211> 424
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 248

tagatagatc aacgtanggt tctttttcct tcaaccttca ttctacatnt tttccttaaa 60

caaagacatg catgatttta ctattgtatt tcttctccat ctcttccatt gaaaagtgca 120

ttttttgtac tattttattt ttctttcttc cattgtatat atatatatat atatacctat 180

tgatttctta ttgcagtcat gatttgagtt tttagagcaa actctttgag tcgatggtgc 240

tactatcttc gaaaatcctt ctatgaatct tcgatagtat ccaaccaatc caacaaaatg 300

tgtaatctct atagctatct tatgggcgtt tcactgcaaa attgtgtcta ccttggaagg 360

atccactaca ttgctaccca ccaagatcac atgacctaag atccgtacct catcaagtca 420

aaac 424

<210> 249
<211> 376
<212> DNA
<213> Glycine max

<400> 249

gcaactagga tgttcggaag tatcaaagta atctgggaat ggaacattgg aaagctataa 60

agaaagttat gagatactta caaggaacaa aagatcacat gcttacatat aggaggtcta 120

atcatcttaa ggtgattggg tattcagact catactttgt tggatgtgtg gttatgagaa 180

aattcactct tggctatgta tttcttttag tcggaggagt aatatcatgg aagagtgcaa 240

agcaaccagt tgttgttgtt gcatctacca tggaagtaga atttgcagca tgttttgagg 300

ctacaagtta agctaattga ctgcgaaact ttatctcagg gctctgaatt gacttacgac 360

tgctaggcat tgaaat 376

<210> 250
<211> 298
<212> DNA
<213> Glycine max

<400> 250

atcctctttc gaaacttcta gatgatattt acccttttact gatgctaaaa atagcggcga 60

ggaacgtcga gaagcagatc ccgtcggagc cgtactgggc attcttgatt ctgtacacat 120

cagtgacact agaataatat cgtctctgcc gatctgtctg ttcgctgctg tatatgtttg 180

ctagtcaagg gatattttca ttagaatcaa aatgtgctct cagcgttata acaggagaga 240

cgacaaatgg atttggacag gacaacagag gcttgtgtga gagaaacgtt agaacctt 298

<210> 251
<211> 132
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 251

tcacanaagt ttgtatggct tgaaacaagc accgaggcag tggtacaaga agtttaatga 60

gtttatgagc aactcaggat tcaaaagatg tgacatgcac cattgctgct atgttaaaaa 120

atatactacc ac 132

<210> 252
<211> 470
<212> DNA
<213> Glycine max

<400> 252

tgacactata aaactaagct tccataggtt attccaagat catgatgaag accaagtcaa 60

cttgtgtctc atgacaaaat ctcatgagaa caacaaagaa gaatctgtaa ggaagaagtg 120

gtacatcgac agtggatgtt ccaagcatat gacaggagat gtatccaaat ttacaaccat 180

ttctcctaag aaaagtggac acgttacata tggcgacaac aacaaaggca aaattattgg 240

agtcggtaaa ataggtacga gttcttctac tcctattgaa aatgttatac ttgtacaagg 300

tttgaagcat agcctattaa gtgttagtca attatgtgat aaaggatata aagtatcttt 360

tgattctgaa aaatgtgtta ttaagaatga gcatgataaa gatatcgaac atatatggtt 420

cagagaatat aatgtctaca tgattgattt ataacaacaa cctgatatga 470

<210> 253
<211> 433
<212> DNA
<213> Glycine max

<400> 253

ctcatctatc tccactatgt tgcctaatgc ctgaaatgtt atttctgatg gcagtgttcc 60

taaatgtagg gaagaatttc tctaagaaca cccgcttaag gtcatcccag ctgaaaatat 120

acctgcgagc aagggaatat agccaatctt ttgcactccc tccagagaat gaggaaaagc 180

ctttataaag atatgatctt cttggacgtt atggggcttc atggtggaac atacaatatg 240

gaactcctta agatgtttat gaggatcttc acctgcaaga ccgtgaaact tacgcagcaa 300

ttgtattatt ccagtcttga gaacatatgg aacaccctca ttaggatatt gaatgcacaa 360

gctttcataa gtgaaatcag gtgcatccat ctccctaaga gttctttacg aggtggaggt 420

tgaccatgtt ctt 433

<210> 254
<211> 415
<212> DNA
<213> Glycine max

<400> 254

agcgtctcaa tatattattg gcctgaatca gacatccgaa tcaaaagtta tggctgttta 60

actatgccat gtgcttccat gttcaatttt gagcatctcg atatattatg cacctgaatc 120

gggcatctga gtgaaaagtt atgccatatg agttagccga gagcttcgtt gttcgatttc 180

gagcgtcatc gacatattat tggcctgaat cggacatccg agtcaaaagt gatggcagtt 240

taaactttac atgtgcttcc atgtttaatt ttgagcatct cgatatatta tgcacctgaa 300

tcggacatct gagagaaaag ttatgccata tgagatagct gagagcattc gttgttcatt 360

ttcgagcgac tcgatatatt atcggcctga attggacatc cgagtcaaaa gttat 415

<210> 255
<211> 450
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 255

gcttataatg tcttacggga aataacccac taacacacac aagggccata agatcaagtt 60

aacatgctta aaaaaacttc ctttaatctt tattatatat attaacataa attcttttt 120

taatttcaag aaaacatttt cacaatatat aatacatttt ttaaaaaata aatatagagg 180

tgttacactg gtggttggga gcataggttg aggtggtagt ttatgactan ggtaataatt 240

ctcctacaaa tgagctatac tattggaata tatatttcta caagacggtt ggaatatgtt 300

agagagatta aatgttacgt tattgctata aggattggtt tgatatcata aaaaattggt 360

gtagtgaact ttcatcgcat agtttaaaga catcacaact aaaactaaca cgagtgttgt 420

attaatgtct taacatacgt cttaatcaat 450

<210> 256
<211> 400
<212> DNA
<213> Glycine max

<400> 256

gaagaaattc atatggtcat aactattcac tcggatgtcc gattcaggtg tatcacatat 60

caagacgctc gaaatttaac aacggaagct ctcgataaat tcaaattgtc atacctttc 120

acacggaggt cctatttatg cgcttaatat atcgagaagc tcgaaattga acaacggaag 180

ctctcgggaa atcaacatgg tcataactta tgactcagat gtccgattat gcgaatcata 240

tatcgagaag ctcgaaattg atcaatggaa gctctcgaga attccaatgg tcataacgtt 300

taacatggag gtctgaccat gcgcataata taatgacacg cttgaaattg aacaacggaa 360

gctcttgaga taaccaaatg agcattactt ttcacacgga 400

<210> 257
<211> 463
<212> DNA
<213> Glycine max

<400> 257

ctgtcttgac ttatttatac ccataccccc caatattata ctataatatc tatatgtaca 60

ctatgatatt gttgagtcta attaataatc aaaatgttat tgtgtattgc ttgatttgtc 120

acatgttatt gatgtgaaat atttatcaac tttagtgata agttaatgac taattgctat 180

tgacagagtt ggctaaccac atctatcagg gtctattccg aactattatt tttcatacac 240

aagtagtggc aaagtcaaat atttttttaa tggggtgaaa aaatagttat aatattttca 300

tagatgaaaa ataatatgag ttttattaaa atggtactaa aggaattaga aatggtaaaa 360

attaaaaagg gtaagtggat aaaaatagta ccaatttatc tattttcact tttaacttttt 420

ataacttttt atattcatct tttttttaag aaaattatct tat 463

<210> 258
<211> 351
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 258

gcttnctaga cgcctactnt agatacaact agatcagaat gcatcctcca cacgaggaga 60

aaatggcatt catcattgaa gatgccaact tttgctatag ggtcatgcca ttcagcctaa 120

aaaatgcagg cacaacataa caacaactaa tggaccgagt cttcaaacaa cagataggac 180

aaaatgccga ggtatatatg gacgacatga ttgtcaagtc tcaaactata ccccaacatg 240

tggtggacct ggaagaagtt ttcggggaac tacgaaaata cgacatgcgc ctcaaccttg 300

aaaaatgcac tcttggggta ggcaaccaca agtccctcac tacagcactg g 351

<210> 259
<211> 343
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 259

aagtttgaat atgatgtata agaaaatgaa tgtgaacctt tctccccttt gaaagacttg 60

taaaaaaaat gttttaaaaa tacttttaat taatatctga attttttttc cttattagta 120

tatatgtgag gggtagaggg tgtcacatcc tgcagcaaat aatgtgcaat atcataaccc 180

ctaaactgta tatatcaact ttggcaatta ttggtgcact ttntagccat tcaggtgcca 240

tgtaacctat tgttcctttt aaattagtgg ttgttctagt ttggtctttg agtaatagct 300

tggaaagcca aaaatctgca atctttgttg tgtgattggc atc 343

<210> 260
<211> 473
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 260

tattaactct atacaagagt gaagctctga taccacttgt tagacaattg gcctcaggta 60

tcttaaaaag gggggtagaa ttaagataca caagctgtcc cccaattaaa atttaactgt 120

ctcttttatt aacaatgcaa tcctctatta tgaattactc taagaacaat tcaaaaacaa 180

acttctttaa agcaaaatat aaacaataat aaataataga aatttaaggg aagagagact 240

acgaactcag tttttatact ggttcgacca cagcctgtgc ctacgtccag tctgcatgca 300

acccgcttaa gagttccact atcttgtaaa ataccttta caaagtctga agcacacatg 360

aacaaccctt cccttgcgtt caaaaacctt acaacttaag agaacatcgg tactttaatc 420

aatctctttg agtgagaata agaagaagac ttctctatnt aggagaaaga tat 473

<210> 261
<211> 413
<212> DNA
<213> Glycine max

<400> 261

tatgctgcaa acatttacaa tagacctcct caacctcagc agcaaaatca atcacagcag 60

aacaattatg acctctccag caacagatac aatcccggat ggaggaatca ccctaatctc 120

agatggtcta gccctcaaca acaacaacaa cagcctgctc cttccttcca aaatgctgct 180

ggcccaagca gaccatacat tcgttcacca atccaacaac agcaacagcc ccagaaacaa 240

caaacagtta aggctcctcc gtaaccttcc ctcgaagaac ttttgaggca aatgactatg 300

caaaacatgc agtttcaaaa agagaccaga gcctccattc agagcttaac taattagatg 360

ggacaattgg ctacacagtt aaatcaacaa cagtcccaga attctgacaa gct 413

<210> 262
<211> 465
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 262

ttcacctgtc tntacataat cagagccatc aacagacttc ataaacatgg taccagcttg 60

agagttaata gaaaaattaa tgatgcatct ttgtttccga tcagtccatg catcggacat 120

aatagtacaa ccatacttga cccattgctc cctatggcct ttcatcaaat ttttagtata 180

ttcaacttcc ttcttcaaga gtggaactct gatgtcatga tagctaggaa tgggcaaatg 240

tggcccatat tgaccaatgg ctgcaaccat tttctcaaag cttttcaata taatgaggtt 300

gaatgacaaa cttgcttggt accaaaagcg agcaatatgt taatgcacct ttcaatactt 360

cattcttatc cattgactct cttatgttca tttgcctcag catctccatt tttctccgat 420

tgattgcatt ttctggattc ttacaaaatt atgccattgg tcctt 465

<210> 263
<211> 450
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 263

agcttcttac atagtccgct nttgcttgtt ctttatgctt aanaatagaa acattaggca 60

tagacaaaag atcaagatga gttagtaggt taaaaccata aacaacttca aaaggagaac 120

aattagtagt gctatgaaca actctattgt aagcaaactc aacatgtggt aaacaagctt 180

cccaagtctt taagttcttc ctcaaaactg tcctaagcaa agttcccaat gtcctattaa 240

caacttctgt ttgcctatca gtttgtgggt gacaagtggg tgaaaataac aatttagtgc 300

ccaacttgcc ccacaaagtc ctgcaaaaat ggcttaggaa cttagagtcc ctatcactaa 360

caatgctcct tggcanacca tggagtctca cacntctctt gaaaacaaat cagccacatg 420

ggaagcatca tcaactcttt tacatggaat 450

<210> 264
<211> 389
<212> DNA
<213> Glycine max

<400> 264

gcttgagaat ggagaattgc actaagcaat cactacgcat agctccaaac tcgaaggtgg 60

aggacacatg aacgaaaaca caattcatgg ggctccgaaa aaggggttga gaatggagaa 120

ttacactaag caatcactac gcatagctcc aaactcgaag gtggaggaca catgaacgat 180

aacgcaattc atggggctcc gaaaagattg agaatggaga attgcactac gcaatcacta 240

cgcatagctc caaacgcgaa ggtggaggac acatgaatga acacgcaatt catggcgctc 300

cgaaaagatt gagaatggag aattgcacta agcaatcact acgcatagct ccaaactcga 360

aggtggagga cacatgaatg aaaacgcaa 389

<210> 265
<211> 435
<212> DNA
<213> Glycine max

<400> 265

gctggcttgc tggctcctgc ttcaattggt gtggctcttg cttcaattgg gtgcttactg 60

actggttgct tccttcgctc aagtgtgtgc ctttaccccc ttactcctag taagtgtttt 120

taaagtaaat aaaatttata tatttttgtt aataaatatt ataagtttaa gttagctagt 180

attaacacat attgtaagtt agtttatata gtattgtgta gttattctaa gctagtatta 240

acaaaaatac taagtttaag ttagttagta gtagtattgt gtagttattt tttacgtatt 300

aatattaata gatataccaa tggtaggtta gttactatga aaatattatt tggttagtta 360

gaatgaaaat tttatttagt tattgcatga tctaactata tgtgtgatat atctatatat 420

atctatatat atata 435

<210> 266
<211> 330
<212> DNA
<213> Glycine max

<400> 266

ggctaaccca tggaagctcc taatatctcc cacactcttt gtggtgggcc attcttggat 60

ggccttgagt ttctcacggt ccacttggac cccatttcta ccaactacaa aacctaagaa 120

aactatatta tctacacaaa aggtacactt ctctatattt gcatagaggg tgtttttcct 180

aaggactgat agaacttgtc tgagatgtcc taagtgaaaa tctaggtctc tactatacac 240

taaaatatca tcttaatata caactacaaa tctacctatg agaatcctta tgacatgatg 300

cataagcctc atacaggtgc ttggggcatt 330

<210> 267
<211> 444
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 267

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tgcttccttc atcaattttt cataaggtca caaaatcacc caccactttg tctctaaatc 120

ttattagaaa cttatattgt ttcattcatc agcttttcat aaaatcaaaa aattcctacc 180

actctttctc tcaatcttat tgcaaaaagt aaattcacta ctataaaaat tggtttttct 240

agacatttaa catcggttat gaaccaatgt tagaatgagt gccaataaaa gatgaccatt 300

gttaacattg gttataaaaa tcaatgttga aatctactat ataagtatgg ttctcaccan 360

aaccaatgtg atatactagc aaatagacaa aattatttaa gaattaattc tttntactta 420

taatttatat cattctacat actt 444

<210> 268
<211> 422
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 268

atctacttca atacactgat tggaaatgat gtggcctaaa actatacctt gctcaaccat 60

aaaatgacat tattcaaaat tatgaacaac gttagtttca atgcatctat tcacaacttt 120

ttccatacta ttcaaacaac catcagaaga ggatccatat acagtgaaat catgcatata 180

cacctctatg caattttcta aaaaatcact tgaaatacta atcatgcacc actggaaggt 240

accaggggca ttgcacaggc cgaaaggcat tctcctatag gcaaaagtgt cgaacgggta 300

ngtgaatgtg gacttttcct gatcctcacg agcaatagta atttgcatat aaccagaata 360

accatcaatg aaacagtagt gggatatagc tgccaggcgt tcaagcatct ggacaatgaa 420

tg 422

<210> 269
<211> 400
<212> DNA
<213> Glycine max

<400> 269

atgcattggt taacatggta acccatctgt ccttgaacca caaatctgta cccgtcgcaa 60

gggtctgtga tctgtgctcc tctgctgacc accatacaga cctttgccct tccatgcagc 120

aacctggagc aattgagcat cccgaagctt atgctgcaga catttacagt agacctcctc 180

agccttagca gctaaatcaa ccacaataga acaattatga cctctctatc aacagataca 240

accctgaatg gaggaatcac cctaatctca gatagtctag ccctcaacaa caacaacagc 300

agcttgctcc ttactttcaa aatgctgctg gcccaagcag accatacatt tctccaccaa 360

tccaacaaca gcaatagccc cagatacagt caacagttga 400

<210> 270
<211> 365
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 270

tacttttgtc ttgaaggcag ttctataagc ccataatgca tcatccaact ngcttgacca 60

atccttttta gtggaggcta cagttttctc caaaatcttc tttggctccc tgttagaaac 120

tctagcttga ccattcgttt gcgggtgata cgatgagact actctgtgcg tgacattgta 180

atggctcacc atcttctgaa gttggttgtt gcaaaaatga gagccccgat cactgattag 240

gaccctcgac accccaaagc aagcaaaaat attcttcttc aagaacctca ctatacgttc 300

agcatcgctc tttgggcagc cactgcttca acccactgga gacataatca cagcccaagg 360

atatt 365

<210> 271
<211> 435
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 271

gctggtgagg gtganaatct cagctgggag ctgcccagag aagaaattgt ggctcatgtt 60

gagactagtg aggtttgtga agatgatgaa ttgcttccct gaaaccacac ctcccaattt 120

cttcatggaa aggtctatgg aagttacaat tgttgagtca ttgttacact tgatgccgga 180

ccaagaacat gcataggatt tcccagttaa ttttcctcca gagggcacca cccaattgtg 240

caagctgttg tcatcatcta caagctccga ttttaggctg agaagtgcct ctgagtaagg 300

gtcaattgct agaactgctg atgataccat gaagaaggta acaagaataa gatttttgat 360

gtagaaagca ttgaaaatct ccattggaac ttggagagca tcacaaggta gagagggaca 420

atngtaagta cccta 435

<210> 272
<211> 431
<212> DNA
<213> Glycine max

<400> 272

gagacaactt actcgagaag ctagagctta gctacacaca cccctctaat aactaagctc 60

acctccttga gaagcttcct tgagaagatt cctaaagaag ctagagctta gctacacata 120

cctctctaat agctaagctt acctccttga gatgagaagc tagagcttag ctacacaccc 180

cctataatag ctaagctcac cccatgacag aaaacatgag aatacataaa aaaaagtcct 240

tactacaaag actacttaat agaatggcca aaatacaagg cccagacgaa agaataacct 300

attctaatat ttacaaagat aatcgggctc atacttagcc catgggcttg aaatctaccc 360

taaggctcat gagaaccctc gggccttccc ttggatctct agcccaatct acttggagtc 420

ttctacccaa t 431

<210> 273
<211> 447
<212> DNA
<213> Glycine max

<400> 273

agctatggag aaccaagcca atcagaatgc tatacgaaat atagatggga atagaggtaa 60

caatggtggt aatgacggac cgaggcagaa ccgggttgag ggagtaaagc tcaatgttcc 120

tcccttcaaa ggtagaagtg atccagatgc ctacctggac tgggaaatga agactgagca 180

cgtatttgcc tgcaatgact acactgatgc gcagaaagtc aagctagcaa cagctgaatt 240

ctccgactat gcccttgttt ggtggcataa ataccaaaga gaaatgttga gagaggaaag 300

gcgagaggta gatacatgga ctgagatgaa aagggtgatg agacaaaggt atgtgcccac 360

tagctataac agaaccatgc gacagaaact ccaagggctg tcccaagggg aattaaccgt 420

ggaagatatt ataaagagat ggaaatg 447

<210> 274
<211> 476
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 274

nggaacatat aaaattcaat acaaggccct ctcaaggatt tattcaaaac atatgcaagt 60

tgattgtttg aactaacaaa ctcggtagaa atctaattgg acagtagctt tccctcataa 120

aatgacaatc aatttttatg tgcttagttt tatcatgaaa cacttgatta gaagcaatat 180

gaaagtttgt ctggttatca caatacaatt tcattggcta aatttcatag aattgtagtt 240

cttgaaggag atgtttgatc cacaccgact cacatgtggt tgtggccatg gtcctatatt 300

cggcttttgc actacattga gcaacattaa actgtttctt actcttccta gagataagat 360

ttccaccaat ggagacacta tcttgtgtta aagagtctat ctataggaga acctgtgcaa 420

tcaaaatcac aatacccaaa gaattgcgca tctcatttat cttcatgata taacta 476

<210> 275
<211> 398
<212> DNA
<213> Glycine max

<400> 275

agctctctta agacgaatcc tatttatgct agagcttagc tacacatacc tctttaatag 60

ctaagctcac ctcctttaga tgagaagcta gagcttagct acacaccccc tataatatct 120

aagctgaccc ccatgacaga taacatgata ataaaacaca agtccttatt acaaagacaa 180

ctcaggatgc cccgaaatac agggctgata ccctatacta ctagaatggc caaaatacca 240

tgccttgacg aacgaaaaac ctattctaat atttacaaag ataagcgggc tcatacttag 300

cccatgggct cgaaagctac cctaaggctc atgagaaccc tagggccttt ccatggatct 360

ctaccccaat ctacttggag tcttttaacc aatgccct 398

<210> 276
<211> 448
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 276

agctngacga tgttganaag aaaatatgtt gtcataattg aagaatgaac atgtagcttc 60

taatgactct gaaatgtcct acattaatat ataattgtta tgctacaaat tcacataatt 120

cttagtatgt tacgttaaat ttaattggca aacgtgtata acttatggat atactattat 180

gtcattaata cgaataccta gtacatttaa cggttaccta atttaaaata atttgttaac 240

attaacccta atatttagag gaataaacag agaataaaaa ttataatcca aaataactta 300

tcatttacaa aatgtgtggg aaaaccaata tgtttgcaaa tacatgaaaa ttatatacat 360

actcgacata tgaaaatata acatggatga tgtctatggc tgatccgtgc gctgccttct 420

tcgcgacttg acataaacat tgccatct 448

<210> 277
<211> 441
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 277

ttacggacct atgaaactca gctatgctgc nacattacaa tagacctcct caacctcagc 60

agcaaaatca accacagcag aacaattatg acctctccag caacagatac aaccctggat 120

ggaggaatca ccctaatctt agatggtcta gccctcaaca acaacaacag cagcctgctc 180

cttccttcca aaatgctgct ggcccaagca gaccatacat tcctccacca atccaacaac 240

aacaacagcc ccagaaacag ccaacagttg aggctcctcc acaaccttcc ctctaagaac 300

tcgtgaggca aatgacgatg cagaacatgc agtttcaaca agagaccaga gcctccattc 360

atagcttaac caatcagatg ggacaattag ctacacaatt gaatcaacaa cagtcccaga 420

attctgacat gctaccttct c 441

<210> 278
<211> 374
<212> DNA
<213> Glycine max

<400> 278

agcttgtgct cgaggccttg acctcataat tgtctcatca ctgtgtttga tccattctga 60

gagtttccag ggcttctgcc acttccattt aaactgtagc agccattgat gatgacttct 120

cttccacttc caaagttttc cggcttgtcc tatagctgct agcctcttcg ttgacaactc 180

tccaatgggt atcatctgga tataaaccca ttaaaactta ttgagaaata aacactatca 240

tcatcatcat cagggaaata gaatctagca aacatacctt tcgtgcttca tctaaaaatg 300

tagctgactc cctgcctgac caattaacaa ctccaggagt gaatttgagt tgctctggtg 360

caggaagcga catt 374

<210> 279
<211> 408
<212> DNA
<213> Glycine max

<400> 279

agcccatgtg tcgttcctgt catattggtg ccaaagaatg atggaagctg gaggatgtgc 60

tcacattgca gagctttcaa caacatcacc attaagtaca ggcatctcat tcccaagcta 120

gatgatcttc ttgatgaatt gtatggatca tgttacttct ctaagataga tttgaaaagt 180

ggatataatc agattacgat tagagaaggt gatgaatgga aaacaacttt tataaccaag 240

tatggcttat atgagtggaa ggtaatgcca tttggtttaa caaatgacct tagtactttc 300

atgaggttaa tgaatcatgt tttgagagag ttcttacgac aatatgtggt tgtctacttt 360

gatgacattc ttgtgtatac cacaaatgtg gatgagcatt tgcaacat 408

<210> 280
<211> 479
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 280

tagttggatg anattccatg atcacacctt atagtaagta gataaacatc ctanatcagg 60

aagaacaagt tgatctagct acctagaaat caaatgtgta atcctaacct atgaagtatg 120

ccagggatgt cctaccttct ctcttacata ttgcggcaga gcaattgatg ccaagttgca 180

cacagccgtt tctgttggac ttgtatactc aattatctca gtgcacaagt ttcatgactt 240

gattgtgccc aaattctgtt ggttgctttt cctattgcaa gtgtcctagg atatagaaaa 300

atgaagaggt ttcaatgaaa ataaatacaa aatgcactga cagaaactta gcaaaagtca 360

aacaagcatt tgtaaaccac cttataaaat atgtaaggag ttccagtttc tatctgtgac 420

ttcaaaattt caaaccagag agattctgtg cctgaacaac cttctttgct tttccccat 479

<210> 281
<211> 436
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 281

agctntgatg atgtcgagaa gaaatcacat gtttgtcatc atcaaaaagg ggagaatgtg 60

attgtatgta tacatgattt tgatggtgaa gaatcaaaac aaggcttatt tgcttcaaga 120

ttaatacaag attgtttcaa caaacaaagc cttgattcaa gatttcttca agatcaagcc 180

ttacctcaaa acgaaaggtt tcaagtcaac caaggcacat gtaattgatt accaatacat 240

gtaattgatt accaatggtt tgaaagtgtg taatcgatta ccagagactt tgaacgttgg 300

gaattcaaat tttaaatgaa gagttacaac tattcaagaa aaataactat gtaatcgatt 360

acactaatgc tgtaatcgat taccagagag gattntcaac gaatatcgcc aacaatcaca 420

tcttatcatt tggatt 436

<210> 282
<211> 455
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 282

taacanaagg catgcgaagt gggtggaatt cctagagcaa ttcccttatg ttatcaaaca 60

taaaaaggga aaaggtaata ttgtagccga tgctctttct cggcgtcatg cattactttc 120

tatgcttgaa acaaaattga ttggtcttga atgtttgaaa agcatgtatg aaaatgatga 180

aacttttgga gaaattctta aaaattgtga aaaattttca gaaaatggtt tctttagaca 240

tgaaggcttt cttttcaaag aaaacaaatt gtgtgtgcct aaatgttcta ctagaaattt 300

gcttgtttgt gaagcacatg aaggaggttt aatggggcat tttggggtcc aaaagactct 360

agaaacatta caagaacatt tttattggcc tcatatgaaa aaggatgtgc agaaattttg 420

tgaacattgc attgtatgta aaaaggcana gtcta 455

<210> 283
<211> 458
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 283

agcttganat tgaacaacgg aagctctcca gatactctta tggtcataac ttatcacacg 60

gaggtccaat tgaggcgcat aatatatcga gacgctcgaa attaaacaac gaatactctc 120

gagaaattca aatggtcgta acttatcaca cggaagtccg attcaggtgc ataatacacc 180

gagacgctca aaattgaacc acgaatgttc tcgagaaatt caaatggtca taaattttca 240

aacggcagtc cgatttaggc gcataataca tcgagaatct tgaaattgaa caacggaagc 300

tatccagaaa ttcaaatggt cgttacttgt cacacggaag tccgattcag gcgcataata 360

tatcgagacg ctcgaaattg aanatcggaa gctctcgaga nattcaaatg gtcgtaactt 420

ttcaaacgga aagtccgatt aagcgcataa tatatcga 458

<210> 284
<211> 431
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 284

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ttgctaaacc actgagtaat ctgatgaaca aggatgctgt gtttatgttt aatgatgaat 120

gcttagaagc ctttaatacc cttaaagcca agttggtctc tgctcctgtg attacagcac 180

tagactgggg actagagttt gaattaatgt gtgatgcaag tgattatgca gtangtgctg 240

tgctgggaca gggaaagggc agaatttttc ataccatcta ctatgccagg aaagtgttga 300

atgatgctca gatcaattat gccaccactg agaaagaatt gttggcaatc gtttatgcac 360

ttgagaaatt ccgatcttat ttggtggngt caaagatagt aatttacact aatcatgcaa 420

caattaaaca t 431

<210> 285
<211> 465
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 285

tagaaaggtc tactcanatg gatgtatgtt aagttgataa gtaaaaaaaa atgcaaaaag 60

tagaanatgc aggatcatca cgtgcccatt gattcttggt ttctaatatc aaataattaa 120

taacaagaag aaattcaatt aaataatttt ttgaaatcac caaatttaat ttcctaattt 180

gataaatcaa aggcattaat tatataacta aaccttacca tgaaaaattg gcatcattat 240

gtatccttct actcctattt taaattttat tatattgaac ttatattttt ttagtcaaca 300

ttgccaagat gtggatcagg tttggccttc caaagacaat atcaatgatt tataataatt 360

tatcaaatca tttgatattt tgatttataa taatttaaga caatatcaat gatttatatt 420

aatttataca ctctgatgaa ctanatccct tgacaaatag ttaat 465

<210> 286
<211> 464
<212> DNA
<213> Glycine max

<400> 286

atgttctgca ggaaacttgt gtccctttta agtttatgac tttcggtcta gatttatttt 60

aaaaaattgc aatagttgta gtatggtaat atatgcttct caccgaaccc tctctggaat 120

ttgagactac tctctctgta gtctttaagc tatagttctt ttgcctcttc aatttttgtt 180

ataccctttt tagctgtttt ttgatgcatt atttgtagct gattattaga tttgactgct 240

tgtggacaat aatttctagt ccatattctt tataaaaatt gagaatgact ctgatatgct 300

ttagcttttt aaacaaacct ttggccggca ccaaatactg ttactttata tacttataac 360

tcaattgcag gtatagattg gcatattcat caaactatag ccatatcttg gatccgttaa 420

ttgagaacaa ttaccaatta ttcatgatcg agaggcttat aatg 464

<210> 287
<211> 397
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 287

agcttgtgcc ttttcacgtc tggaatatga atgtagcata tagatccaaa gacccttagg 60

tgctttgctg atggcttctt cccgttccaa gcttcaattg gagtcttgtc ttttacagac 120

ttagttggac atctgttgag tatgtaaaca gcagtgtaga ctgcttcaac ctagaatgtg 180

ttaggtagtc ccttctcctt gagcatcgat ctagccattt ccataactgt gcgattcttt 240

ctctcggaca ctccattttg ttgaggagaa tatgcgattg taagttttcg ctcaatgctt 300

tcatcctcac aaaatctttc aaactcgcga gatgtgtact ttntgttgcg atcacttctt 360

agtactttta tccgttttcc acttttgatt tcagcaa 397

<210> 288
<211> 315
<212> DNA
<213> Glycine max

<400> 288

tcattccttg tttcactcat gtgtccaagt ctttgatggc atatggttga attgttgaca 60

gccttagtaa ctgctaccat atactcatct gcaatcatgt aaagagatcc tcgcttcttt 120

ccacgagcca caatgagatt gccttttgtt accttccaag ctctatatcc aaaagtggtg 180

taatgcccct cattatccaa ctaccctata gatgttagat ttccctttaa ggcaagaata 240

tgtcaaacat tgtacagtgt ccatagggat ccactagagg tcgtgatgtc aatatcacct 300

cttccgacaa tgtca 315

<210> 289
<211> 377
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 289

ggactcatgt tatctacaat cacttgttac gttgattctt aagaaagtcc tctaagacaa 60

caccccatat gccatgtctc tcattnggtc ccatgactcc tatctgatgt ccctgcatca 120

ccaataattt aagtgcccaa ctaatggttc catgcatatc cttatgtcta tataaatatt 180

caaggccgca agcattgagg accaacacaa atcattcaca tcataaagtg tttgaaatta 240

aaattctcaa cacttctctt caaccattct cttctcagat caatacaaca atgggatttc 300

gttacctggc atatataggc attcaaagcg gtgacgcacc taaggctatc ttgcagtcta 360

tgtcggagag aaattga 377

<210> 290
<211> 260
<212> DNA
<213> Glycine max

<400> 290

aagatctttg gatgccgtca gaaattttat gactatgagt gtgagtattt ggtacttgtg 60

aattcattac tcttctatgt agaaatttat tgatttacac cccttgcaaa ctcagcattt 120

gttacacaaa gcttaaaatt cagagagaac gcaccttgtc ctatgtatta ttaaattcgc 180

ttcacaaccc cttgctaact cagcacgctg caagccataa tgcattcatg tgatatattg 240

ccgtgcgaca acaacaacat 260

<210> 291
<211> 374
<212> DNA
<213> Glycine max

<400> 291

tggccccaca tagagaatgg ccaaggtgta tccatgacgt tcaaaggtat ggtggagcat 60

taacattatc agtgaaggcc tgacacttat ggcatttcct cacatggatg caacaattgc 120

tctccatagt gagctagtaa tacccagttc tcagaatttt ctaggccatg gcatgtccat 180

tggtatgcgt tccaaaggat cctttatgca cctctactag aatttgctca gccccttag 240

catccataca ccgaagtagt accatgtcat ggttattctt gtataggata ttcccactca 300

ggaagaagtc ggtcgccaac cttcacaaca ttcttttatc gttgtcagag gcctcccgtg 360

ggcattcctt gtct 374

<210> 292
<211> 380
<212> DNA
<213> Glycine max

<400> 292

ttaactcgga ggtccgattc aagcgcataa tatatcgaga cgctcgaaat taaccaacgg 60

aagctctcga gaaattcaaa tggtcataac ttttaactcg gaggtccgat tcatgcgcat 120

aatatatcga gacgctcgaa attgaacaac ggaagctctc gagaaattca aatggtcata 180

acttttcaca cggaggtctg attcaggcgc ataatatatc gagaccctct aaatttaaca 240

acggaagctc tcgagaaata ccaatggtca taacttttca ctgggatgtc cgattcaggc 300

gcatcataca ttgagacgct ccagattgaa caacggaagc tcttcagaaa ttcagatggt 360

cataactttt cactcggatg 380

<210> 293
<211> 164
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 293

gcgtctgtat atgtgatgcg cctgaatcgg acatccgagt gaaaagttat gaccatttga 60

atttctcgag agctttcgat gtttaattnt gagcgtctct atataatata agcctgaatc 120

tgacatcagt gtgaaaactt atgaccatan taacttctgg agag 164

<210> 294
<211> 452
<212> DNA
<213> Glycine max

<400> 294

tcaagaaaaa gatggcctca gcaaattcct tatttccaga atggaattct atcaatagac 60

ctccaatctt taatggagag ggttaccact actggaaaac ccgaatgcaa atttttatcg 120

aggcaataga tctaaatatc tgggaagcca ttgaaatagg gccttatata cccaccacag 180

tagaaagagt ttcaatagat ggtagttcat caagtgaaag cataaccata gaaaaaccta 240

gagatagatg gtctgaagag gatagaaaac gagtacaata caacctataa gccaaaaaca 300

taataacatc tgccctagga atggatgaat atttcagagt ttcaaattgc aagagtgcta 360

aggaaatgtg ggacactctt cgattaacac atgaaggaac tacagatgtt aaaagatcta 420

ggataaatgc actaactcat gagtatgaat ta 452

<210> 295
<211> 333
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 295

ctaagcttat ccaggggaga cggaccatct caagtgctng aaagaatcaa tgacaatgct 60

tacaaagttg agctgcccgg tgagtataat gttagttcca ccttcaatgt ctctgattta 120

tctctttttg atgcagatgg agaatccgat ttgaggacaa atccttctca agagggagag 180

aatgatgagg acatgaccaa gagcaagggc aaggatccac ttgaaggact tggaggacct 240

atgacaaggg ctagagcaag gaaagccaat gaagctcttc aacaagtgct gtccatacta 300

tttgaataca agcccaagtt tcaaggagaa aag 333

<210> 296
<211> 441
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 296

tgcttctata gatggtaggg accaagcaag gaaatattca catccttcaa gggtccacta 60

tgacaggatc aactatttca caatatgaga gccatgcgtc caatggctca tccaatgata 120

attctctatg gcatctgtgt ctgggcccat aagtgaaaac ataataaaag ttttgagcaa 180

gcgaggctta cttggaaaac ataaggttga acctcttcag ttttgtgagc attatgtcta 240

agggaagtaa cataggacaa aatttctaaa ggttgttcac actacaaagg gcattttgga 300

ctatgntcca tttgactact ggggggactt tgagagttcc atcactgaga ggggaaaggt 360

atttcctctn catcatcaat gnatactcca caatgacatg ggtattcatg atgaagtaga 420

aatctgaagc ttaccaattt t 441

<210> 297
<211> 398
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 297

agcagcaaga ggtcttgcaa agattcatgc ttagtacagt gcagccaaag tgcctcacgg 60

gaatgtgaaa tcctccaacg tgcttctaga caagaacggt gttgcatgca tctccgattn 120

tgggttatca ctcctattaa acccggttca cgccattgcc cgattgggag ggtacagggc 180

cccggagcaa gaacagaaca agaggctatc tcagcaggct gatgtgtata gtttcggagt 240

attgttgtta gaagttctca caggaagagc tccttcatcg cagtaccctt caccggctcg 300

tccccgaatg gaggtagagc cggaacaggc tgcggtggac cttcccaaat gggttcgctc 360

ggtggtgaga gaagagtgga ctgcagaggt ttttgatc 398

<210> 298
<211> 345
<212> DNA
<213> Glycine max

<400> 298

gagtagtgtc ccactggtaa aactaacttt ccaaattttt gccttcgcag gaaatggccc 60

cgaggaagct tgcctcaaag aggtccagga aggacaaggc agccgaagga actagttccg 120

ctccggagta tgacagtcac cgctttagga gcgctgtaca ccagcagcgc ttcgaggcca 180

tcaagggatg gtcgtttctc cgggagcgac gcgtccagct cagggacgac gagtatactg 240

atttccagga ggaaatagct ctacggagtt ttaaaagact ggctaagaat ttggtaaaac 300

ataagcactt agacaatgaa ggaaagctgg agttgctgac atgat 345

<210> 299
<211> 304
<212> DNA
<213> Glycine max

<400> 299

atctaggtcc ttatatggat ggagctcaac cttgtctctc acttacatat taagttcact 60

aaggaaccta gcaatacttg ttctttcctc cttcctaagt ccagctctca aaatgagtag 120

ttccatttgt tgcctatact cttcaacact cacactccct tgtctaagcc tttggagctt 180

gtccataagc tccctttcag agtaggaggg gatgtgcctc ttcctaaggg cactattcaa 240

gacaatccta tacctactag aggatcccca tgaatccttc tttccctagt gatgcaatcc 300

tacc 304

<210> 300
<211> 166
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 300

atgaagcaac aatgatgtaa gctccattgg agcttgtang cctaggatct tcttcatcaa 60

tggattcctt tgcttcttgg aagatgaatg gcagcggaat ggagaaagga agagagagag 120

gagacgccac ttcaaggaga agatgagtct agaagaagct caccac 166

<210> 301
<211> 400
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 301

tcttagtctc acctgatgaa ttcatggcta cttcatgcac tcctctaatg acaatagcat 60

cacttctgac actaaattgc tgggagtttg aagccatctt ctcaattaaa tttctggctt 120

cagcaggggt catgtctcca agggctccac cactggcagc atctatcata cctctcttca 180

tgttgctaag tccttcataa aaatattgga gaagaagctg ctctgaaatc tggtggtaag 240

ggaaactagc acataatttc tttaatctct cccagtattc atacaggctc tctccacaga 300

gttgtctaat acctganata tcctttctga tggtcgtggt cctggaagca gggaaaaaaa 360

tatctaagaa tactctcttg aggccattcc agctcgtgat 400

<210> 302
<211> 349
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 302

tgtgtcacga ttcactgtga cagtcaaagt gccattcact tagcaaatca ccaaatgtac 60

catgagagga caaagcacat agatgtaaaa ctacacttca tcagagatgt gattgaatct 120

aagaaggtga aggtggaaaa ggtttcaaca gaagaaaacc cagctgatat gttcacaaag 180

tccctctcta gtgtcaagtt caagcactgt ctgaacttga tcaatttcga agatgcctaa 240

agctgattgg tagaagtgca gccctgaatc acaagataga cactngctaa tttggagtca 300

aggtggagat ttgtggtgtg tgactcanaa tcacaattgg cacaagtga 349

<210> 303

<211> 325
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 303

ntactgaaga aagctagggg tgactcacct tgcattagta ctatgcccat ggccgtgccg 60

gaggcgtccg tttcgagtgt gaatggacgg gaaaaatctg gcagagctag cactggtgcc 120

tgtgtcatgg cacgcttaag agagtcaaac gcaagttgag aatcctcgcc ccaatggaaa 180

ttatccttct ggaggagtga agttaacagc gccgcaaagg cagcataatc acggatgaac 240

ttgcggtaga agtccgttaa acccaaaaaa ccacgcacag attgggttgt catgggtgta 300

ggccaattca ccatagcttc tatct 325

<210> 304
<211> 289
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 304

gctacgctct taactgacac gctcttaata ttcgaagagt atccttgtgg aaccttcacc 60

cgacgaagac actgacaaan acttatatta ttcttctttg acaaagtatg gcaggatagg 120

gacaaagtaa atttcttccc atcagacctt ggatgcaact gtgatcgtat acccatatca 180

gctagatctt gacgggtatt caagccatcc ttcgtcttgc cttgaatgtt aaggagcgtc 240

ccaatcacac tgtcacaaac atgtttcttc acatgcataa catcaatac 289

<210> 305
<211> 307
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 305

tatcgagacg ctcgtaattg aaaacagaag ctctgagcca attcaaacga caataacttt 60

taactcgggt gtccgattgt gtcctgtagt atattgagac gctcgaaatt gaaaacagaa 120

gctttgagca aattcaaacg acaataactt ttgactcgga tgtccgattg tgtcccgtag 180

tatatcgaga cgctcgaaat tgaaaactga agctctgaga aaaatcaaac gacgataact 240

ttttactcgg atgtccgatg gagacccgta atatatcgag acgctcgtan ttgagaacag 300

aagctct 307

<210> 306
<211> 273
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 306

cacttgttga atatgcttct ttgctntcct tgcgctagcc cttgtcatag gtcttccaag 60

atcttcaagt ggatccttgc ccttgctctt ggtcatgtcc tcatcattct ctccctcttg 120

agaaggattt gtcctcatat cggattctcc atctgcatca naaatagata agtcagatac 180

attgaaggtg gtactaacat tatacttatc gggtagctca actntgtaag catcattgct 240

tctttcaagc acttgacatg gtccatcttc cct 273

<210> 307
<211> 435
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 307

gcttanacat tgagaagaca gtatgagctt cttgctatgg atgagactga atcaatagct 60

gagtatttca ccaagattct cacactcacc aataagatga agtgttgtgg agaacagatt 120

aaggaacaac tggtggttga gaaggtgctc agaacactga catcaaagtt tgatcacatt 180

gtggtggcca ttgaagaatc aaaggatctt acatctttca agcttgaaga actacaaagt 240

tcacttgaag cgcatgagca gagattaata gacaggaatc ctgagaagca caatgatcaa 300

gccttacaag ctcaaacagg cataaagttt gacaagcaat gagacaaatc caaaaagaac 360

aaaggatagt ggtgtgatga gaagtggaga aagactgaag attccatatg tggtgattct 420

ggatcatctt cacag 435

<210> 308
<211> 352
<212> DNA
<213> Glycine max

<400> 308

cggcgtttgt agaacctgtt acatgaggtc ttttaggctc ttgtggtccg tgatgataat 60

gaaggggtac ccgaggaggt aatggcgcca ttttcgaact gccgaggtaa tggcatgaag 120

ctcgtgaatg taagtagatg catgttgaag gcgtgggcag aacatcttac tataaaaggc 180

gattggatgt gatctctgtt gaagaatggc acccatggca atagcaaagg catatgtttt 240

gaggacaaaa ggcaatgaga aatccgacga ggccaacacc ggagcctgag tcattacttc 300

cttatgacga aggaaggagt gggtagcctc ttcagaccat tagaattgat ct 352

<210> 309
<211> 431
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 309

gcggtagaga gattgagatg atattgtagt cttcatttta ctgtcaacat gcaagggaca 60

tttctctcgt tttagacatt gtttcacaaa ttccaacggt ggagatgtgt gaaaatggat 120

tccaaagtcg gtgtccaaat tgcacaatga tccaacggtt aacgagtcca ggatcatagt 180

tttaatgaga taggttttgg gtctctacga gaaaagagaa agctagaatg cgaaggatat 240

ttctctcacc tctgacgttn tttggcaaat ttcaacggtg agaatatttg aaagtgagtt 300

ctaaacctgg ttctcaaatt tcatgatgat ccaacggtta acgagtctga gatcgttgtt 360

ttactaagat atgtttgagt gtatgcgana aanagagagg aatttggaaa gaggagaagg 420

gaaaacgaaa t 431

<210> 310
<211> 354
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 310

agaaccaaag aagagcaagt tatattgaga catgaacttt ggttatgcga aaaacttttt 60

ggatgagaaa acatatatct ggatatggtt tataattcta tacttaagac atttaaaata 120

gaactgaggg aatcaaactt aggtcaattt aattctagtt tacgatatgt actcatggtt 180

aaattntatt ttagtgattt taatttaatc tttataaatt atttagatat gttatgtgat 240

atgtcactta catagttatt aaagtaacat atatgatttg ttatatatta catcatttca 300

tgaataaatc ttttttatta tgcagaaaaa gcaatggatt ntttaattat tttt 354

<210> 311
<211> 447
<212> DNA
<213> Glycine max

<400> 311

tagactaact tcagcctacc attctcatac tgatggccat actgaacgga ccattcagtc 60

attgaaggac cttctaagag cgtgtgtctt atagtagaat gaaagctggg agagttttct 120

tccatcgata gagttcactt ataacaatag ttttcactct accattggca tggatcccta 180

tgaagctctg tatggtagaa ggtgtatggc acccttatgt tggctagagc ccagagaagg 240

ccttaccttа tgacctaaag tggtacaaca aaccaccgag aaagtcaagt taatccagga 300

taggatgatg actgctcaca gtaggcatac aagttatcat gataagagga ggaaagatct 360

ggaatatgag gatggtgatc atgtattctt gagagtcact tcgtggactg aggttggtcg 420

agcattgaaa tcccgaaaac tcacacc 447

<210> 312
<211> 355
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 312

agcttggact tcctatgttt tgggaacctc tccttcctca ggtgtaccca aacccaatca 60

cctggttcaa gcacgacttt ctttctgctt ttgttggttc tccttgcata gcttgcattt 120

ttgttttcaa tttgagcctt cacttgctta tgcaacttct tcacatactt agctttagcc 180

tctgcgtcct tatgcttaaa catagcaatg ttagtcatag gcaacaaatc aagaggtgtc 240

aaaaggattaa atccatacac tatctcaaat ggtgaacaat tagttgtgct atggacagcc 300

cgattatagg caaactaaac atgaggcann acatgcttcc aagtttaaga ttttc 355

<210> 313

<211> 216
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 313

tgcctatgtt gctgcggatg attgcttcat atntacctgn gtcaactcta tcagagagaa 60

atcacacacc ttcgaagtat tcaaagagtt gagtctaaga cttcatagag atgaagactg 120

tgtcatcacg agaatcacga gtgaccatgg cagagagttt gaaaacagca ctgttactga 180

attctcacat ctgagggcat actcatgagc tctcta 216

<210> 314
<211> 384
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 314

agctnggcaa ggttcttttc ttgacaatgt gtcacccttt aaccaatggg caaactgaag 60

tgataaatca aactctttct caaatcctat gacacttcat taaaggtaat ttgaaagctt 120

ttgaagattg gctgccccat gtggaaattg catacaataa gggaaccaac tataccattc 180

ttcttttgaa gttgtttatg gttttaaccc tttgtctctt cttgatttga ttcctttgcc 240

taatattgat tctatgttga ataaagatgg atttttcaaa gcttctttta ttaagaactt 300

gcatgagcaa gtgaaggctc aaattagaag gaagatggaa caatatgtta aacaagccat 360

caaagggagg aagaagatgg tgtt 384

<210> 315
<211> 397
<212> DNA
<213> Glycine max

<400> 315

ggctgcagct ttagattttt aataaaagac ctatgattat tgaagaatct atccatgttg 60

cttttgatga gactaaccct ataggccaag aaaggaaaca cttgatgata ttaacggatt 120

cattataaga tatgcacttg gtgaaagggc acaagacaag gaaatggaaa tgaaaaagac 180

tttcaaattg atgaaaataa aataaatata gatcttccaa gagagtggag aacttcaaga 240

tatcatcctc ttgataatat catcggtgac atctcaaaaa gggtaacaac tcgacactct 300

ctcaaagatc catgcaataa tatggctttt gttcctttaa ttgaatctaa aaatttaaat 360

gaagccataa ttaatgaaca ttggattatt gttatgc 397

<210> 316
<211> 321
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 316

agctntagca actctntctt tttgtttagt ctagacttct aatgctctta atctctcctc 60

gtctaaatca actaactcat ctgacatcat tttccaataa tggtcgatcg gaatgtccat 120

ttgtttttgt actctagctg attgcaaatg tatttcgacc ggaagtatag catcgtgccc 180

ataagtcagt cgaaatgggg tagtattagt tgattcctta ggagaatttc tacatgccca 240

tagaacttga tctaacgttt tattccaatt tcttggcttt tgggcaatgt gtttttaat 300

caagttaatt acaatcttat t 321

<210> 317
<211> 399
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 317

agctntctta agatcaagcc ttgcctacaa ggaaaggttt caagtcatcc aagggacatg 60

taatcgatta ccaatggttc gaaagtgtgt aatcgattac acatcatatg taattgatta 120

ccagagactc tgaacgttgg gaattcaaat tttaaatgaa gagttacaat tgttcaagaa 180

aaacaactgt gtaatcgatt acaccaattc tgtaatcgat taccagagag gattttcaag 240

gaatatcgcc aacagtcaca tcttatcatt tggattttga atggccatca aaggcctata 300

tatatgtgtg acttgggaca aaattagaga gagttttgct ggtccaaaat gtcttatcct 360

ctcanaataa aatgagagag atntccagag aacttcatt 399

<210> 318
<211> 408
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 318

atccttttca ttttacaagc ttgaaaagtt nttgaaaggc tttaaaagcg ttactcttag 60

aagatacgaa taaagtccag gtatatatag agcagtcatc tacaataacc aaagcatagt 120

aattccctcc gttgctcatc gttctagaag gaccaaaaag atctagatgt aaaagttcaa 180

gcggtctaaa ggtagaaaca acatttttag atttgaaaga tgctctagtt ttctttccat 240

tntgacatgc attacataat tcatccttca caaatttgag ctttaggagt cctctaacta 300

actccttaga cactagctta tttaaatgat tcatgtggat atgagttatt ctcctatgcc 360

aaagccaaga gagatcatca ctacttatta aacaagtcat gtttgagt 408

<210> 319
<211> 368
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 319

gtgccttatg aatcctcccg tgcttatgcc accagtacct ggaatgcctc tcattntgta 60

catgacaatc ttagacgagt caatggggtg tatngctggg caacatgacg aatccgggaa 120

gagagagcgc gcctgttact acctaagtaa gaagttcacg acctgtgaga tgagatactc 180

cttgctcgaa agaacgtgtt gtgctctagt gtgggcatcc catcgcctaa ggcagtacat 240

gctgagctat actacctcgt tgatatccaa gatggacccg gntaagtaca tctttgagaa 300

gccagctctc acgggacgaa tcgcccggtg gcaagtcctg ctatgcaagt ntgatatant 360

ctacgtca 368

<210> 320
<211> 236
<212> DNA
<213> Glycine max

<400> 320

agcttaacta cacactcttg gcgcgtatga tgaatgaaca gcgcttggcc atgacattca 60

tgtggctcca aatgaaagcg cgaaacggag actcgccgta tacaactcgg caacctcatt 120

cgcggagctc cagactccta ggtggaagac acatgaacag tgctaggcaa tgacattcat 180

ggggctccga agaaagggga caatggagga ctgccctata agggacacac ttaagc 236

<210> 321
<211> 367
<212> DNA
<213> Glycine max

<400> 321

agcttgctaa cccatggaag ctcctaatat ctcccacact ctttggggtg ggccattctt 60

ggatggcctt gattttctcc tagagaggga aactacaaac cctaagaaaa ctatattatc 120

tacacgaaag gtacacttct ctatatttgc atagagggta tttttcctaa ggactgaaag 180

aacttgcctg agatgtccta aatgatcatc taggctccta ctgtacacta aaatatcatc 240

aaaataaaca acttcaaatc tgactatgaa atcccttaag acatgatgca taagcctcat 300

aaaggtgctt ggtgcattag tgagcccaaa agacatcact agccattcat accaaccaaa 360

cttggtc 367

<210> 322
<211> 371
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 322

agctntgaat tagtgtctgg gttgaggata aattttgcta aaagtaaatt cagggcaatt 60

agcaagtcac atcagcggat tcaaaatgcg gcaaattacc ttaagtgcag agtattggcc 120

attcccttct tgtatttggg tatccctatt gaggcaaacc caaagcgtag tgtgatatga 180

gaccctatag ttgagagatt tgagagaaaa ctatcaaagt ggaaccaaag acatctatct 240

tttgggggaa ggatcactct tataaagtca gctttaaatt caatccctgt ttttttctttc 300

tttctttttt cagggtccca aagaacgtgg ccatcaaatt ggtgaggctg caacgatggt 360

tcttatggga t 371

<210> 323
<211> 192
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 323

tgctgaccac catagagacc tttgttcttc catgcatcaa cctggagcga ttgagcaacc 60

tgaagcttat gctgcanata tatacaatag acctactcaa cctcagcagc acaatcaacc 120

acagcagant aattatgacc tctccagcaa cagatacaac catggatgga tgaatcaccc 180

tagcctcaca tg 192

<210> 324
<211> 401
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 324

gctccttcaa ctgcacaagg ctcttaatat ttgaagagta tccttgtgga accttcaccc 60

gatgaagaca ctgacaaaaa attatcttct acttcttgga caaagtatgg caggctgggg 120

gcaagtaaat tttcttccca tcagaccttg gatgcaattg tgatcgtata cccatatcag 180

ctagatcttg acaggtattc aagccatcct tcgtcttgcc ttgaatgtta aggagcgtcc 240

caatcacact ttcacaaaca tttttctcca catgcataac atcaatacaa tttctaacgt 300

caagatcaca ccagtacgga agatcaaaga aaatggatct cttcttccat atgcaactct 360

gacttttatc cttctttngg gtcttcccaa atacaatatt c 401

<210> 325
<211> 252
<212> DNA
<213> Glycine max

<400> 325

atgaatttca agaaatttcc aaatgtccta agtgtggggt atcacagtac aaagtgaagg 60

atgatgacga gtgtagtagt gacgaaaact caaagaaggg ccacccaacg aaggtgttgt 120

ggtatcttcc catcattcca aggtttaagc gtctgtttgc taatggagat gacgcacaag 180

accttacatg gcatgcaaat gagagaaact gcgatggaat gctctgtcaa tggttatcta 240

agtccattga tt 252

<210> 326
<211> 470
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 326

tgctggtaca tacgacatcc tcacggatca gtaccaagtc cttgctctct tgcaattctg 60

tgtaaaagga cacaatatag taaggagccg cttgtgttcc cctggccttg taatcttcaa 120

gacctgtaga aaccatgtgt ggcgtctgga ctgcaagaaa aaaacgaata cgtattgtga 180

gactacgatg gaagtgttga aaaagaaaac actcggaata aataaatcat tctttacatg 240

tcttttttaat aatatttcac gttctgtaag tagaaaattt gttaagagga agcatgtcca 300

taactatgtg cagggagaga ttagaattcg atttcttgat aggtaaggta tatccaaagg 360

gtgtcaacag tagtttatat gaatctagaa actgtccagg acctagtggc aaatattaac 420

atctttntat atatgtaact aanactgcat ctctttctcc aggctcggga 470

<210> 327
<211> 437
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 327

acgagcgtct cgatatacta cgggacataa tcggacatcc gggtaaaaag ttattgttat 60

ttgaatttgc tcataggttc tgttttcaat tacgatcgcc tcaatatatt atgggattca 120

ttcggacatc cgagtaaaaa tttattgcca tttgaatttg ctacgagctt ccgatntcaa 180

ttacgagcgt cttgatatac aacgaaaaac aatccgacat ccgagtaaaa agttattgtc 240

gttagaatat gcttagagct tctgttttca attacgagcg tctcgatata ttacgggact 300

caatccgaca tccgagtaaa aagttattgt catttgaatt tgctcatagc ttctgtnttc 360

aattacgatc gcctcgatat atcatgggat tcattcggac atccgagtta aaatttattg 420

cctgttgagt ttgctac 437

<210> 328
<211> 436
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 328

tgcagcaaat tctaacgaca gataactttc actcggaagt tcgattgagt cccgtaatat 60

atcgacacgc tcgaaattta aaaccgaagc tcatagcaaa ttcgaacgac aataactttt 120

cattcggaag tctgattgag tcccataaca tatcgagacg ctcaaaatag aaaacagaag 180

ctcgttgcaa attcgaacga caataacgtt ttactcggat gtccgattga gccccgtaat 240

atatagagac gctcgaaatt tanaaccgaa gctcgcagca nattctaacg acaataactt 300

ttcactcgga agtccgattg agtcctgtaa tatatcgaga cgctcgaaat ttaaaaccga 360

ggctcgtagc aaatacgaac gacaataact tttaactcgg aagtacgaat gagtcccgtt 420

acatattgag acgctc 436

<210> 329
<211> 400
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 329

agcttgaagg anaacttaat gccttggtca acctagtaac ccagcttgcc atgaataaga 60

aatctacgct tgttgcaaga gtctgtggtc tatgttcttc tgcagatcac catacaaatc 120

tgggtccttc tttgtagcaa tctggagtca atgagcaacc tgaagcttat gctgcaaaca 180

tttataatag acctcctcag tagcaaaacc aataacaaca gaataattat gacctttcaa 240

gtaatagata caatccaggt tggaggaatc atccaaatct gagatggaca agtcctccac 300

aaaaacaaca gtctgtccct cattntcaga atgctgctgg tccaagcaag ccatatgttc 360

ctcctcaata cagcaatagg aaccacaaca gtcaccacaa 400

<210> 330
<211> 401
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 330

agctttgatt tcctttgttc cgganacctt tcttttctca tgtgcaccca aacccaatct 60

ccgggttcga agacaacctt ctttctccct ttgttggctt gtttagcata gcttttattt 120

ttcctctcaa tttgatcttt gactctctca tgaagcttct tcacatagtc cgcctttgct 180

tgaccttctt tatgcttaaa aacagaaaca ttaggcatag gcaaaagatc aagaggagtt 240

agtgggttaa aaccataaac aacttcaaaa ggagaacaat tagtggtgct atgaatagct 300

ctattgtaag caaattcaac atggggtaaa caagcttccc aagttttaa gttcttcctc 360

aaaactgtcc taagcaaaga tcccaaagtc ctattaacaa c 401

<210> 331
<211> 258
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 331

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ttattaacat tggttttgtc caaaaccgat gttaagttaa acgcggtgac atatttgtaa 120

ataaagtatc cttcttaaca tcggtttttc caaaaaaccg atgttaacta atgatgttaa 180

catcggttat tggaaaaccg atgttaacgt atgataatgt aacattgatt ttttggaaaa 240

ccgatgttaa tgcatata 258

<210> 332
<211> 391
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 332

nttcccacat aactcttcca atctttgatg gagagaatta tgatctttgg gaagtgaaaa 60

tgcaatccta catggagtct ttggatttat gggatgctgt ggaagaggat tatgaaatat 120

atccgctgca tgaaaatccc accatgtccc aaattaaaaa tcacaaggaa agaaagatga 180

agaatgcaaa ggcgaggtca tgtttgttca ctggtgtttc acaaatgata ttcatcagaa 240

tcatgactct taaatcaccc aaagcaattt gggattatct gaaagaggaa tacgctgaag 300

atgatagaat acgaagcatg caagtgctga atttaaggag ggaatttgag cttcaaagga 360

tgcaagagtc agagacaatc aaagaatact c 391

<210> 333
<211> 478
<212> DNA
<213> Glycine max

<400> 333

gacactatca aactgaagct cgtgtccagg aggatatcca tgtttctgta acattcatca 60

acaatgtgat ttgtgaatcc agaatgtgta caaaccttgt ttcctttccc attagaactc 120

cctctgccag agcctccttg gctacttctt cctcctctag aagtatagtt tggaggaaaa 180

ccacttttcc tataacatct gcccactgtg tgattatctc cacaaacatc aagttgaaca 240

aattgagctt atctttcatt gactccgcta ccacattagg cggcaccacc gactcctttc 300

cctctagcat caaaatgtgc agcatcttat tccatgagct tctttgatag agtttacagt 360

tatgccccac ctttgtcgcg gtttgtcgga accaattatc atttctttca tccacaatgg 420

atctccattt acatgcctct tgtcctatgt atcttagaat attcatcata aacacata 478

<210> 334
<211> 469
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 334

cgcttctaca tttatcacct ttatagatgg atgttcgtga tatatgaata tttatttgct 60

tcataacaaa aataaagcat tggatccctt caaagtcttt aaggctgaag ttgagaacca 120

atgtggtaag aaaataaaaa tagtgagatt agatagaggt ggagaatatt atggcaaata 180

tactgagaat ggacaagcac ctggtccttt tgcaaagttt cttcaagaac ataggattgt 240

tgcccggtac actatgcctg gttctccaaa tcaaaatggt gtggcaaaaa gaaggaaccg 300

aacattattg gacacggtac ggagtatgct tagcaactct gatcttccta aatccttgtg 360

ggctgaagca ctaaagacgg cagtgtatat attaaactat gttccaacca aggctgtcca 420

aaagacacct tntgagttgt ttaaaggttg aaaacaaagt ttgaaacat 469

<210> 335
<211> 427
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 335

ctctcanagc cttgagacta cacatatcat aaacaacttt ctttatctcc tcctcagtat 60

atatttctcc ctaacatctc aatctcctct tgaaccaaaa ctgtaaattt acctcttaag 120

caaaaaggtt aataatctgc cacttcagtg aataaattcc tatagaaaga agtcaccatt 180

tcttctaaat ctatcgaatt aagcacccaa tagccctttt cattcaatag cctagcatat 240

aagttagatt gctttcttaa nagagtggtg caatgaaagt aatgagaatt cttatctcca 300

aatttaagcc acttgcacca agacttttga aaccacaaaa cttcttggaa caatatctgc 360

tctaactccc cacataaatc ttnttgtagc cttaaatggt acttattatc cttaatcctt 420

caacttc 427

<210> 336
<211> 455
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 336

tgctcaccac tactagagga gaagccttta ggttgtttca tataaacctc ctcttctaaa 60

tcaccattaa gaaaagctat tttcacatcc atttgttgca actcaaggtc aaaatgagca 120

actaatgcca agattatacg aagataatct ttcttagata ctggagaaaa agtctttgtg 180

taatctattc cttctttntg agtaaattcc ttagcaacaa gtcttgccat gtatctctca 240

atgttgccta atgaatccct tttggtctta aaaacccatt tacatccaat ggcctttgcc 300

ccattaggca tctctacaag gttccaaact ttgttactct gcatagaatt catctcatcc 360

ttcatgacat cataccatan nattgactct ttacaactct nggcttgatg caaaagttca 420

ggatcatttt cagctccata ttatagcata ttcta 455

<210> 337
<211> 429
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 337

agctntgaat gctctattca atggagttga caagaatatc ttcagactga tcaacacatg 60

cacagtggcc aaagatgcat gggagatcct gaaaaccact catgaaggaa cctccaaagt 120

gaagatgtcc agattgcaac tattggctac aaaatttgaa aatctgaaga tgaaggagga 180

agagtgtatt catgacttcc acatgaacat tcttgaaatt gccaatgctt gcactgcctt 240

gggagaaaga atgacagatg aaaagctggt gagaaagatc ctcagatcct tgcctaagag 300

atttgacatg aaagtcactg caatagagga ggcccaagac atttgcaaca tgagagtgga 360

tgaactcatt ggttcccttc aaacctttga gctangactc tcggataggg ctgaaaagga 420

ggcacatga 429

<210> 338
<211> 455
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 338

tgcttgaagg gttgtacatg accaaatctt tagttaatcg tctttacgtt tagcagtctn 60

tgtattcgtt taaaatgcat gaagataaat cagtacgaga acaattggat ttgtttaata 120

aactgattct tgatcttgaa aatatcgatg tcactattga tgatgaggat caagccttgt 180

tattgttgtg ctctttgctt aagagttact ctcatttcaa agagacttta ttgtttggaa 240

gagactctgt ttctcttgat gaagtgcaag ttgctctgaa ttcaaaggaa ttgaatgaaa 300

gaaaggaaaa gaagtcttct ataagtggtg aagggctgac agcaagagac aagaccttca 360

agaaagatag taaatctgat aagaagaagc ataagccaga taatcatatg aatggtgaat 420

gaaacatgtt caaaatcaat tgtatcactg taaaa 455

<210> 339
<211> 417
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 339

agcttgtaat cgattacaac atttgtgtaa tcgattacca gacataaaaa ttcaaatttc 60

aagtctcaag agtcacaact cttcagaaac taattgtgta atcgattacc acatttatgt 120

aatcgattac caataaggaa ttttcgaaaa gtacacccaa gagtcacaat tgttcaagaa 180

gtttttgaat ggccatcaaa ggcctataaa taggtgactt gngatacgaa attctttaga 240

gtttttttctg aacaacattg tcttatcctc tcaaaaccaa attgtcttat cactctcaaa 300

atattccttg gccaaaacac ttgcaaattc aataaggaat cttgatcgat cttcaattgg 360

aatatccttc tcttaaagag agaaaatgct tcttcttctt attcaaagag atctgtt 417

<210> 340
<211> 457
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 340

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ttcaaacgtg actcaagtgt ttgttgatca actatcacga ctaaacacgt tgggtttgaa 120

cgctccccac actcaccctc gaggcactga gatccttata gtccttgagg gtactctcta 180

tgttggattt gtgacttcca atcaagatgg aaatcacctc ttcaacaaag tgctgaacaa 240

gggtgatgtg tttgtgttcc caattggtct cattgatttc tgcatcaatg tgggatatgg 300

caatgttgcc gccattgttg gtcttagcag ttaaaatgca ggaggcatta ctattgcaaa 360

tgctttgttt aaagctaatc cacctatntc ttctaaggtt ctcaccaaag cttgccaggt 420

ggacaagagc ataattgatt atcttgaana gcaatct 457

<210> 341
<211> 403
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 341

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ctatnttcag attgggaatg cctctaacag cacttttgtc aaggaatttc ttcatgcctc 120

ttaagtgcag atgtccaaac ctttgatgcc atattctgac ttcatcttct ttggaggata 180

gacatgtgga ggagtagctg gtttcttggg gtgtccatag gtaacaaatg tcctttgatc 240

tgctgccctt cattagaact tcactcttct catttgtcac caagcattct gactttgtga 300

agtttacatt gaatacttca tcaaacagct gactgatgct gatcaagttt gcagtcagtc 360

ccttcaccag cagtactttg ttcagactag gaagtccatc atg 403

<210> 342
<211> 374
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 342

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ctatacgaga catcttgcca aacaaagtca agttcacgat aactcgcctg tgctttttct 120

tccatgctat atgtagcaaa gtgattgatc cagtaatgtt tgatgagttg gaaaatgagg 180

ccacaattat actatgccag ttggagatgt attttccccc tactttcttt gacatcatga 240

ttcacttgat tgtgcatctg gttagagaaa tcaaatgctg tggtcctgtt tatctacggt 300

ggatgtaccc ggttgagcga tacatgaaga tcttaanagg gtatacaaag aatctatatc 360

gtccagaagc atct 374

<210> 343
<211> 451
<212> DNA
<213> Glycine max

<400> 343

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tcatatagaa atcaaaagac aaccaaccat tcttcaacac ccaaaagaaa gaaggaagga 120

aaatagactt cagatgtaat gtaaaaagaa atctctattg tagatctaag cttacacttt 180

tactcttttt ttgtagattt ttcaatccaa aatatgcctt tctgcaaatg cctgaatata 240

tgatcacata taagatagat tatataaaaa caaattattc aaatgccata tgaatttaac 300

atcatttcca caagaaaaac cttgtggcaa tatcatgatc agctaaatag taatatgcac 360

agccacataa caacaatgcc tctaaattat tttcatcttc cttgagaaga aacccagact 420

cagcaatagc actctcatac tctttatcag c 451

<210> 344
<211> 393

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 344

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agcaagaaat gaagagccaa tggttgatac atggacggag atgaataaga tcatgaggaa 120

gcggtatgtt ccggctagtt actcaaggga cttgaaattc aagctccaaa aactaaccca 180

aggcaacaag gtggttgagg agtatttcaa ggaaatggat gtgctcatga ttcaagcaaa 240

tattgaagaa gatgaggagg taactatggc tcgatttctt aatggtttga ctaatgatat 300

ccgtgatatt gttgagctgc acgagtttgt tgaaatggat gaattgcttc acanagcaat 360

ccaagtggag caacaattaa aaagggaagg agt 393

<210> 345
<211> 450
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 345

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agttatgtcc ccgaatcgga catctgtgtg aaaagttatg accattcgat tttctcgaga 120

gcttccgttg ttcaatttcg agcgtctcga tatattatga ccccgaatcg gacatctgtg 180

tgaaaacgta tgaccattcg attttctcga gagcttccgt tgttcaattt cgagcgtcta 240

gatgagttat gtccccgaat cgaacattcg agtgaaaact tatgaccatt cgaatttctc 300

gagagcttcc gttgttcaat ttcgagcgtc tcgatatatt atgttcccga atcggacatc 360

cgagtganat gttatgacca ttcgattttc tcgagagctt ccgcttgttc aattcgagcg 420

tctcgatata ttatgtcccc gaatcgacat 450

<210> 346
<211> 480
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 346

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tccacccaag acttgatatc atcccatatc tctagcccat cagaagcata aggatagtcc 120

tcgatcaaaa gtcaaactcc atggggagca gatggatcct taacagcaac tcctctgaat 180

taaaagcacc caaataacat tgattagcat aagagttata tcaagcctga agccttttt 240

cttcttatgt cattgatgac tttttatatc atgcattcat gtgccactac tctgtcaaag 300

ccatgaactg tcaaagccat catttaggat gaaacagtct ttgtctttcc aaaatctgaa 360

atacgagcca cttgagcatc tgctaaacga tatttcgtgc caccaatagt aacctcagat 420

gaaacagtct ccacatccaa cacaatataa tccaccaatt gtctactagt aagtaatgac 480

<210> 347
<211> 440
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 347

taaacattca atttcgagag tctcgttata ttacgggact ctatcagaca tccgagtaaa 60

aagttattgt cgtatgaatt ggcttatagc ataaacattc aactttgagc ctctcgatat 120

attacgggac tcaatcagac atccgagtaa aaagttattg tcgtttgaat ttgctcatag 180

gttcaaaatt caatttcgag cgtctcgata tatttcggga ctcaatcaga catccgagta 240

aaaagttatt gtcttttgag ttggctcaga ggttcaacat tcaatttcga gcgtcccgat 300

atattacgtc actgaatcgg acatccgagg aaaaagttat tgtcgtttga atntgctctg 360

agcttcaaca ttatattacg agcgtctcga tatattacgg gactcaatca gacatccgag 420

atacaagtta ttgtcgtttg 440

<210> 348
<211> 431
<212> DNA
<213> Glycine max

<400> 348

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atatatcgac acgctcgaaa ttgaatggtg aagctctagg cctattcaaa cgacaataac 120

gttttactcg gatgtccgac tcagtgacgt aatatatcgg gacgctcgaa attgaatgtt 180

gaacctctga gccaactcaa acgacaataa ctttttactc ggatgtctga ttgagtcccg 240

tattatatcg agacgctcga aattgaatgt tgaacctctg agccaattca aacgacaata 300

actttatact cggatgtctg attgagaccc ataatatatg gagacgctcg aaatggaatg 360

ttgaacctct gagccaattc aaactacaat aactctatac tcggatgtcc gattgagtga 420

cgtaatatat c 431

<210> 349
<211> 463
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 349

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gcttctgaag ctgttgctga agtcagagca gaggtggata agctcgctga gagggtgagc 120

ctgcttctca tattatcttt ggttattgaa acataataac tggagctgag aatgaggata 180

tgagtgattt tgatttgcaa gtatctgtct tggaagtggc tgtggatgga gggaccaggg 240

tttctgacaa agagtttttg atgtccacag agttgcttat gaggcaattg ctgaaactgg 300

atagtattga ggctgaaggt gaagtaaagc tgcagagaaa agctgaggta gtgtttatgg 360

tggttagaat tataacttaa attctaacta attgcgtatt agntattgtg tttattttgg 420

tatttacaaa atcccaccta ttagtaagtc atggacactg act 463

<210> 350
<211> 427
<212> DNA
<213> Glycine max

<400> 350

tttccgacta tgctctcgtg tggtggaaca agctacaaaa ggagagagca agaaatgaag 60

agccaatggt tgatacatgg acggagatga aaaagatcat gaggaagcgg tatgttccgg 120

ctagttactc aagggacttg aaattcaagc tccaaaaact aacccaaggc aacaaggggg 180

ttgaggagta tttcaaggaa atggatgtgc tcatgattca agcaaatatt gaagaagatg 240

aggaggtaac tatggctcga tttcttaatg gtttgactaa tgatatccgt gatattgttg 300

agctgcagga gtttgttgaa atggatgatt tgcttcacaa agcaatccaa gtggagcaac 360

aattaaaaag gaagggagtg gctaagagga gttttaccaa ctttggttct tctagttgga 420

aagacaa 427

<210> 351
<211> 352
<212> DNA
<213> Glycine max

<400> 351

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gagttatgtc cccgaatcgg acatctgtgt gaaaagttat gaccattcga ttttctcgag 120

agcttccgtt gttcaatttc gagcgtctag atatattatg accccgaatc ggacatctgt 180

gtgaaaacgt atgaccattc gattttctcg agagcttccg ttgttcaatc tcgagcgtct 240

agatgaatta tgtatccgag tcgtacattc gagtgacaac ttatgaccat tcgaatttct 300

cgagagctta cgtagttcaa tttcgagcgt ttagatatat tatgtccccg aa 352

<210> 352
<211> 442
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 352

ngtgaatgta tatctatcat tcccaacttg caagtaaggt cttgaagttg ctccgtggga 60

agtccttggt aagggatgta ttcggtggct ataagaccac tgtctaattn ttccttaata 120

aaatgtcgat taatctctat gtgctttgtt cgatcatgtt gaactggatt gtgtgcaatg 180

ctgatggcaa acttattatc acaaaccagt cccataggaa cttcatattt tattttgagg 240

tcatcaagta tgatattcat ccataacaac tcacaaacac cttgagccat agctctgctt 300

ttgcacttga tcttgcaacc acattntgct tcttactcct ccacgttact aaatttccac 360

ccaagaacat gcagtatcct gtggtagatc tcccatcaac aatngatcct gcatagtcag 420

catcagtata tactttcatg at 442

<210> 353
<211> 439

<212> DNA
<213> Glycine max

<400> 353

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atctaaatca actaactcat ctgacatcat tttccaataa tggtcgattg gaatgtccat 120

ttgtttttgt accctggctg attgcaaatg tatttcgacc ggaagtacag catcatgccc 180

ataagtcagt cgaaatgggg tagtattagt tgattcctta ggagaatttc tacatgccca 240

tagaacttga tctaacgttt tattccaatt tcttggcttt agggcaatgt gtttttaat 300

caagttaatt acaatcttat tggctgcttc gacctgacca tttgcttgcg cgtaatatgg 360

tgttgaggtt aataatcgaa agccagtttt ttgggcaaat tcttgcattt ttcgtccagt 420

aaaaactgaa ccttgatca 439

<210> 354
<211> 423
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 354

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ttcttttgca agaagaaggg acacatgaaa aagaattgcc ccggattcca ganatggctt 120

gagaagaaag gtaaatcaat ctcattagta tgttatgaat ctaatatggt tagtgttaat 180

attaacacct ggtggattga ttctggatct actattcata ttgcaaattc tttacagggt 240

atgcataacc taatgaaacc agtgggaagt gagcaaagca ttttatcagg caataagcta 300

ggctcacatg tggaggccat tggaacttgc attctgactt taagtagtgg ctgtatttta 360

aaattagaaa ggactttcta tgtanccaag ttttcccgaa acttgatttc tatttcaagg 420

ctt 423

<210> 355
<211> 378
<212> DNA
<213> Glycine max

<400> 355

atgacaattt gaattgctct agagattcca ttgttcaatt tcgagcgtct cgatatatta 60

tgaatatgaa tcggacctcc gagttaaaag gtatgaccat atgaatttct cgagagcttt 120

cgttgttcaa tttcgaggcg tttgatatat tatacgcctg aatcggaact ccgtgtgaaa 180

agttatgacc atatgaattt ctccagagat tccgttgctc aatttcgagc gtctcgatat 240

attatgcgcc cgaatcggac ctccgggtga aaagttatga ccatataaat atcttgagag 300

cttctggtgc tcaatattga gcgtcttgat atatatgctc cagaaattga cttgcgagta 360

aaagtatgac catttgat 378

<210> 356
<211> 303
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 356

tcggatgtnc gatntaggcg natattatat ttagacactt gatattgaat aacagaagct 60

ctcgagaaat tcgaatggtc ataacttttc acacggatgt ccgattcggg cgcataatat 120

gtcgagacgc tcgaaattga acaacggaag ctctcgagaa attccaatgg tcataacttt 180

tcactcggag gaccgattca ggcgcataat atatcgagac gctcgaactt gaacaacgga 240

agctcccgag aaattcaaat ggtcataact tttaactcag aggtccgatt ccggcgcata 300

ata 303

<210> 357
<211> 460
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 357

tcaaactatt tgcttcccga gggaaattct ataaacagac ctcccatctt taatggagtg 60

ggttaccact actggaaaac ccgcatgcaa atcttcatag aggcaataga tttaaatatt 120

tgggaagcca tagaacaagg accttatgtt ccctctataa tagccggaag tgcaacaata 180

gaaaaaccta gagcagattg gactgagaaa gaaagaagat tagtacaata taatttaaag 240

gccaaaaata ttattacata tagcttagga atagatgaat actttagggt ttcaaattgt 300

aaaagtgcta aggatatgtg ggatacacta caagtaacac atgaaggcac aacagatgtt 360

aaaagatcta ggataaacac tttgactcgt gaatatgaac tttntaggat gaatgtaaat 420

gagagtatac aagacatgca aaagagggtc acacacatag 460

<210> 358
<211> 443
<212> DNA
<213> Glycine max

<400> 358

tggatactct gagtcacctg cagctgcagc ttgaattgat acatcatttg tgtaatcttt 60

taccagacac aaaagaaatt caaatttcaa gtctgaagag tcacaactct atagaaacta 120

actgtgtaat caattaccac atttatgtaa tcgattacca tgaagatatt ttcgaaaata 180

actcccaaga gtcacaactg ttcaagaagt ttttgagtgg ccatcaaagg cctataaata 240

ggtgacttgg gatataaaat tccttagagt ttttttgaac aacattgtct tatcctctca 300

aaaccaaatt gtcttatcac tctcaaaata ttccttggcc aaaacactcg caaattcaat 360

aaggaatctt gatcgatctt caattgtaat atccttctct taaagagaga aaattcttgt 420

tcttcttatt caaagagaat tga 443

<210> 359
<211> 382
<212> DNA
<213> Glycine max

<400> 359

aaaatgaaga tacaataaaa tagtgagaaa atatatagat ttctaaatta tttaatatga 60

aatattcaaa atataaaata aaagtttctt gcccgtacaa caattctatt tataataatt 120

ctatttaatt cacataagat tacatttaat agaagataca catcatttaa acaaaaatta 180

aagtttatag atggacaact agaaactaag gaagctatag ctagctaagc tactacatat 240

taataaagaa caaaacatta caagaaaagg aaataattaa aaaaggtaga taaagaaaaa 300

agtgaggtga aagtttcaaa ttttgtgtgg ttccaggctt gcaaaccaat cctccagaaa 360

ggaattgttg agaaaaagta at 382

<210> 360

<211> 447
<212> DNA
<213> Glycine max

<400> 360

tataatatat tattacgctc gaaattaaac atcagaagct ctcgagatat tcaaatggtc 60

ataacttttc acccggatgt ccgattatgg cgaatcacat atcgagacgc tcaaaattga 120

acaacggaag ctcttgagaa attctaatgg tcataatttt aactcggatg ttcgattcag 180

gcgcatcaca tatagaagcg ctcgaaaagg aacaacggaa gctctcgaca aattcaaatg 240

gtcataactt tccacactga ggtccgatta cggattataa tatatcaaga cgctcgaaat 300

taaacatcga aagctctcga gaaattcaat tggtcatcac ttttcacacg gatgtgcaat 360

tctggcgcat aatatgtcga cacgctcgaa attgaacaac ggaagctctc gagaaattca 420

aatggtctta actcttcaca cggatct 447

<210> 361
<211> 461
<212> DNA
<213> Glycine max

<400> 361

agctttcaag aaacttgcaa aagttattca aaatgaaaaa gatttgaaaa ttaagacctt 60

gagaagtgat catagaggtg aattccaaaa tgaagatttt aaaacttttt gtgaagaaaa 120

tgggatttca cgtgattttt ctgctactag aacttcacaa caaaatgggg ctgcagagag 180

gaaaaatttg tgtttgcaag aactagcaag aactatgtta aatgaaacta acttagcaaa 240

ttatttttgg acggatgcca taagtacaac ttgctatgtt ctcaatagga ttttaataat 300

acctatttta aaatccacac cttgtgaact ttacaaagga agaaagccta acatatcaca 360

cttaagggtc tttggaagca aatgctttgt tttgaataat ggaaaactat accttgggca 420

agtttgattc caaactcaat gaagcactct ttttacgata t 461

<210> 362
<211> 590
<212> DNA
<213> Glycine max

<400> 362

gacactatag aaactaagct taacattgaa tttcgagcgt ctcgatatat tacgggcctc 60

aatcagacat ccgagtaaaa agttattgtt gtttgaattt gctcagagct tcaacattca 120

attccgagcg tctcgatata tgacgggact caatcagaca tccgagtaaa aagtcattgt 180

cgtttgaatt ggctcagagc ttcaacattc aatttcgagc gtctcgatat gtgacgagag 240

tcaatcagac atccgagtaa aaagttattg tcgtttgaat gggctcagag catcaacatt 300

caatttcgag cgtctcgata tattacgaga ctcaatcaga catccgagta aaaagttatt 360

gtcgtttgaa tttgcctcag agcttcaaca ttcaattttg agcgtctcga tatatgacgg 420

gactcaatca gacatccgag taaaaggtat tgtcgttgga ttggctagaa cttcacaatt 480

aatttcgagc gtcttgatat atgacggact caatcagaca tccgagtaaa agttatgcgt 540

ttgaattgtc taaagcttca caataaattt gagcgtctcg gtttatgacg 590

<210> 363
<211> 488
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 363

agctttgagc caattcaaac gacaataact ttttactcgg atgcctgatt gaggcccgta 60

atatatcgag acgctcgaaa ttgaatgtgg aagctctgag ccaattcaaa cgacaataac 120

tttttactcg gatgtctgat tgacgcccga aatatatcga cacgctcgaa attgaatgtt 180

gaagctctga gcaaattcaa acgacaataa ctttttactc ggatgtctga ttgagtcctg 240

tcatatatcg agacgctcga aattgaatgt tgaagctctg agccaattca aacgacaata 300

acttttttact cggatgtctg attgagtccc gtaatatatc gagacgctca aaattgaatg 360

ttgaagctct gagccaattc aaacgacaat aacttttttac tcggatgtct gattgagtcc 420

tgtcatatac cgagacgctc ganattgaat gttgaagctc tgagccaatt caaacgacaa 480

taacttttt 488

<210> 364
<211> 301
<212> DNA
<213> Glycine max

<400> 364

gtaagctggt tgttaaacca aactttagca atataaaata gtttatgtta cacgggactg 60

aagtgtccca aattgcaaac tgataaaaga caagaaattt tgtttgcagg tacttactcc 120

ttcgtactcc ctccaaggag gcttccccat gaacatttct ataattgtac aacccaaact 180

tcaaatatca acaacgaaag caacgtcaaa gctgttatct ttttgcacaa ccgcttgaaa 240

aagctacatg tatgtggaat aagtgtttat agagaatgca tgagacatca tgaagtaaaa 300

t 301

<210> 365
<211> 600
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 365

agcttcatgc ttaagtatgt atggcaaaac tttgttactg ttgttcaaga catacaagtg 60

agcttgtaac aaatgttcta cacttggagt gatcacatgc agtcctcttg aacccttacc 120

acccactctg tcttcatgcc gagactcgag aaggctaaca ggtttagcct tctctaagta 180

ttctgaacaa aattcaatgg cttcttctgc aatgtacctc tcaacaatag atgcttctgg 240

acgatataga ttctttgtat acccttttaa gatcttcatg taccgctcaa ccggatacat 300

ccatcgtaga taaacaggac cacaacattt gatttctctg accagatgca caatcaagtg 360

aatcatgatg tcaaagaaag caggggggaaa atacatctcc aactggcaca gtataattgc 420

ggcctcattt tccaactcat caaacttgac aggactaatg actttgctac atatagcatg 480

gaagaaaaat cacaggcgag ttatcactaa cctgactttg tttggcaaga tgtcttgtat 540

agcccaccac taacaaatgg ttgcatgagc acatganaat cgtgagactt ttaaccctac 600

<210> 366
<211> 464
<212> DNA
<213> Glycine max

<400> 366

tgatgaagaa tgcttggaag ttttttagac tttgaatgaa aaccttgtat ctgccgcaat 60

aatggttgta tctgactaga gtaaggagtt tgagttgatg tgtgatgcca acgactatgc 120

tgtgggtgca aatctaggac atcgacgaga caagatattc catgccatat actatgtcaa 180

caaggtcctg aataacgcac aattgaatta tgcgactact gaaaaggaaa tattggtcaa 240

cgtctatgcc ttagagaagt ttcaatgctt tctggtgggc tccaaggtcg tcatcttcac 300

agatcatgca acaatcaaat atcttcttac caaggcagat tcaaagccaa ggttgataag 360

atgggtcttg ttgattcaag agtttgacat cgtcttcaaa gacaagaaat gatctgagaa 420

tgtaatagct gaccatttct cccggttagt gaatgaagaa gtga 464

<210> 367
<211> 256
<212> DNA
<213> Glycine max

<400> 367

caccggcgag cctttgaatt gcttcgatta agtatctatg agacacatgt ttcctaccat 60

acccttttgac cagctcctga gcaagtaata tgttatcctg gatattccta ccaggaataa 120

aagctgaatg agtgtttttc accacactat ttatcacatc actcagtctg ctagtcaaaa 180

tcttcgatgt gaccttataa attgtgctac aacatgatat tggcctcatg tctttgatgg 240

tttttgcctc cgggga 256

<210> 368
<211> 368
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 368

ntgagcaaat tcaaacgaca aaagcttttt actaggttgt ttgattgagt cccgtaatat 60

atcgagacgc tcgaaattga atgttgaagc tttgagcaaa ttcaaacgac aacaactttt 120

tactcggatg tctgattgag tcccgtaata tatcgagacg ctcggaattg aatgttgaac 180

ctctgagcca attcaaacga caatcacttt ttactcggat gtctgaatga gtcccgcaat 240

atattgagac gctataaatt gaatggtgaa gctttgagca aattcaaaca acgataacct 300

tgtactcaga tgtctgattg cgtcccgtaa tatatcgaga cgctcgaaat tgaatggtga 360

agctctga 368

<210> 369
<211> 420
<212> DNA
<213> Glycine max

<400> 369

agcttcaaca ttcaatttcg agcgtctcca tatattacgg gactcaatca gacatccgag 60

taaaaagtta ttgtcgtttg aatttgctca aagcttcaac attcaaattc gagcgtctcg 120

ttatattata ggactcagtc agacatccga gtaaaaagtt attgacgttt gaatttgctc 180

agagcttcaa cattcaattt cgagcgtgtc gctatattac gggactatat cagacatccg 240

agtaaaaagt tattgtcgtt tgaatttgct cagagcttca acattcaatt tcgagcgtct 300

ccatatatta cgggactcaa tcagacatcc gagtaaaaag ttattgccgg ttgaatttgc 360

tcaaagcttc cacattcaaa ttcgagcgtc tcgctatatt acaggactca ctcacacatc 420

<210> 370
<211> 533
<212> DNA
<213> Glycine max

<400> 370

agctttagag gactacacgt cttcgccttc agaggactac tagtcctcgc cttcagagga 60

ctacacgtcc ttgccatcag agggctacac gccttcacca ttagaggact acacgtcctc 120

gccatcacaa gactacatgt cctcacaatc agagggcaac acgccctaac ctttagagga 180

ctacacgtcc tcgccgtcag aggacttcac gtcgtcacct tcagagggct acaagccttc 240

acctttagag gactacacgt cctcgcaatc agggggctgc acgccctcac cttcagagga 300

cttcacctcc tcgccatcag agggcagtac gccctcacct tcagaggact acacgtcctc 360

gccatcagag gactacacgc cctcaccctt agaggactac acgtcctcgc cattagagga 420

ctacacgccc tcgccatcag aggactacag gtcctcccct ttaaaggact acacgccctc 480

ccttttagac gactacccgc tctccccttt aaaggcttcc acgccctccc ctt 533

<210> 371
<211> 471
<212> DNA
<213> Glycine max

<400> 371

tacttttttc tttcctatag atggtttcag ttactatatc ttttatgaca gtcttgagct 60

ggtcacaaaa ggtcaaacaa tagactatgg aatgaacctg cactttgtga gcttaattga 120

tatgtcaagt tacaatttgt ctggaataat acctccccaa atgttcagcc tcattggatt 180

gtactccttg aacttttccc acatcaaatt aacaggacaa ataccaaatg agattggcaa 240

cattgaaaac ttggagtccc ttgatttctc aacaaaccaa cttcggggtg aaattcctca 300

aggcctttcc aatttgtcct ttcttgcttc cttagacctg tcatttaaca atttcacagg 360

caaaatacca tcaggcacac agctttaagg gtttcgtgca ctcagctata taggcaatcg 420

caatctttgg gacctccact ttcaaaattt tgctgcaggg tagtgaacct a 471

<210> 372
<211> 462
<212> DNA
<213> Glycine max

<400> 372

agcttatcct taaataagaa aaagtatccc tcccattata atccaaagtt tgataaaaaa 60

aaaaaaagaa aaaacattgc tgtttcaata gcaatatcct tacaatatct ctgcggataa 120

gctcctgaag tttaaacata atgcgttgac gagtggtgat aggagtattt ttccatgaag 180

gaaaagcttg cttggctgca ctaactgcag ctttaaactc ttcatatata gttaaatgaa 240

cttgagatac aacttcttgc gttgcctgag taaagataaa tattcaaatt acttttttaca 300

taaaccatca caatgctaag aaaatttcaa gcaaatatca ttgaaaaaca tatcaactta 360

cgggatttat aacatcaatg attacagaac cctgagaatt tacaaatttc cccccaataa 420

aatttgagac ctttagctac ataccaataa aaaaggccat aa 462

<210> 373
<211> 262
<212> DNA
<213> Glycine max

<400> 373

agcttttatt ttctgatgag taatcgttct agtatgtctt gaatgagctc ctcgaaaact 60

tgatgtaaat aaacgaattt ttgtccttcg tttccgagct atatatcctc gtttaattct 120

ggtcattgaa taattgagac tttgatgaat aactatttga tttttcagct attcttttct 180

tcttactagt ctattaataa cacaaatgga ttcttccaat gtataaaaaa agaacttcac 240

aggctcttgc tactataacc tc 262

<210> 374
<211> 551
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 374

tgagttaagc aagcctaaag agggtcgagg tttagtactt tctgctatag catagaacac 60

aaaagcatga ttgattagag aaatatcctt atatgcatca acttgtttgt tagaaatacc 120

caacactttt gtagaagcaa gcttcatgat gatgaaccaa gtaattttga tgatgccaaa 180

agcccaaatg attgattcaa gattgattca agacttcaag atcaagcatc aagaatccaa 240

tccaagattc aagattcaag agaagaaatc aagaagcaac aagtcaagac ttcatatagg 300

ataagtatta aaagaanttt tcaaaaacca aatagcacag ttttgtttta caaaagaatt 360

ttttcaaatt ttctaagtta ccagagtgat tactctctgg taatcgattg cctgttatca 420

gtaatcgatt accagtgacc aatttagttt tcaaatgttt gcaacgttcc aaaatgattt 480

tcaaatagtg taatcgatta cactatatta gtaatcgatt acaagtgaat cggaacgttg 540

gaattcaaaa t 551

<210> 375
<211> 531
<212> DNA
<213> Glycine max

<400> 375

tgtaggcgtt ggatcttctt catcaatgga gtcatttgct tcttgaatat catggcagcg 60

gaatagagaa ggaagaaaga tgattggaga ccccacttca aggagatgat gagtcaagaa 120

gaagctcacc accacaggaa gccatggata agagcttgaa ggaaggcgaa gatgagtgga 180

gggagaggga gagaaggggc acgaaatttt atgcctcaaa tgaggtctga actttgaagt 240

gtaattctca aatgatcaaa gttcaaaata atgcacacac atggcctcta tttatagcct 300

aagtgtcaca caaaattgga gagaaatttg aatttctatt caaatttcac ttgaatttga 360

aattgaattt gtggagccaa aatttcaata attatgatta atggaattta gatatggttc 420

agcccactaa tccaagatca agtccaagat tcttcactaa gtgtgcttag gtgtcatgag 480

acatgtaaaa catgaatgac atgcacaagt gtgactatat gatgtggcaa c 531

<210> 376
<211> 354
<212> DNA
<213> Glycine max

<400> 376

agcttgttgg agagagcaat gtcaatattg tcatcaactt cagccctaat agttgggcct 60

ggaaactgac cgttgattcc catcagaacg tgttccaagc aatctggttt tctgatcatg 120

tactccacat caaacttgta gtgtctcact attcctccga ttgacaattc taccaaaccc 180

aaccatatta tgcacccaac aaaaagagct ttgaagctca ttcttaatta attttgatca 240

gagaaagcct aattagcaat ataacaggaa ggtatcaagt agtagaacga agctattgat 300

gaacaaattg aaagaatagg tatagaggat cgaggatttg gattgctggt accc 354

<210> 377
<211> 248
<212> DNA
<213> Glycine max

<400> 377

ctcagtccct gagaaactga ttcccagaag acaacaggga gtgtttattg ctgaaaaccc 60

tagccttgca acaagttcta gggaagtaga caaggagatg gacaagaaaa tccgcagtat 120

cgtgagtagc attttaaaag acgcctctgt tcctgaagct gatgaagatg ttccaacatc 180

ttccaccccg aatgtttctg tgcctgatgt tgagaaagat gttccaacat actttcggtc 240

caaatgct 248

<210> 378
<211> 333
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 378

agctttgagc anattcaaac gacaataact nttgactgtt ttttccgatg tgccccgtag 60

gaaattgagc cgctcggaat tgaaaaacgg aggctctgag aacaaactaa cgacaataac 120

ctttaactcg gatgtctgat agaaccctgt aatatatcaa gacgctcgaa attgaaaacg 180

gaagctctaa taaaagtcct acgacactaa cttttgactt cgatgtccga ttgagccccg 240

taatatatcg agacgctcct aaacgaaaac agaaactttg accaaattct aacgacaata 300

acctttgact tcgatgtccg actgcgcccc ctc 333

<210> 379
<211> 395
<212> DNA
<213> Glycine max

<400> 379

tgactagttt gcaaaatggc atacttgaaa tatatatgtt ggatcaagtg gcctcggaat 60

aattaagaag ggggggttga attaattatt gatgtgcctt gactaattaa aaatctatcc 120

ttcttaatgt tactagattt aattaagttt ttactacaaa gttaagaaag taaagaacag 180

taattgaaac ttaaccaaaa gtaaaaacga taattaaaag agcacaacga aaattaaaag 240

tgtagggaag aagaagacaa acactataat tttatactgg ttcggcaaca acctgtgcct 300

acatccagtc cccaagcgac ctgcggtcct tgagatttct tttcaacctt gtaaaaacct 360

ttacaagcaa agatccacaa gggatgtacc cctcc 395

<210> 380
<211> 474
<212> DNA
<213> Glycine max

<400> 380

tgttgattta agcacagata atccatcaat tgcttctgat ggtttagcag catttcagcg 60

tgtaagcaaa ttgacaagaa aagtgaacct ttttgaaaag gattatatct tcatccccat 120

aaactatagt cttcactgga gtttgaatgt catttgtcac cctgctgaag tcatgacatg 180

ctacagagat gaagaaacta aaggatctcc caaagaagct tgcatcttgc acatggattc 240

ccgaaaagga attcatcaag atctacacaa tgttttccaa agttatctat gtgaagaatg 300

gaaagagagg cacaacaatg tgagggatga tgatgtttct tctatatttt tacatcttcc 360

attcgtgcca cttgagctgc ctcagcaaca aaatgcatac gattggggca tctttttgtc 420

cactatgtgg aacgttttct ggacatgctt caatcaactt caaccgtcca tgat 474

<210> 381
<211> 647
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 381

ccgcaagctt cctgcacaat gactatatta ttaagatttg ttctcaagct ggtataatct 60

tatcatgctt cagcgagtca gtggcactta cactaatcaa gtgtcaagta ccaacgaagc 120

atcagtaagg aaagttagtt tacaataatt tatctccaca agtaatactg agttctggca 180

acaaagaaaa accataccaa gaataaatta gaaaaggcac aaaacagtct accttgcatc 240

aggaattcca tggcagatta cttcattaac tgacctgtta gataaagcaa atttcattct 300

taacatatac catggcaata agagaaaaat atgacattac agaaggaaag tacctacgtg 360

cagcaagatt tagggaagaa aaggtaattg agaggtgatg gatatcctcc tgaaaaagta 420

aaaagtcaga aaaaaattca ttaccaatga ccatttgtaa tagccatatg acaatgacat 480

catgaaactc aatgaaccat catttggaag aggaattata acaaagttag gaagcatcct 540

ctctgtaatg ctcaaggctt ttttttgact ttttcaaatt ctggtaagca gatagcagcc 600

ttgatataca ttntggtatt tttttggccc ccccttctct gacccat 647

<210> 382
<211> 344
<212> DNA
<213> Glycine max

<400> 382

cttttctagt tagagaccaa cgtcttgggg ctaatgtatg atctgctcaa ggacctacag 60

gtttaggtaa atatctaatg cgttccccga caggagaagt tatttttggg ggagaaacta 120

tgcgtttttg ggatttgcgt gctccttggt tagaacctct aatgggtccg aatggtttag 180

acttgagtag actgaaaaaa gatatacagc cttggcaaga acgccgatct gcggaatata 240

tgactcatgc ttctttaagt tccttaaatt ccgtgggtgg cgtatcttca gagattaatg 300

cagtcaatta tgtctctcct agaagatggg tagctacttc tcat 344

<210> 383
<211> 187
<212> DNA
<213> Glycine max

<400> 383

agcttggtct aaaattcccg aaaaattagc tttttatgat tatatcggaa ataatccagc 60

aaaaggggggg ttatttagag caggttcaat ggacaatgga gatggaataa ccgtcggttg 120

gatacgacct tctgtgtata aagaaaaaga tgggcatgaa ctctttgtac gctccccccc 180

ctccttt 187

<210> 384
<211> 546
<212> DNA
<213> Glycine max

<400> 384

ttctccacta agttgcctga tgcctgaaat gtcttttctg atggcagtgg tcctagatgc 60

agggaagaat ttctccaaga acaccctctt aaggtcatcc cagctgaaaa tggacctggg 120

agcaaggtag tatagccaat ctttggccac tccctctgga gaatgaggaa aagtctttag 180

aaagatatga tcttcttgga catcgggggg cttcatggtg gaacaaacaa tatggaactc 240

cttaagatgc ttatgaggat cttcacctgc aagaccatga aacttgggca gcaaatgtat 300

tagtccagtc ttgagaacat atggaacacc ctcatcagga tattgaatgc acaagctttc 360

ataagttaaa ttaggtgcaa ccatctccct aagagtcctc tcacgaggtg gagggtgagc 420

catgttctaa gtaggaaaat tagtagtgga atgctcacaa ttagatattc agaatcaccc 480

ttaacagaat gctcaaaatg cacagaatga ccaggatgca cactatgcct aactaatcta 540

tgaaag 546

<210> 385
<211> 435
<212> DNA
<213> Glycine max

<400> 385

tgccttgccc cttgatatat ttgagggact catggtcact atgaatgaca aattccttgg 60

gataaaggta gtgttgccat gttttcaaag cccgtactaa ggcatacaac tccttatcat 120

aagttgaata gttaagggta tgaccactta acttttcact aaaataagca attggatggc 180

cttcttgcat caacacagcc ccaatcccaa catttgaagc atcacactca atttcaaaag 240

atttttgaaa gtttggcaac gcaagtatcg gggcattagt aagcttttgc ttaagaacat 300

tgaaagcttc ttcttgtttc tctccccatt tgaaaccaac atttttcttg agcacttcat 360

tgagaggtgc tgccaatgtg cttaaatcct tcacaaatcg tctattaaaa cttgcttagc 420

catgaaaact tccta 435

<210> 386
<211> 323
<212> DNA
<213> Glycine max

<400> 386

agcttcttac aagagactaa gaaatttttg acgaaatttt tttagaggaa agatcttggg 60

gaagcctcga tcttgcggaa gcctcttttg tattaggaat caagatatta agagatcgct 120

cttaaggtat cctaaggttg tcacaaaaga gttatatcga taaggtccta gatagattca 180

acatgaaaga tagtaaacca ggagatatcc cgatagctca aggagacaaa tttagtctca 240

aacaatgccc caataatgac cttgaaagaa tagagatgca caagattctt tatgaatcaa 300

cagttggaag tctactgccc cct 323

<210> 387
<211> 504
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 387

taagaccatt tctaatgggt tagataatnt atttttaatt gtttatccta tgctaattag 60

tccttataat atcacattat aattaaataa tttatatatt tcttgtttca ataagtaatt 120

cttaaataat aagaaaatat tttttctcat aagtaattat tattatatat atataattat 180

aggttaattt taaacaattt aatgtgacat ataaataatc taccatagtt aaaaaaatta 240

acaattatat ctaaaaataa accaatcgtt aaataatgag cattgaagat gctctaagat 300

aggaatactc ccataaataa taaatcatgc cattatgtta ttcctgtatg aatatctaat 360

catgtttctt tttttactcc ccaattttat tacctatata tcctttgaaa aatatactat 420

aaatattttg atgtattttt taagagaaca aaggctcctg gtttaacaaa aagccaagac 480

aggggaatta aggccattta aaaa 504

<210> 388
<211> 293
<212> DNA
<213> Glycine max

<400> 388

atgcaagctt ttaactggga aatgctccaa gaaacactat cttctttttc cgattctctg 60

gctgcttgct ccagtaaagc acaagaagaa atatgagcac cagcagattg ccccattaga 120

taaatcctat tacatagtaa caaaaaaaag gaaaagataa atctcagttg aatgtctaaa 180

tatatgatga aaaggaatct tgtatcatag tagcacgcca cctattaggg tcacctccat 240

aattagctat gttgttgatg atgaacgaaa ttccccgcga agtatcattt acc 293

<210> 389
<211> 605
<212> DNA
<213> Glycine max

<400> 389

taagcttgca aactagcttg tttaaataat aataataata ataagaataa ttattattat 60

ctataccatt tttatggcat tatgaatgac agtatgaagt agcataatgt gcttagagag 120

ttcacttgca ttggaaaatt ttcaaaaaga aaaaaactta agttaaaagg ataatgcaac 180

cagattaata cttccaaaga aaaaaatgtt ttgtaaaaac attttcagac aatttaaata 240

tttttatttg actatattag tataaatcat ctctaatcca tatattttta atattatgtt 300

ctttttttt cattttcttt tgatatactt tgtgttttaa taacttgaat tcaatatgat 360

tttgtttatc aattattttt ggatttgtgc attacttata cgaaatttta taagtttctt 420

cttttggtta gtatgttagt atttcacgag gttttaaaat aattaattga ttaaagacgt 480

ctttaagcag actcttaaat aggttcgtag gccgataagc cgagtcgagc ctttaaaaaa 540

agctatgaca gataatgagt cgaactcaaa tcttacgtag ttaacttaag tcaaactcca 600

atcta 605

<210> 390
<211> 419
<212> DNA
<213> Glycine max

<400> 390

tgcctgaaac tatatgagat ccctttgtcg ttgccttcca actagggtta agcttaagga 60

gaacccaatc tcctatctgg tagttcactt cacgacgttt cccatcagct tggcttttca 120

tagcagcttg ttccttagaa gcttatttcg aatagcttgg aaagtgttat ccctatcagt 180

taacatctct tcaacggcct caatgttcga agaccctgta atatattcag gaaagttaaa 240

gggttttcgg ccaaaggtga caccatactg attggctcca gttcccgcat tccatgaagt 300

attatgggac cattcgaccc acgggaggag ctatcccccc atgcttggcc cacgatggat 360

gaaggctcgc aaatattgtt caattatgca attcaaaacc cttgtctgtc catcaattt 419

<210> 391
<211> 573
<212> DNA
<213> Glycine max

<400> 391

agcttccaag aatcaagatc aagattcaag atttaatatt catgaatcaa gagaacactt 60

aatcaagata agtatgaaaa agtttttca aatactaagt agcacatgga tttttctcaa 120

aatctgttta ccaaagagtt tttactctct ggtaatcgat taccagatta ttgtaatcga 180

ttactagtag cgaaaatggt tttaaaaaaa cttttaactg aatttacaat gttccaattg 240

atttcaaaat gttgtaatcg attacaatgt tttggtaatc gattaccagt gtgcttgaac 300

gttgaaattc aaattcaaat gtgaagagtc acattctttc acaaaaaagc tttgtgtaat 360

cgattaccag tgaaagtttt tgaacaaatc aaaagatgta acttttaaa tagtttttga 420

ctctttcaaa ttggctttaa gtttttctaa aagtcataac tcttctaatg gttctcttga 480

ccagacatga agagtctata aaaacaacgc tttgttttgc attcttacag ctattcaatc 540

caatcaatct tatacaatcc tttacaagcc ctg 573

<210> 392
<211> 453

<212> DNA
<213> Glycine max

<400> 392

tccaccttct atgtactcat aaatcagtat cttctctgaa ccatttaggc accaaccgta 60

gagtgtgacc aggtttggat gtggccaacc aaagccatga ccactcagaa cctccatttc 120

agccttgaat tccttctcac cctcaagacc ttccctttga agcttcttca ctgccacttg 180

tctgccatct gaaaacactc ccttgtacac tgttccaaac cctccttttc ctataactct 240

gtcctctgag aagctgctag ttgctttcag aatgtcggca tgtgtgaaaa ctgtcttgtt 300

cagacggata accttaactg tgtcagacat ccatgatgag gatccggagc tgctggaatc 360

atgccattgt tttgtatccc tcaagaggta tcttggttcc tctgaagggc ttttcaccga 420

tacacagact aggatcgtaa gaagcccgat act 453

<210> 393
<211> 548
<212> DNA
<213> Glycine max

<400> 393

agcttgtgca tccaataccc tgatgaggat gtcccatttg ttcttaaaac tagacgaatc 60

catttgcttc caaagtttca tggccttgca ggtgaagacc tgcacaaaca tctgaaagaa 120

ttccatattg tctgctacac catgaaaccc ccagatgtcc aggaggatca catatttatg 180

aaggcctttc ctcattcttt agagggagtg gcgaaggact ggctttatta ccttgctcca 240

cggtccatca cgagttggga tgacctcaag agagtattct tagaaaaaaa atttccctac 300

ttccaggacc acggtcatca gaaaggatat ttcaggcatt agacaactca gtggagagag 360

cttgtatgaa tactgggaga gatttaagaa actatgtgcc agttgccctc accactagat 420

ttctgagcag cttctcctcc aatattttta tgaaggactc aataacatgg agaggagtat 480

gatagatgct tgccgtggtg gagctcttgg agacatgacc cctgctgaaa ccagaaattt 540

aattgaga 548

<210> 394
<211> 230
<212> DNA
<213> Glycine max

<400> 394

tccattattc aaaagttgcc tgtgcttctt caacccgtgg ctgttaatgg taatttagtc 60

cccctcggac aaagaaaact gatgtgtaat gatgactgtg ctaagttaga gcggaaaagg 120

gttcttgcag atgcttttga gattaccgct ccaaatctgg attcactcca ttttggtgag 180

aattcggttg cttctgaatt gctggctgac atgttgagac gtgattctaa 230

<210> 395
<211> 466
<212> DNA
<213> Glycine max

<400> 395

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ctttacaagt tgccattgcg ggttcccaaa gatgaccaag aatatgctgg tttatgggga 120

ggaacttttg gttggcctcc tggaaagcct tctgaagaca agcctggaaa ggctttattc 180

tttcttctgc tcttttatga ggagttccag ggacaacagc ttcttattgc aacaaaaatt 240

ttggaaggca cacactatgt gttacatcct aacgtgtcag caatgtttac agcaaatatc 300

aatgatcctt catccgaacc ctttccctgg gacactgatg cagactcggt tccagtgaat 360

atcaagcaag ctttcgtggg agagggtatt gcaagtggtt acgggttcag ataccctgga 420

tcaaagcctg gttccctctt tgttttagaa aatggtatcc ttgcct 466

<210> 396
<211> 430
<212> DNA
<213> Glycine max

<400> 396

taaacattca acttcgagcg tctcgatata ttacgagtct caatcaatca tccgagaaaa 60

aagttattgt cgtttgaatt tgctcagagg ttcaacattc aattttgagc gtctcgatat 120

atgacgggac tcaatcagac atccgagtag aaagttattg tcgtttgaat tagctcagag 180

cttcaacatt caatttcgag cgtctcgata tgtgacggga ctgaatcaga catccgagta 240

caaagttatt gtcgtttgaa tttgctcaaa ggttcaacat tcaatttcga gcgtctcgat 300

atattacggg actcaatcag acatccgagt aaaaagttat tgtcgtttga attggctcat 360

agcttcaaca ttcaatttcg agcgtctcga tatatgacgg gactcaatca tacatccgag 420

tgaaaaggta 430

<210> 397
<211> 461
<212> DNA
<213> Glycine max

<400> 397

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atatatcgag acgctcgaaa ttgaatgttg aagctctgag ccaatccaaa cgaccataac 120

tttttactcg gatgtctgat tgagtcccgg aatataacga gacgctcaaa attgaatgtt 180

gaagctttga gccaattcaa acgacaataa ctttttactc ggatgtctga ttgagactcg 240

taatatatcg agacgctcga aattgaatgt tgaagctctg agccaattca aacgacaata 300

actttttact cggatgtctg attgaggccc gtcatatatc gagacgctcg aaattgaatg 360

ttgaagctct gagccaattc aaacgaccat aacttttac tcggatgtct gattgagccc 420

cgcatatatc gagacgctcg aacatgaatg ttgaacctct g 461

<210> 398
<211> 553
<212> DNA
<213> Glycine max

<400> 398

tgcatccatg tgcactagtt attgtattat tgaagagaaa gaataaattt gaggtagaga 60

ctacagagtg tagcatacat gtccacttgc tgtttctgac agttggcggg tccataaatt 120

tgaaagattc aatgaaccat ctttcagaga cattgctatt cccattgttg cagctgagtg 180

tgatgataga ttgctggaat atgaagcaca agaaacatta aaaggattgc taaaacaggc 240

aaaagagtat gttcaatttg atttactgaa tacaaaatta cccaccgagt tgtttgcacc 300

ccgattagtg cacgcagacc agccgaggcc acaacctcta ctgacgaaac ttctgaaagt 360

tgatgcctaa acacagcagt agcagctcca ccaccttcat ctccattcac tgctaaatta 420

cctccaatcg taacagcatt gtgctttgat aactgagaac tgaattcact tgtcatagcc 480

attctgatac tcataaacgt aataaaatac acaaacaatc agaccaaaaa caaagaagtg 540

cttaacacat taa 553

<210> 399
<211> 357
<212> DNA
<213> Glycine max

<400> 399

agcttctata gaaggttcat tcctaatttc tctacaattg catcacctct caatgagctg 60

gtgaagaaga atgtggcatt taccttgggt gataaacaag atcaagcctt tgctttgctc 120

aaagaaaagc ttactaaggc acctgttcta gctcttcctg acttttctaa aacttttgag 180

ctagaatgtg atgcctctag agtgggagtt ggagttgtat tgttacaagg tgggcaccct 240

attgcttatt ttagtgaaaa acttcatagt gccccccttc actaccccac ctatgataaa 300

gagctttatg ccttaataag agcccctcaa acttaggaat attaccttgt ttccaag 357

<210> 400
<211> 400
<212> DNA
<213> Glycine max

<400> 400

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tcttacgaaa gggggttgaa ttaagatatc acaaactatt tccccaatta aaaatttatt 120

ttactttcta ttcaagttat aaattccctt aaaaatgaac ttcttaaata ttgattcaaa 180

taaagcaatt tgaatatgaa tataaaacaa taataaataa aggagtttaa gggaagagag 240

attgcaaact cagacttata ctggttcggt cactcccttg tgcctacgtt cagtccccaa 300

gcaacccgct tgagagttcc actatcttgt aaaagcctat tacaagatct gaaccacaca 360

aggacaaccc ttcctttgtg tttagatttc tttacaacaa 400

<210> 401
<211> 111
<212> DNA
<213> Glycine max

<400> 401

agcttgcata actgaaacca tcttttgggg tattttattg gtaaaaacag cagcaccttc 60

aacagaattc attgaataac cacatggctt aaaagtaaag tcacaaatct c 111

<210> 402
<211> 387
<212> DNA
<213> Glycine max

<400> 402

aatactaagc tcgcttctac atttatcacc tttatagatg attgttcgtg atatatgaat 60

atttattcgc ttcataacaa aaataaagca ttggatccct tcaaagtctt taaggctgaa 120

gttgagaacc aatgtggtaa gaaaataaaa atagtgagat tagatagagg tggagaatat 180

tatggcaaat atactgagaa tggacaagca cctggtcctt ttgcaaagtt tcttcaagaa 240

catacgattg ttgcccggta cactatgcct ggttctccaa atcactatgg tgtggctaaa 300

agaacgaacc gaacattatt ggacacggta cggagtatgc ttagcaactc tgatcttcct 360

aaatacttgt gggctgaagc actaaag 387

<210> 403
<211> 426
<212> DNA
<213> Glycine max

<400> 403

tgatgaagag tgcttgacag cttttcagac cttgaatacc agtctcgtgt ctgctcccat 60

aatagtgaca cctgactgga gtaaagagtt tgagctcatg tgtgatgtcg gtgactatgc 120

aatgggtgca attcttggac aacagcaaaa caaggtattc catgccattt attatgccag 180

caaggtccta aatgatgcac aactgaatta tgccaccatt gagaaagaaa tgctcatcat 240

tgtttatgcc ttagagaagt tcggatccct atttgttggg ctccaaagtc atcatcttta 300

ctgatcatgc agctattaag tatcttctaa cgaagaccga tttggagcca agggtaatca 360

catgggttct tctgattcaa gagtttgata tagcgattaa agacaaatag ggctaagagt 420

aaagtc 426

<210> 404
<211> 609
<212> DNA
<213> Glycine max

<400> 404

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ccgattgata aatgagaaag agagctttct tgtctctctt tcttgactcc ttcaacgtct 120

cctttacacc ttggcttagc gaggcttcat cttgttcctc gaagccattc tctatgatat 180

cccacacatc ttgagctcct agtagcgcct tcatcttgat actccaatta tcatagttgt 240

tctttgtgag catcggcatt tggaaaggaa aacctccatt cgccatcttt tgaggatctt 300

gaagctctga taccactttg ttggaaataa ggctttttat gtttaggaaa agtgtttagg 360

aatattggag actttgaata ggaaggagaa ttctctatgg aggagagaac tttgtatttt 420

tgcttgatac aaatgtgtag gattacatct ctatttatac tactctaagg agaactctag 480

acacactaat tctagagagt tctcaactct agagatccaa agaggattct agagaatatt 540

aaaaccataa gaaatatcta gacacttcaa acactacaaa aattctctag aacatgaccc 600

ataattact 609

<210> 405
<211> 353
<212> DNA
<213> Glycine max

<400> 405

gcttaaggag accactttga acttttttcac gaacaatatg gcaatctaag tcaatgtgtt 60

tagtacgctc gtgaaaaact tggttaaaag agatctggat agcgattgat tgtcacacca 120

aaaattgggg ggtgaaccta ccaaacacgt aaatcttgaa ggagatatgt gagccattgg 180

agctcgcaag tagtggaagc caaggctcga tactcagctt cggaggagct gcgagacaga 240

gtgggctgtt tctttgagca ccaagaaata atggaattgt cgagatagac ggagaagccg 300

atgatggaac gtcgagtgtc atgacaaccg gcccaatcag aatcactgaa tgc 353

<210> 406
<211> 577
<212> DNA
<213> Glycine max

<400> 406

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tgtatcagaa aggtgtaata gaacattaat ggatatgatt aggagtatgt taatcaattt 120

gactttaatc atatctttgt ggatgtatgc cttgaaaact gtcatgtatt tgttgaatag 180

gattcctagt aaggcagttc caaagacacc tttgaactgt ggacaaatag gacacctaat 240

atgaggtacc tgcatgtttg gggttggcaa gcagaaataa ggatttataa tctgcaagaa 300

agaaaattgg atgcaagaac aatcagtggc tatttcatta gttatccaga gaaatcaaag 360

gggtatatgt tttattgtcc taatcataat atgagaattg tcgaaactgg aaatgcaaga 420

ttcattgaaa atggtgaaat cagtgggagt acagttccac gagaagtgga aattaaagaa 480

gttagagtgc aggtcctttt tgcttgggcc tctaacagta aggtgattgc tcttttaatt 540

ggtgttgcat aattaatgaa gaggagcaac acattaa 577

<210> 407
<211> 331
<212> DNA
<213> Glycine max

<400> 407

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tcaccggagt tgacaaagtc aatgatgatt tctcctgaga gcacctttc tctcacaaag 120

tgacagtcaa tttctatttg gttagtctgc tcatggaaga tcggatttga tgcaacgtgg 180

agagcaactt gattgtcgca tagtatcttg agtgtctcca aattttagtt ggtggagaaa 240

ttgcctagcc atgtaacctt ggatgcaata gctgccatag catgacactt agcttcaaca 300

ctggatatag caattgtttc tgcttcttac t 331

<210> 408
<211> 136
<212> DNA
<213> Glycine max

<400> 408

atacgcctga atcaacatcc gtgtgaaaag ttatgaccat ttgaatgttt cgaaagcttc 60

ctttgttcaa tggcgagcat atagacataa tgagagcccg aatctgacca ccgtgtgaaa 120

agttatgacc atttga 136

<210> 409
<211> 448
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 409

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ggctgatcat tagaattgat gaactcagtg gtaatctcct tggacaataa tttttctcga 120

atgaagtgac aatcaatctc tatgtgcttg gtcctctcat gaaagactgg atttgatcca 180

atgtggaggg ctgcctgatt gtcacaaaat aacttcattc gtgtaacttc acaaaacttc 240

aattcttgaa gaagttgctt aatccacata agttcacatg tgaccaaagt catagatcgg 300

tactcagcct ctgcgctgga tcgagcaaca acagtttgtt tcttgctttt ccaagagata 360

agatttcctc caatgaaaac acagtagcct gaagtagatn tcctatcaat aggacaacca 420

gcccaatctg catacaatat ccagatac 448

<210> 410
<211> 445
<212> DNA
<213> Glycine max

<400> 410

tcaacctaga ggagacggac cattccaagt gttggataat atcaacgaca atgcctacaa 60

gattgacttg cctagtgagt ataatgtaag tgccactttc aatgtgtctg atctatctct 120

ttttgatgca gatggagggg ccttgtattt gaggacaaat ccttttcaag aaggagggag 180

tgatgatgac ataaccaagg gcaaggacca tgaagcactt gaagggccca tgaccagagg 240

cagacttaaa caagcccaac acgtcataga gacaaggctg gtcatttgta tagctaccat 300

tgatgatgat tgaaggccca agtggagaaa gatgaatgcc cacaggcata ggcactacca 360

agactactaa ttgttgctga acgcccaagt taaataagtt tttagttata atttatttt 420

attgtaactt tggcccaaac tgttt 445

<210> 411
<211> 375
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 411

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cagtttcatg ctccatgtag gtgaattgtt ctgttttatt ttctgtggag ttttttttcta 120

tttacttggt gcatggtttt tcagttatgt caacacttgc attgcttttc agtttcatgc 180

aaccatggca tgatttacat tgcaaaattg aaggccgtgc tgcatatgat atactcacta 240

attntgagca gcgctggaga aaagccacca aatggtctga gatgggtcgg aaactcaaga 300

gagtatctaa cttgaacgat gattctttga tcaagataga acacatttct tggattctta 360

gtctttcgaa ttact 375

<210> 412
<211> 451
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 412

ntcccataga ccatctaaaa tggtgatatt ccaatgggag tcttgaaggt agtcctgtaa 60

gcccataggg catcatccaa cttcacaacc aatccttcct tgaggatgca acaatattct 120

ccagaatttt cttcaattct ttgttggata cctcggcctg gccatttttc tgaggatgat 180

aaggtgaaac taccttacgt ttgacattat aatgcccaat accttctaca actatctatt 240

gcagaaatgt gaaccctatc actgattatc actctggaga ccccgaagcg ggagaaaatg 300

tttctcttca ggaatttgat gacaatcttg gcatcattct ttgaggcaac cacaacttcc 360

acccacttgg acacttaatc aacaaccacc aagatgtact cattcccata agaggatggt 420

agagggccca caaaataaat accccaacag t 451

<210> 413
<211> 452
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 413

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tgtttgcaaa ttaaacaaat ccttgtatgg tttgaaacaa tcctctaggc aatggaataa 120

gagatttggt gaatttatgg ctcatataaa gtttcataga agtcaccatg atagctgtgt 180

ttacttcaaa ttttcttcta aagctgagtt tgtgatattg ctactatgtg ttgatgatat 240

cttgatagca agtaataaca agagtgaagt tgaaaaattg aaatgtagga tttgggaaca 300

actaggagga tattgggaat agaaatcaaa caggacagaa aaaggaaatt gttatatttg 360

tcttaagagt tatatatcag aaaagttctt gaaaggtttg gaatgtcaaa ttccaaacct 420

gtaactactc ctatgtctta gcagtttaag ct 452

<210> 414
<211> 450
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 414

tatgctgcan atatttacaa tagacctcct caacctcagc agcaaaatca accacagcag 60

agcaattatg acctctccag caacagatac aatcctggat ggaggaatca ccctaacctc 120

agatggtcca gccctcagca acaacaacag cagcctgctc cttccttcca aaatgctgct 180

ggcccaagca gaccatacat tcctccacca atccagcaac agcaacaacc ccagaaacag 240

ccaacagttg aggcccctcc acaaccttcc ctcgaagaac ttgtgaggca aatgactatg 300

cagaacatgc agtttcagca agagaccaga gcctccattc agagcttaac caatcagatg 360

ggacaattgg ctacccaatt gaatcaacaa cagtcccaga attctgacaa gctgccttct 420

caagctgtcc aaaatcccaa aaatgtcagt 450

<210> 415
<211> 418
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 415

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caggtatatc tagagtagtc atctacaata accgaagcat aataatttcc tctaatactt 120

atgggtctag aagaaccaaa aagatcttaa cgtaaaagtt caagcactct cgaggtagaa 180

actgcatttt tagatttgaa agatactcta tttgttttcc cttttgacat gcattacata 240

atccatcctt ttgaaatttt agctttggga gacctttaac taattcctta tagactagct 300

tatttagttg atccatgagg atatgagtta ttctcctatg ccaaagccaa gagagatcat 360

cattacttct taaacaagcc atgtngaagt gagatgcact ttctacatta agcatata 418

<210> 416
<211> 462
<212> DNA
<213> Glycine max

<400> 416

actaagcttc ttatccaggc acattcttgg tggtgaaact ccttcttcca tggcttattc 60

ccttgtggat ggagcctccc ctctcctctt ctcctttgcc ttccgctgca tctccatggt 120

ggaaaatcac cattgaagct caaagatcca gcctccatag aagcttcaca tgcaagcttc 180

catcagagtt agtgcaactc gatgtcaaaa caacctttct ccatggaaga ttggaggaag 240

acattttgat gcaacaacct gaaggttttg aaatggaagg gaagaaaaat tatgtatgta 300

ggttgaaaag gtttatatat gggttgaaac aatctccaag gaagtggtac cagagattcg 360

atgagttcat tattactcat gggtacaaca gaagtgccta tgattcatgt atctattata 420

gtaaggtggg ggatggtttt cgcatctagg tgctactcta tg 462

<210> 417
<211> 457
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 417

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tattntcaga ttgggaatgc ctctaacagc acctttgtca atgattttct tcatgcctct 120

taagtgcaga tgtccaaatc tttgatgcca tattctgact tcatcttctt tggaggatag 180

acatgtggag gagtaactgg tttcttgagg tgtccatagg taacagttgt cctttgatct 240

gctgcccttc attagaactt cactcttctc atttgtcacc aagcattctg actttgtgaa 300

gtttacattg aatccttcat cacacagctg actgatgctg atcaagtttg cagtcagtcc 360

cttcaccagc agtactttgt ccagactagg aagtccatca tggactagct ttcccattcc 420

agtgatcttt cctttagagc catctccaaa tgtcaca 457

<210> 418
<211> 466
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 418

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ttaaacattt tataacaacc ttctgaaatt tgaatttaaa ttttaaagac ctgtaatcga 120

ttacaacttg tgtgtaatcg attaccagac atgaaaattc aaatttcaaa tctaaagagt 180

tacaactctt cagaatctaa ctgtgtaatc aattacaata gttatgtaat cgattaccag 240

taaggaattt ttgaaaataa ctcccaagag tcacaattat tcaaaacgtt ntttggatgg 300

tcatcaaagg cctataaata ggtgacttgn ggtacaaaat tccttagatt tttcctgaac 360

aaatttttctt atcctctcaa taccaaattg tcttataagt ctaaaaaaag aattctttgg 420

ccaaaacact tgcaaattca gtaaggaatc ttgagtgatg ttcaat 466

<210> 419
<211> 443
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 419

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catccagtag aggtatgttt acctctactc ttctaaatgt ttccaagatc tccttctccg 120

cctcttccat tttcttgttg gaaattgctc ttggtgggaa tggaagaggg atatgctact 180

actgtaagtc agaattacca gtagaagatt cacctgcata gaaattgtta ggcaacttac 240

tctttaaatt tttgtcatca tctttttctg gagttgagtg acgttgggca ggttcatttg 300

cagatgagga agatgctact agttgaggtc cttgatactg ttttcccaac ctcaatgtaa 360

ttgcactcac attcttggga ttctgtacag attgagaagg taatctgtca gaattctggg 420

actggttttg atttaactat gta 443

<210> 420

<211> 443
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 420

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tacattcatc aggaaaacat cagagtggaa ggaaattgca gtgctgtgat ccagaagatc 120

cttccaccca agcataaaga tcctaggagt gtaacgattc cttgttcaat tggagaagtc 180

aatgtgggaa aagctcttat tgacctgcga gccagtatca atttgatgcc attctccatg 240

tgcggaagat tgggagagtt ggaaataatg cccactcgaa tgactntaca attagctgac 300

cgctccatta ccaggccata tagagtaatt gaagatgttn tggtcagagt aaaacatttt 360

aacttcccgg cagactttgt ggtaatggat atctctgaag atactgacac ccctgtatta 420

ttgggaaggc tattcatgtt gac 443

<210> 421
<211> 180
<212> DNA
<213> Glycine max

<400> 421

aatgaagtga aatccaacat ctatatgctt ggttctatca tgatgaacct gatccctggc 60

catgtatata acactaaggc tatcacagta gatattaaca tactcttgat taataccgag 120

atcatttatc agacctctta gccaaattcc ttcctttggc agcttcagta agagtcatat 180

<210> 422
<211> 469
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 422

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gtctaggtat tcccgaagaa aatctgcctc accgtgataa aaaatgagaa ggatgagctg 120

attcctactc gagtgcagaa cagttggaga gtatgcattg actataggag gctgaaccag 180

gttaccaaaa aggaccattt ttcactgcca ttcattgacc agatgcttga acgcctggca 240

agtaaatctc actactgttt ccttgatggt ttttctggtt atatgaaaat cactattgct 300

cctgaggatc aggaaaagac cacattcacc taccccttgg acactttagc ttataggagg 360

atgcctttcg gcctgtgcaa tgcccctggt accttccagc ggagcatgat tagtattttt 420

agtgattntt tagaannatg catagaggtg tttatggatg atttcactg 469

<210> 423
<211> 424
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 423

agcttcaacc ctttcccaaa actcggcaag gtacgcgaaa tgttattccc actcagatcc 60

aacaatgtca aagatttcaa actagtccaa ttactcggta tcgtaccact aatatcatta 120

cctcccaacc ttatctcaac aagagaatct aacttggcaa cagaaggact caaagtccca 180

ctaagattaa acttttccaa aataatcatg tccacctttc cgtccccatt gcaccttatc 240

cccaaccatg gcccgtgaca agggtcattt ccactccaag aatcaaccaa aatccaagga 300

taccccaacc ctccaagaaa ctccaacaac accatcactt caaaagcaca cataaccccg 360

gcctttgcct cacaaaattc attgttctca taactcactt tactcgctgc anattccggg 420

atcg 424

<210> 424
<211> 311
<212> DNA
<213> Glycine max

<400> 424

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gagtctagaa gaagctcacc accataggaa gccatggata agagcttgaa ggtaagaaaa 120

gatgaatgga gggagaggga gaaagggagc atgaaattta atgcctctaa agaagtttga 180

actttgaaag ttaattctca aatgatcaaa gttgaaaaaa tgcacacaca tagcctctat 240

ttatagccta agtgtcacac aaaattggag ggaaatttga atttctattc aaatcttact 300

agaaatttga a 311

<210> 425
<211> 322
<212> DNA
<213> Glycine max

<400> 425

gcaaaccaat agcagcagaa taattatgac cttttaagaa acagatacaa tccaggttgg 60

aggaatcatc caaatccgag atggacaagt ccttcacaac aacaacagcc tatccctcct 120

ttccagaatg gtgctggtcc aagcaagcca tatgttcctc ctccaatgca gcaacagcaa 180

caacaacaaa gacaacaagc aactgaggcc cctcctcaac ctttcttaga agagttagtg 240

aggcaaatga ccatccagaa tatgcaattt tagcaagaga caaaagcctc cattcagagt 300

ctaacaaatc agatggggct ga 322

<210> 426
<211> 436
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 426

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gtgtttgcag cttctcccca aaaagccttt ggcagtcctg cacttagaag catgcacctt 120

actctttcca aaatggtcct gttcattctt tctgccaaac cattctgttg tggagtgtga 180

gggactgttt tgtgcctttt gatgcctatt ttcctgcaaa actcattgaa ctgctctgaa 240

acaaactcca ggccattgtc agttcttaaa acttttaatt ttgtaccaag ttgatttcca 300

acaagagtat gtcattctct gaatttttga aaagcttccg acttattttt canaacatac 360

agccatactc ttcttgagaa atcatctatg atggtgagaa agtatgagct tccaccatga 420

gttttcactc tagatg 436

<210> 427
<211> 416
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 427

agcttcatgc ttaactatgt atggcaaaac ttcattactg gtggtcaaga catacaagtg 60

agcttgtaac aaatcttcta cacttggagt gatcacatgc agtcctcttg aacccttacc 120

acccactctg tcatcatgtc gagactcaag aagcccaaca ggtttaacct tctctaagta 180

ttctgaacaa aaatcaatgg cttcttctac aatgtacctc tcaacaatag atgcttctgg 240

acgatataga ttctntgtat acccttttaa gatctttatg tatcgctcaa ccgggtacat 300

ccaccgtaga taaacaggac cacaacattn gatttctcta accagatgca caatcaagtg 360

aatcatgatn gtcaagaaag angggaaaa tacatctnca ctggcacagt ataatt 416

<210> 428
<211> 459
<212> DNA
<213> Glycine max

<400> 428

actaagctat gctgctacat ttatataaac ctccacagca gcatatcctt tatcagataa 60

ataattatga cctttcaagc aacagataca atccatgttg aaggaatcat ccaaatctga 120

gatggacaag tcctccacaa caacaacagc ctgtccctcc tttctagaat gttgctggtc 180

caagcaagcc atatgttcct ccttcaatgc agcaatatca acagcatcaa caaagacaac 240

aagcagttga ggctcctcct caaccttcct tagaagagtt agtgaggcaa ataaccatcc 300

agaatatgca atttcagcaa gagataagag cctccattca gagtctgaca aataagatgg 360

ggcagatggc tactcagatg aaccaagccc agtcccaaca ttctaacaaa tagtcttcac 420

aaactgtgca gaatctgaaa aatgtgagtg ccatcacct 459

<210> 429
<211> 333
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 429

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tcaagaggaa cctcactctt atgatgaggt cataagcaac aaggacaatt caaaatggat 120

tgaagctatg gaagaagaaa tgtcttttct aaaaaagaat tgtcctaaag ggcagtaaat 180

tgttggatgc agatggctat tcaagaggaa agaaggtttt gaaggagttc aaagtgtaag 240

gttcaaagct aggctagtag cctgtgggtt tactcaaaag gaaggagtag attntgtaga 300

aatcttctca cctatggtaa aacatagttc aat 333

<210> 430
<211> 339
<212> DNA
<213> Glycine max

<400> 430

gcccataggg catcatccaa cttcacaacc aatccttcct tgaggatgca acaatattct 60

ccagaatttt cttcaattct ttggtggata cctcggcctg gccatttttc tgaggatgat 120

aaggtgaaac taccttacgt ttgacattat aatgcccaat accttctaca actatctatt 180

gcagaaatgt gaaccctatc actgattatc actctggaga ccccgaagcg ggagaaaatg 240

tttctcttca ggaatttgat gacaatcttg gcatcattct ttgaggcaac cacaacttcc 300

acccacttgg acacttaatc aacaaccacc aagatgtac 339

<210> 431
<211> 412
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 431

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aatcactacg aggccaaaaa gattttgtgt ccagtgggaa tggagtacaa gaagatccat 120

gcatgcccta atgattgcat attgtataga aatgagtatg cagaactacg gcaatgcccc 180

acgtgtgggg tatcatgata caaagtgcaa catgatgaat taactgatga tgcaggaacc 240

aaaaattgtc gtcctgccaa ggtgtgttgg tatcttccaa taataccaag gtttaagcga 300

ttgtttgcta atacacatga tgcaaaaaac ctttcatggc attcggatga ccgaaaatct 360

gatggattac tgtgacatcc tgccgattcg ccgcagtgga agacaattga tc 412

<210> 432
<211> 455
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 432

ngtctctaca gaagaaagaa acaaaaataa gagtagattc attgtagata attctttgca 60

gtgatcaaga ataattatga accaaccaat caatcaacaa gcataaattg aaaattggtc 120

ccacattcta aaaatggtca tctcagtgct tcaaaaaaat ttctcaaaag aaatagaaag 180

tacaaaatca tacataaaag cttagaagca aagtttgagg gttttatctt acttttgata 240

tcctgtgtcc acacctttgc tggggatgaa ccaatttctt catctcccag agtgttattc 300

caattggcac tttctttctt caaatgacca agctcgctca acaaatattc aacattgatg 360

taatggcatt ccctccgagt cttccagaaa aggagttcca caaacaagag ggggtgcttt 420

ttcattntct ttagcatctt tctgaccaaa caagt 455

<210> 433
<211> 378
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 433

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ggattgctgc tcactccttt gagtattttg caattggtat ctctatttag atattttctg 120

agagaagagg tcaatggaag gcagcagctc aatcccagga atttattcga acactacagc 180

gttattataa caacacatat ttagatggtg ataagcaaaa agcaattaac ttgtaagtca 240

aataagccaa ttttttattt gtatttacaa ctgttttcat atgtaatatg gtttacagca 300

aacacaagtt atgtatatat gtgattgcat tataatgatt tactaattgg tgggtctgat 360

tttgtttggt tcacactc 378

<210> 434
<211> 420
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 434

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ctgagattaa ggataattgc attgtgttcc ttctgcaata gtgctttctt atccccatca 120

gccatcatct tttcgagttt ggcttctcca tcaagtgctt ccaccaggcc ctgctgaaca 180

agaaaagctc tcatcttcaa tcgccataac ccanaatcat tttgccctgt gaatttttca 240

acctcatact tggccgagcc catttcttga atcgaactca aaatcgatcc acactcaccg 300

caccaatttg ttgtgccaag atcagatttt acttcacaaa agaatgagtt tcttgtatga 360

acaagaataa gcaaaatgca gaaaaatgaa ccataaactg cacagaactc acaacagtca 420

<210> 435
<211> 397
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 435

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tcagggtcca cttggacccc atttctacca actaccaaac ctaaaaaaac tatattatct 120

acacaaaagg tacacttctc tatatttgca taaaaggtgt ttttcctaag gactgaaaga 180

acttgtctga gatggtctaa gtgatcatct agcctcctac tatacactaa aatatcatca 240

aaataaacaa ctacaaatct acctatgaaa tcccttaaga catgatgcat aagcctcata 300

aaggtgcttg gtgcattagt gagcccaaaa ggcatcacta gccattcata caaaccaaac 360

ttggtcttga aagcagnttt ccactcatca ccctttt 397

<210> 436
<211> 394
<212> DNA
<213> Glycine max

<400> 436

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ggactaccct ttattaaccc ccgtgaataa ctttgggaag gatggttact tggaaagcaa 120

tttaaaatga ggttttccaa ggaagcaaac ttatgagcta agaagccacc cgagctaata 180

catgctgaca tctgggggcc aatcaagcca agctcactag gtaaaaataa ctatttcctt 240

cttttcattg atgatttttc aagaaaaaca tgggtttatt tcttaaagca aaaattaaaa 300

gtcttttctt gcttcaagaa gttcaaagct gcagtggaga aagaaaatga tcaagatatc 360

aaagccatga ggactgatcg aggaggataa ttca 394

<210> 437
<211> 446
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 437

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acacttcctg agcaggtacg agcagttatg caagtgggat cagcaacttt cattatcaga 120

gtaatcaagc acagcggtat ctgtagtggc gacagcaaaa ttctgcaagt tgcaagtcgt 180

ttcccggatg tcaagacatc tcacgtgaca tcagctttct gctccccctg tctccatgct 240

cttactgctg tgaagcagtt cactgcagca tcttctatca gctactagtc ttttccagga 300

tgtcaagaca tctcatgtga catcagcttt ttgctccccc tgtctccatg ctcgtactgc 360

atcttctatc agctactagt ttcagtagct tacatcaatc atcatcagca gcagcagtct 420

gcccctagaa tcatatacat acaact 446

<210> 438
<211> 397
<212> DNA
<213> Glycine max

<400> 438

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ctctaatagg aaagctcacc ttcttgagat gagaagctag agcttagcta cacccctat 120

aatagctaag ctcaccccta tcccaaaaat acatgaaaat acaaaaaaaa agtccctact 180

acaaagacta ctcaaaatgc cctgaaatac aaggctaaaa ctctatacta ctagaatggc 240

caaaatacaa ggcccgaaag aaggaaaaac ctattctaat atgtacaaag ataagcaggc 300

tcatacttag ctcatgggct cgaaatctat cctaaggcta atgagaaccc tagggccttc 360

ccttggatct ctggcccaat ctacttggag tcttcta 397

<210> 439
<211> 421
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 439

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tntttctcac taacatctct ttttataaca ttaatctctt taatcctctc atttgtacta 120

attactttat cttacatttt tcttcctttt cttctcatct ccttttctat taaaaaagtt 180

gcccgatttt gttatataaa tgcaatttct cttttcattn taccaaactc tatataaaga 240

tattttattt gtttcaccag gacatatttg ctgctggaac tgatacttca gcatcaacac 300

tagagtgggc tatggcagaa atgatgagaa atccaagagt gagggagaaa gcacaagctg 360

aattgagaca agctcttcga gaaaaggaaa taattcatga aagtgatcta gagcaactta 420

c 421

<210> 440
<211> 437
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 440

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atttacctgn gtcaacttta tcagagagaa atcggacacc tttgaagtat tcaaggagtt 180

gagtctaaga cttcaaagag aaaaagactg tgtcatcaag agaatcanga gtgaccatgg 240

cagagagttt gaaaactgca agtttactga attctgcaca tctgaaggca tcactcatga 300

gttctctgca gccattacac cacaacaaaa tggcatagtt gaaaggaaaa acaggacttt 360

gcaagaagct gctatggtca tgcttcatgc caaagaactt tcctatgatc tctgggctga 420

agccatgaac acagcat 437

<210> 441
<211> 371
<212> DNA
<213> Glycine max

<400> 441

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agaataccgg cctcgtagtg atgaacaatg agacggagga gctgattcct actctggtgc 120

agaacagttg gagagtctgc atcgactata ggaagctgta ccacgttacc acaaaggacc 180

atcttcccct atcattcatt gaccacatgc ttgaacgcct ggcaggaaaa tctcactact 240

gtttccttga tggatgttct ggtcatatgc agattactat tgctactgag gatcacgata 300

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gcaaaggccc t 371

<210> 442
<211> 459
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 442

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catctcaata tattacggga cttaatcgga catccgagtt aaaagttatt gttgtttgca 120

tttgctacga gcttccgttt tcaattacga gcgtctcgat atattacggg actcaatcca 180

acctccgagt taaaagttat tgtcatttga atttgctacg agcttccgtt ntcaatttct 240

agtgtattga tatattacgg gacttgatcg aacattcgag ttaaaagtta ttgtcatttg 300

catttactca cagctttcgt tttcaatgac gagtgtttcg atatattacg ggactcatcc 360

gagttgaaag ttagtgtcat ttgaatttgc cacgagcttc tgttttcaat tntaagtttc 420

ttgatatatt tcgggactca atcggacatc cgagttaaa 459

<210> 443
<211> 454
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 443

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tccgattcag gtgcataata tatcgggaag cttgaaattg aacaacggaa gctcttgaga 120

aattcaaatg gtcataactt atcacacaaa agtccgattc aggcgcataa tatatctaga 180

cactcgaaat tgaacaacgg aagctctcga gaaattcaaa tggttataac ttatcacacc 240

gaagtccgat tcaggcgcat aatatatcga gacgctcgaa attgaacaac ggaagctctc 300

gagaaattca aatggtcata acttatcaca cggaggtccg attccggcgc atagtatatc 360

gagacgctca taattgaaca acgaaagctc tcgagaaatt caaatgctca taacttatcc 420

cacggaaggt cgattcatgc gcatgatata tcta 454

<210> 444
<211> 405
<212> DNA
<213> Glycine max

<400> 444

agcttggaaa tgaacaacag aagctcacga gatactacaa tggtcataac atgtcacacg 60

aaagtccgat tcaggtgcat aatatatcga gacgctcgaa atagaacatc ggaagctctc 120

gagaaattcc aatggtcata actttcaca cggaagtcct attcaggcgc ataatatatc 180

gagaagctgg aaattgaaca acgaaagctc tcgagagact caaatggtca taacttgtca 240

cacggacgtc cgattcaggc gcataatata tcgagacgct cgaaattgaa caacgtatgg 300

tgtcgagata ttcaaatggt cataacttgt cacacggaag ttcgattcag gcgcataata 360

tatcgagacg cttgaaatga acaacggaag ccttgagaaa ctcaa 405

<210> 445
<211> 430
<212> DNA
<213> Glycine max

<400> 445

ctacaatgga ttaggtatcc catttcaaca aaaaagattt acttaacaga ttaaattctg 60

caaaaatatt ttccaagttt gacatgaaat ccggattttt gcaaatccaa atacaagaat 120

cggataggta caaattgctt ttacaatacc ttttgggcaa tatgagtgga atgttatgcc 180

attcagtctg aagaacgccc cttcaacttt tcagaaaatt atgaatgata ttttcaatcc 240

ttattataat ttatcattgt ctacatgtgg aagcaatgcc ttccaagatt attttgatga 300

tgccaaagaa tcaagagtca tacaagtttc aagaatcaag atcaagattc aagattcaag 360

attcaagaat aatcatgatc aagattcaag attcaaataa agaatcaaaa ctcaagattc 420

aagaatcaag 430

<210> 446
<211> 410
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 446

gtctcacgat tgaacatgct catgcaacaa ttgttagtcg tggctatacg agacatcttg 60

ccaaacaaag ttaggttagc gataactcgc ctgtgattnt tcttccatgc tatatgtagc 120

aaagtcattg atccagtcaa gtttgatgag ttggaaaatg aggccgcaat tatactgtgc 180

cagttggaga tgtattttcc ccccgctttc tttaacatca tgattcactt gattgtgcat 240

ctggtcagag aaatcaaata ctgtggtcct gtttatctac ggtggatgta cccggttgag 300

cgatacatga agatcttaaa agggtataca aagaatctat atcatccaga agcatttatt 360

gttgagaggt acattgttga agaagccatt gaattttgtt cagaatactt 410

<210> 447
<211> 435
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 447

ntgatggtgt tgagaagaaa tcacatgttt gtcatcatca ttaaggggaa gaatgtgaat 60

gtatgtatac atgattttga tgatgtcaaa agaagaatca aacaaggctc gcttcaagat 120

taatacaaga ttgtttcaac aaacaaagcc ttgattcaag atttcttcaa gatcaagcct 180

tgcctcacaa tgaaaggttt caagtcattc aaggcacatg taatcgatta ccaatggctt 240

gaaagtgtgt aatcgattac acatcatatg taatcgatta ccagagactc tgaacgttgg 300

gaattcaaat tttaaatgaa gggtcacaac tgttcaagag aaacaactgt gtaatcgatt 360

acactaattc tgtaatcgat tactagagag gattttcaag agatatcgcc aacagtcaca 420

tcttatcatt tggat 435

<210> 448
<211> 347
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 448

agcttacccc tcattgtacc aacaagtgtc cttatgaggt tctctttggc tccaaacccg 60

attgccataa tctntgtgtt tttgggagtc tatgttatcc atggctacgc ccttactcaa 120

ataaaagcat gccatgtgtg tttctaggtc cctctcccca acaccatgca tacgaatgct 180

atcatattct aactcaaaaa atatacctct ctagacatgt tgtctttcat gaatcaatct 240

tcccctcact acgcctcatt tggtccctac cttcccaacc tcaaaccatg atatgacctt 300

acttatctct tgccatcctc tcatactaca acaactccat acaaaca 347

<210> 449
<211> 412
<212> DNA
<213> Glycine max

<400> 449

tctattctga atttcaagcg tctcgatata ctatgggact ttatcgaaca tccgagtaaa 60

aagttattat cgttggaatt tgctaagaac atccgttttc aattacgagc gtctcgatat 120

actacgggac ataatcggat atctgagtaa aaagttattg tcgtttcaat tttctaagag 180

catctatttc aattttgagt gtctcgatat attacgggaa tcaatcggca tctgagttaa 240

aagttattgt catttgaatt tgctacgagc atatgttctc agttacgagc gtctcgatat 300

accacgggac acaatcaaag atccgagtaa aaagttattg tcgtttgaat ttgcacagag 360

cttctgtttt cagtttcgag catctcgata tattacagga ctcaatcgga ca 412

<210> 450
<211> 403
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 450

ncaagcttga gcaaattcaa acgacaataa cntttcactc ggatgtctga ttgagtcccg 60

taatatatcg agactctcaa aatggaattt cgaagctctg agcaaattca aacgacaata 120

acttttact cgtatgtctg attgagtcct gcattatatc gagaccctcg aaattgaata 180

ccgaagctct gatccaattc aaacgacaat aacttttac tcggatgtct gattgagtcc 240

cgtaatatat cgagaacgct cgaattgaat attgaagctc tgaacaaatt caaattacaa 300

taacttttc ctcggatgtc tgattcagtc tcgtaatata tcgagacgct tggactagat 360

tgccgaagct ttgagcaaat tcaaacgaca atatactttt act 403

<210> 451
<211> 447
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 451

ntgaatgcac tattcaatgg agttgacaag aacatcttct gtctgatcaa cacttgcaca 60

gtggctttag atgcatggga gatcctgaaa atcactcatg aaggaacctg caaagtgaag 120

atgtccagat tgcaactctt ggctacaaaa ttcgaatatc tgaagatgaa ggatgaagag 180

tgtattcatg acttccacat gaacattctt gaaattgcca atgcttgcac tgccttggga 240

gagaggataa cagatgaaaa gctggtgaga aagatcctca gatccttgcc taagagattt 300

gacatgacag tcactgcaat agaggaggcc caagacattt gcaacatgag agttgatgaa 360

ctcattggtt ctcttcaaac ctttgagcta agactctcng atagggctga aaagaagagc 420

aagaatctag ctttcgtgtc caatgat 447

<210> 452
<211> 377
<212> DNA
<213> Glycine max

<400> 452

tgcttgaatg cactattcaa tggagttgac aagaacatct tcttattgat caacacttgt 60

ttagtggcca ttgatgcatg ggagatcctg aaaatcactc atgaaggaac ctccaaagcg 120

atgatgttca cattgcaact cttggctaca aaattcgaat atctgaacat gaaggaggaa 180

gagtgtattc atgacttcca catgaacatt ctatgaaatt gccaatgctt gcactgcctt 240

gggagagagg ataacagatg aaaagctggt gagaaagatc ctcagatact tgcctaagag 300

atctgacatg aaagacactg ctatatatga ggcccaagac atttgcaaca tgagagttat 360

gaactcattg gttctct 377

<210> 453
<211> 410
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 453

catcacatgc cattgcttcg ttgatgaggt tgctgtgatc gagatttgcg gcattatagc 60

gccacacgtc ttcaccgtga gcctttgcaa atgaggggtt gccattggcc atgacgcgag 120

cactcagact gtgccaaggt gccagcatta caggactact ctccagcaag agaaaactag 180

ccatgctgtg ttcgccgttt ctcatcaatc gacgagacag agctgattga gaatagcccc 240

tgctgcaccc gtcgcctttg aatatctttc tttgcaccaa gaacctcatg atgcgcttca 300

gatgtgaagt atcacaccct aaacttgatg atatctccga tagtgtcatg ggacttccat 360

gcttctctat ggcttcagct atgccaagct caatcgcaca ttntatcact 410

<210> 454
<211> 397
<212> DNA
<213> Glycine max

<400> 454

agcttcaaga ttaagatggc ctcagcaaat tccttatttc cggaagggaa ttctatcaat 60

agacctccaa tctttaatgg agagggttac cactactgga aaacccgaat gcaaattttt 120

atcgaggcaa tagatctaaa tatctgggaa gccatagaaa tagggcctta tatacccacc 180

acagtagaaa gagtttcaat agatgatagt tcatcaagtg aaagcataac catagaaaaa 240

cctaaagata gatggtctga agaggataga aaaagagtac aatacaactt aaaagccaaa 300

aacataataa catctgccct aggaatggat gaatatttca cggtttcaaa ttgtaagagt 360

gctaaggaaa tgtgggacac tcttcgatta acacatg 397

<210> 455
<211> 340
<212> DNA
<213> Glycine max

<400> 455

agcttcttag tttcagatga tactgctgag tttgtagcta cctcatgcac tcctctaatg 60

actatagcat catttatggc gctaaactgc tgggagttgg aagccatctt ctcaattaaa 120

tttctggctt cagcaggagt catgtctcca agggctccac cactggcagc atctatcata 180

cttctctcca tattactgag tccttcataa aaatattgaa gaagaagctg ctccgaaatc 240

tgatggtggg ggcaactggc acatagtttt ttaaatcgct cccagtactc atacaggctc 300

tctccactga gttgtctaat acctgagata tctttcctga 340

<210> 456
<211> 386
<212> DNA
<213> Glycine max

<400> 456

gcttgagaaa tatactaccc catgaagttt atcaattagt tcatcaacag cgggaatagg 60

aaagttatct ttgattgtga tggcattcaa ggccctgtaa tctgtgccaa atctccaagg 120

gccatccttc tttttgacaa gaatgattgg aggtgaaaaa tggcttctgc taggggcaat 180

aatcccttcc ttgagcatgt cagctatcat taattacttc aatctgatcc ttccggctgt 240

gaggatacct atatggcttg acttttactg gtccagcacc ttcaaccaat gggattgaat 300

gaatgtgagt tcttctaggg ggtaatcctg atggcaccat caagactgtt ctataagtgt 360

aaagtaaaca gttccgcaat ggcatg 386

<210> 457
<211> 247
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 457

tatcaccttt accagcgatt gaaaaaaact nttagcgaat gtcaagaaca tgaaagtgca 60

ccgatactat taattggtca gcagattctt aagcgggttg aggacattaa tacgatattt 120

cgaaagaccc aaaagaaaaa agtaaaactt gcatatggaa taagaggtcg atattctatg 180

atcttccata ttggtctaat ctagatgtca cacactgtat tgatgttatg catgtggaga 240

aaaatgt 247

<210> 458
<211> 420

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 458

agcttgaagg actacgttac acggatgaag gatggtcaga aggacattta ctacatcaca 60

ggagagagca ngaaggcagt ggagaactct cccttcttgg agagactcaa gaagaagggc 120

tatgaagttc ttttcatggt ggatgcaatt gatgagtatg ctgttggaca actcaaggag 180

tacgatggca agaaattggt ttcagctaca aaggaagggt tgaagctaga tgatgagact 240

gaggaagaga aaaagaagag agaggagaag aagaagtcat ttgatgaact ctgcaaggtc 300

atcaaggaca ttctgggaga caaagtggag aaggttgttg tctctgacag aattggtgat 360

tccccttgct gtttggcgac tggtgaatat ggatggagcg cacacatgga gaggatcatg 420

<210> 459
<211> 407
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 459

gaaatgacaa taactntata cacggatgtt ctgttgagtc ccgtttatat cgagacgctc 60

aaaatttaga tccgaagctc tgaaaaaatt gaattgacaa taactttata catggatgtc 120

cggctgagtc ctgtaatata tcgagacgct gcaaattgaa aacggaagct cgtaggaaat 180

tcaaacgaca ataacttttt actcggatgt tcgattgaat cgggtaatat atcgagacgc 240

tcaaaattga gactagaagc tctgagcaaa tttaaataac aataactttg tacacggatg 300

tccggctgag tcccgtaata tatcgagagg ctccacattg agaacggaga ctcttagaaa 360

attcaaacga cactatactt ttactcggat gcccgacaga gtgtcgt 407

<210> 460
<211> 386
<212> DNA
<213> Glycine max

<400> 460

tgaaggtttg tacatgacca aatctttagt taatcttctt tacctaaagc agtctttgta 60

ttcatttaaa atgcatgaag atagatcagt aggagaacaa ttggatttgt ttaataagtt 120

gattctagat cttgaaaata tcaatgtcac cattgatgat gaggatcaag ctttgctatt 180

gttgtgctct ttgcctaaga gttactctca tttcaaagag actctactgt ttggaagaga 240

cttcatttct cttgatgaag tgcaagctac tctgaattca aagcaattga atgaaagaaa 300

ggaaaagaag tcctctacaa gtggtgaagg gctgacagca agaggcaaga ccttcaagaa 360

agatattata tctgataaga agaagc 386

<210> 461
<211> 401
<212> DNA
<213> Glycine max

<400> 461

cttgagcaaa ttgaaatgac aataacttta tacacggatg ttcggttgag tcccgtaata 60

catcgagacg ctccaaattg aaaacggaaa ctcttataaa attcaaacaa caataacttt 120

ttactcggat gcccgacaga ttgtcgtaat ttatcgagag atgctccaaa ttgaaaacag 180

aagctcgtat caaattcaaa cgacaataac tttttactag tatgtctgat tgagtcccgt 240

aatatatcga gacgctcaaa attatgatcc gaagttctga gaaaattgaa ttgacaataa 300

ctttatacat ggatgaccgg ttgagtccct gtatatattg agacgctcgc aactgataat 360

ggaagctcgt atgaaatgta aacgacaata acttttttact t 401

<210> 462
<211> 341
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 462

agcttgtagt ttattcaaac gacaataact ttatacaagg atgtccgatt gagtgccgta 60

atatatcgag acgctccana ttgaaaatgg aaactcgtag caaattcgaa cgacaataac 120

tttttactcg gatgtccgat tgagccccgt aatatatcga catggtccaa attgaaaacg 180

gaagctcgta caaaattcaa acgactataa cttttcactc agatgtccga ttgagtcccg 240

taatatatcg agatgctcca aattgagaac gggagctcat agcaaattca aacgaccata 300

acttttttact tggatgtccg atggagtccc gtaatatatc g 341

<210> 463
<211> 426
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 463

tcntatttaa atttcgaacg tcttgatata ttacgggact ctataagaca tccgagttaa 60

aagttaatgt cctttgaatt ttctcggagc ttttgttttc aatttggagt gtctcgatat 120

attacgggac tcaatcggac atccgagtaa aatgttattg tcgtttgaat ttgctcagag 180

tttctttttt aaatttcgag cgtctcgata tattatggga ctcaattgga catcggagta 240

aaaagttatt gtcgtttgaa tttgctcaga gcttctgttt taaatttcga gcgtctcgat 300

atataacgag actcaataag acatccgagg aaaaagttaa tgtcatttga atttcttcga 360

agcttctgtt ttcaattttg agcgtctcga tattttacag gactcaatcg gacatccgag 420

taaaat 426

<210> 464
<211> 456
<212> DNA
<213> Glycine max

<400> 464

gcttatcccc taatgcacct attccattcc tcccatggtc atcatcacca taaacagcaa 60

taacctctct ccagccaaag tagttaacaa agtctgctat tgcagtcatt tcataaatgt 120

cactaaaagc agttctaata aagaatggga attgaagtga agaaagagta gggtcagtgg 180

ctgtaaatga tagtagagga acttggagct cgttcgctat atgagatatg acatgagctg 240

ttgtagacgt ctggggaccg attatagcca cagtttgtgt tgccatgagc tgcaaggcta 300

ttacacacaa tttatgtaaa ccaagagtaa taatctgcca aactttgaag taacttgtct 360

aatagaaaaa aagatgcttt taaagtttta acacataaaa aagatgggaa tattgtgaag 420

gacgtaccct cggcaatgct cagaaaacct ctgtat 456

<210> 465
<211> 449
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 465

tctgcaagct ggaaccattt atcctatctc cgacagccaa tgggtgagtc ccgtctctgt 60

agtcccgaag aaaaccggcc tcaccgtgat aaaaaatgag aaggaggagt tgattcctac 120

tcgggggcag aacagttgga gagtctgcat cgactatagg aggctgaacc aggttaccaa 180

aaaggaccat tttcccctac cattcattga ccaaatgctc gaatgcctgg caggtaaatc 240

tcactactgt ttccttgatg gtttttctgg ttatatgcaa atcactattg ctcctgagga 300

tctggaaaag accacattca cctgcccctt cggcactttt gcctatagga ggatgccttt 360

cggcctgtgg aatgcccctg gtaccttcca gcggtgcatg atcaatattt ttagtgattt 420

tttacaanat tgcatagagg tgtttatgg 449

<210> 466
<211> 413
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 466

tgacatgcta ttgaacaagc agttatatac tctgcttcac ttgtagagag tgcaacaaca 60

tcctgtttct tagagcacca ggagatggga gcacctccaa acaataaaac atgccccatt 120

atgctttttc tgtcaagaac atctccacca cagtctgagt ctgaataagc cacaagttgt 180

ggctcaacct tctctttcta atgtggaaat agaacaccaa agtctagtgt gctctcaagt 240

atctcagtat ccttttagct accatcatat gtgaatgtct tggatcactc ataaacctac 300

tgataactcc cacattgaaa gtgatttctg gtctggaatg acaaatgaat ctgagactcc 360

caacaatntg cctatacaag gtacaatcca ctacaggttc agctttacat tta 413

<210> 467
<211> 330
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 467

agccaaaaac tttaacaatg accanagcaa gacatctaca ttcaacttca gtacttgagt 60

gtgcaacaac aaattgcttc ttagaccact aacagatgag attggggctg aagaagacac 120

aagcgtcgaa ggtggaccat ctgtaatctg ggtcagacgc ctagtcagca tcacagaaag 180

tcacaataga aaaaaggtgc agaagcaagc ttgaaatgcg agccccacga gatggttccc 240

ttgagatacc gcggtatccc cttatggtat catagtgtaa cgccctgaaa tttcgctaac 300

tggaaatcga ttttaatgta tttctcatct 330

<210> 468
<211> 357
<212> DNA
<213> Glycine max

<400> 468

ctttagctat gtgtgctgat gttggctaca cagatagagc atctgaaatt ttttatgaaa 60

tgaaaagttc tgggacttgc agcctgaca gttggacatt ttcatccatg attaccatgt 120

attcccgcag tggtaaagtt tcagaggcag aagggatgtt gaatgaaatg atccaatctg 180

gatttcaacc tactattttt gttatgacat cactcatctg ctgctatgga aaagcaaagc 240

gaactgatga tgttgtgaag atatttaaac agctcctgga tgtgggcatt gttccaaatg 300

atcacttctg ctgttctctt ctaaatgttc tgactcaaac accaaaagaa gagcttg 357

<210> 469
<211> 445
<212> DNA
<213> Glycine max

<400> 469

tgaaggtaaa ctagatgcct tggttaacct ggtaacccaa ctggccatga atcaaatatc 60

tgcacctgtc accagactct gtggtttatg ctcctctgcc gaccaccaca cagacctttg 120

tccttctgtg caacaatctg aagcaattga acagcctgaa gcttatgctg caaacatcta 180

caatagacct cctcaacctc aacaggaaaa tcagtcacaa cagaacaatt atgacctctc 240

cagcaacagg tacaatcccg ggtggaggaa tgatcccaac cttagatggt tgaatccttc 300

acaacaacag caacaacaac cttattttca gaatgctgct agcccaagca gaccatatgt 360

tcctccacca atccagcatc aacaacaata acaacaacaa ccccagaaac agcaaacaat 420

tgaggctctt ccgcaatctt ccctt 445

<210> 470
<211> 400
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 470

catgcaagct ntntcacagt caactgtgaa gaccatgcaa ggattgcttc tggatntagc 60

ttcagctata acctcattag caatcaacac accatgaaga atatgccttc ctttcagaac 120

agcagtttgc ctttcatcaa tgaggtgagg gaaaacaaga gccagcctat tagccagaat 180

tttggacact attntataaa cacaccctat aagagagatg ggtctataat cattaagaga 240

ttgagggtta atgatcttgg ggataagggc tatgaaggaa gcattgcttc ctttggggta 300

taagccattg atgaagaact catccaagaa ccgaataaag tcaggtttta gaatctccca 360

naacttcttg ataaaattaa agttcaagcc atccgagcca 400

<210> 471
<211> 443
<212> DNA
<213> Glycine max

<400> 471

tcaagaaaaa tggcctcagc aaacttctta tttccagaat gaaattcaat caatagacct 60

ccaatcttta atggagaggg ttaccactac cggaaaaccc aaatgcaaat ttttattgag 120

gcaatagact taaatatttg ggaagccata gaaatagggc cttatatacc caccacagta 180

gaaagaattg caatagatgg aagcacatca agtgaaagca taacaataga aaaacctaga 240

gatagatggt ctgaagagga tagaagacga gtacaataca attgaaaagc caaaaacata 300

ataacatctg ccctgtgaat ggatgaatat ttcagggttt caaattgtaa tagtgctaag 360

gaaatgtggg acactctaca attaacacat gaaggaacta cagatgttaa aagatctatg 420

ataaacacat taactcatga ata 443

<210> 472
<211> 362
<212> DNA
<213> Glycine max

<400> 472

cctctgagtc acctgctgca tgcatgctag gaccgtgccc aagttgagcc tccaatatat 60

ccaccgttgg gaaatattag actttgagaa ctttagctac tattatatct tggttggtca 120

tattctctag ccttgcttcc ctaccacgac aagggtaaaa gcatgcagtt gtctaaacca 180

cataccttca tgttcctttt tcattatcat cttgacccac ataagccaat tgattccttg 240

tctttgtgga ttagagtccc accaaaaaga attcatcatc tgctacaatt catcttcaag 300

agtggaagga aacatataca cactcatgta ataagtgggt atagatcgag caacagattt 360

ta 362

<210> 473
<211> 430
<212> DNA
<213> Glycine max

<400> 473

cgcttggaaa atgatttcta tacaaaagtt agtcgtataa agcgactaac aaatcttcag 60

taatatcccg ccaaacccag aaaactccta atctcacaca cagacttaag actctcccac 120

ttaagtacaa cttctatctt agaaggatct atatctatac tgccttagga tatcacatgt 180

cctagaaaac taactttatc taaccagaac tcacacttgg acaacttagc ataaagttgt 240

cggttcctaa gggtgtgcaa cacaatcctc aagtgctctt catgctcctt tctagtcttt 300

gagtatacca aaatatcatc tatgaaaact accacagaac tatcaagata tgggtgaaag 360

atcctattca tgtaaactat aaacacacca ggggcattag tcacaccaat gggcatgaca 420

tactcatagt 430

<210> 474
<211> 445
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 474

agctntntat ttttagtaga tgaagatgaa ttcgtggcca cctcatggac tcctctaaga 60

acaatagcat catttcttga actgaattgt tgggagttag aagccatctt ctcaatcaaa 120

ttcctagctt cagtaggggt catatcacca agagctccac cactggtagc atcaatcata 180

ctcctctcca tgttgctaag tccctcatag aaatattgaa gaaggagttg ctcagaaatc 240

tggtggtgaa ggcagcttgc acacaatttc ttgaatcttt cctagtactc atacaagctc 300

tctccactaa gttgcctgat gcctgaaatg tctttttga tggcagtggt ccaagatgaa 360

gggaagaatt tctccaagaa caccctctta aggtcatccc agctgaanat ggacctgaga 420

gcaaggtagt atagccaatc ttttg 445

<210> 475
<211> 339
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 475

agctngcata cattattctc cttgcctgca tcttanaacc ttctggttgg gtcatataga 60

tgtcttcctc taaatcccca tgcaagaatg tagttttaac atctaactgc tccaagtgaa 120

gattctctgc agctactatg ctcagaataa ctctgatggt agtcatcttt acaactggag 180

agaagatctc tgtgaaatca attccttgtt tctgctgaaa ccctttcacc acaagtctcg 240

ccttgtatct tcttctaccg tcagattctt cctttagcct atagacccac ctattctgta 300

atgccttctt tccttctggc aatttaatta aagaccacg 339

<210> 476
<211> 417
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 476

gatgtttatg aattaattng acattatgtt atatntattg atgatcaact tgatagtaaa 60

ttaaaaaaat gtgaactcaa ttggcataag ctatacaata gaataaaatt atgcactttn 120

tacacatcac tgactaaata aaaaaaatgt tgtaacataa actaatttat catcacttta 180

catttctcaa gaacaaaagt gtttatttac accttctttt atctaatgaa attcatgtca 240

aattcattag ttaaggaata aaactcatta aataattaat aagtgatact acataattta 300

ctgaatttta cgtgattgta atttaataat aaaaatgtta ataatatatt aatatatatt 360

tatgaacctt nttcattgcc caataaaaat aaaaaagtta aataattatt gtaatcc 417

<210> 477
<211> 418
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 477

agcttattgg ttntgataat atcactagag aaaatacagc attaaaagta atttanacgt 60

aaaataatca tcaatcttta tactatgtct ctttcttgtc agatctcatt cctggtgatt 120

ttattcatgt tattggggat gctcatattt accgcaatca cgtgaggcct ttgcaggagc 180

agctccataa ccagccaaag ccttttccag tatgtgtaat gtttagcact tctttaagtt 240

tatcttttga ctctcttact tngttacccc ctaatgtact tcattgcaga ctttgaagat 300

aaatccaaag aagaaagata tagattcttt tgtggctgct gatttcaagc tcataggcta 360

tgatcctcac cagaagaatg atatgaagct gtctgtctaa natctgggga ttctcact 418

<210> 478
<211> 489
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 478

tcttcatgtc tctcctcgta tctctaacat ctaggactca tgtgtttatc atagtaaggt 60

ggaagatggt tcccacatct atctactact ttacacggat gacatgctta tagcatccca 120

aaatttgttg ccaattttga ggatgaagtt actactctat aatgaatttg atatgaagga 180

catgggagtt gctgaaaaga ttctgggcaa ggagaataag atggatgaag tccagaagat 240

gatcttctgt gtcagaagga atacattcaa aaattgctaa attgttttgg gatggcatcc 300

gcaaaaatag tatgtactcc cctaataacg tccattcgtt tatctatact caatactact 360

cagtcaaatn tagagaagga atacatgtcg tgtgttcctt atgcaagtgt tgtagctagt 420

ctcatgtatg ctacaccana ccanacctaa cacaagaagt aatggtgtga gtaagtatat 480

tggtattct 489

<210> 479
<211> 389
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 479

agcttcttag tttcagatga tgcagatggg tttgtagcta cctcatgcgc tcctctaatg 60

actatggcat catttctggc gctaaactgc tgggagttgg aggccatctt ctcaattaaa 120

tttctggctt cagcaggagt catgtctcca agggctccac cactggcagc atctatcata 180

cttctctcca tattactgag tccttcataa aaatattgga gaagaagttg ttctgaaatc 240

tgatggtggn ggcaactggc acatagtttc ttaaatctct cccagtactc atacaggctc 300

tctccactga gttgtctaat acctgagata tccttcctga tggctgtggt cctggaagca 360

gggaannatn tttctaagaa tactctctt 389

<210> 480
<211> 504
<212> DNA
<213> Glycine max

<400> 480

cgaatcgttt cagttggaaa aaatcccttg tgcatgaaga tcaaaggata tgaacacaca 60

aagatacatc accaaagaaa taaaataatg aaagatataa atttaaagca gatatctttt 120

atctacattc acacaaacat ctaaacaata ttcactatct caaattttaa tttgacaatg 180

aattacattt atcctctatt taataatgtc aaaataacaa taaattgata tcttgacaga 240

actataatta taataagagt ttaaaataat tgtacattat catctactca tcaatcattg 300

ttgttatgat ttttaaaata atttttatca aagtcaacaa acttatatca tagatgatga 360

ttgaatgata atgtaatctt acattatata atacttttc tcttataata acctatagca 420

aggataaatg cacacattga tccgatgcac agattattag gatcattata tagtatggat 480

tcattgggat gatcgatgat gctg 504

<210> 481
<211> 446
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 481

ntccacttgg cttctaactn ttcgactctt aacttataac ttataagctt ttaattaagt 60

ttataagcta attgtactaa atataatctt aatagttaat ttggtttgat aaatttatct 120

taaatttaca ttttatttta aaagagtaat aacattttaa cacccttttt ttctctccat 180

ctctttcttc ttattaaatc atattaccta tcttagatat actgtatact nttctttctt 240

ctctctcttc tttactcgaa gtgttccata aaacatgaat ctctctntat tntttattct 300

ntataaaaat gtcattatta ttaatattct tttctcttat gagtctcaat ataacctctt 360

ttgtcattta attaggagta ttttatttaa caataattaa tataattaaa tatgagagac 420

attcgccact tttaatttta tcttat 446

<210> 482
<211> 499
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 482

cgcatctttt actaaggcag ttntataaaa tcgtccttgt tttagtgtca tataatctca 60

cttttggagt agtgccaatt gcaatctatg tttctattga agatccttgg ccctttgaaa 120

tattttcttg gcttagaaat agctaaatcc aatagaggta tctcactctc ccaaagaaaa 180

tacactatat ctcttttaga agatacaagt ttcttggcat gcaaaccttc caatcttcca 240

atggatccaa acttgaagct caatcttcat gatggagact tactccttga tcccttagtg 300

tataaaacgt taattggtag attaatttat ctaaccatat cacgtcccga tataacattt 360

ggtgtaaatc acttgagtca atatatgaaa gaacatagag tntgtcacct aaatgttgtc 420

catcatcttc tgcagtatct cacatctact ccaggacaag gtttattttc cctgctcata 480

actctctcaa attcactgc 499

<210> 483
<211> 474
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 483

gcttactcca ggtttcactt gacgtcttct ttctatgcaa tgacgttctc taacgtgaac 60

actnntcttt ttatttattt taattnttta tgattttatc taatgttatg gaatgtctta 120

atttgttaat atttattatt aaatttctta ttatatttaa gtgaagaaat taatgatata 180

tgtaaagtga taattatatt tgatttagaa ttaattntac ataagccaaa tgagtgcaac 240

ttgtgcatag tgcatacccc taatttctta gttntaataa ttaattattt ntgtcgacaa 300

tcgattgtct tatgtaaaaa aatcaatttt ataacataat cgttgattat caaattgatt 360

gtaaaaaaat tatttatcat ctccttttntt ctttntttca aacgtactat atttctcact 420

tgttgttatt cattggattc tatttttttt tcttaatttc atctaacttg ttct 474

<210> 484
<211> 427
<212> DNA
<213> Glycine max

<400> 484

tctatccatg gcgttctatg gtggtgagct tattcttgac tcatcttctt tatgaagtgg 60

cgtctgcaat caccttttcca ctttctccat tccgctgcca ttgatcttca agaagtaaag 120

gactccattg atgaagaaga tccaaggcct aaaagctcaa catggagcta catcactagt 180

agtacttgtt ctttcctcct ccctaagcct aactctcaaa aggagtagtt ctatttgttg 240

cctatactct tcaacactca tactcccttt tctaagcctt tggagcttgg ccataagctc 300

cctttcatag taggagggga tgcacctctt cctaagggta gctttcaagt cattccaata 360

ctctactaga ggatcccatg aatccttctt ttcctaacaa gtgaagtcca cccatagagg 420

gcatacc 427

<210> 485
<211> 380
<212> DNA
<213> Glycine max

<400> 485

tgtgacattt gtcagcatca gatgtatagc gctatctcac ctgtaggatt gctgcaacct 60

cttgctattc cggaacaggt ctgggaggat gtatctattg attttatcac agggttgcct 120

tgttccagag gctatgaagc tattctggtt gttgcggaca ggctgaccaa atatagccat 180

tctgttccat tgaaacaccc ttatactgcc aaaggaattg ttgagatttt ctctgggaag 240

tactgatgct acatggagtt ccacaatctc tcgcgagtga tagagatcct ttatttatga 300

gtttgtcttg gaacgaacta tttaatttac acgcgacaat gctcaagatg agtacaactt 360

accttccgca gactgatgga 380

<210> 486
<211> 480
<212> DNA
<213> Glycine max

<400> 486

taacataagg catgtgaagt gggtggaatt cctagagcaa ttcccttatg ttatcaaaca 60

taaaaaggga aaaggtaata ttgtagccga tgctctttct cggcgtcatg cattactttc 120

tatgcttgaa acataattga ttggtcttga atgtttgaaa agcatgtatg aaaatgatga 180

aacttttgga gaaatcttta aaaattgtga aaatttttca gaaaatggtt actttagaca 240

tgaaggcttt cttttcaaag aaaacaaatt gtgtgtgcct aaatgttcta caagaaattt 300

gtcttgttgt gaagcacatg aatgaggttt aatggggcat tttggggtcc aaaagactct 360

agaaacatta caagaacatt cttataggcc tcatatgaaa aaggatgtgc ataaattttg 420

tgaacattgc attgtatgta aaaaggcaaa gtctaaggta aagcctcatg gactgatact 480

<210> 487
<211> 423
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 487

agcttctata gaagggttct tcctaatttc tcaacaattg cctcacctct caatgagctg 60

gtgaagaaga aggtggcatt tacttggggt gaaagacaag agtaagcctt tgctttgctc 120

aaagaaaagc ttactaaggc acctattcta gctcttcctg actnttctaa aacttttgag 180

ctagaatgtg atgcctatgg agtgggagtt agagctgtat tgttacaagg tgggcactct 240

attgcttatt ttagtgaana acttcatggt gccaccctca actaccccac ctatgataaa 300

aagctntatg ccttaataag agccctccaa acttgggaac attaccttgg tgtcaaggga 360

atttgcattc atagtgatca tgaatcactt aagtacatta gagggcaaag caagttaaac 420

aaa 423

<210> 488
<211> 404
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 488

agcttctatg ttcaatttcg agcgtttcaa tatattatgt gcctgaatcg gacattcgtg 60

tgaaaagtta cgaccatttg aatttcttga gaacttctat tnttcaagtt caagtgcctt 120

tatatatcat gggcctcaat cgtatatcca tctcaaaagt tatggtcgtc tgaattggac 180

aagagctttc gtgttgaatt tcgagcgtct cgatatattg tggacctgaa tcggacatcc 240

gagtaaaact ttatgaccat ttgaatttcc ctataacttc cagtattaaa tatggagccg 300

tttgatatat catgggactt aatcgtacat tcatgttaat agttatggcc gtctgaattg 360

gactaaagct tctgcgttca attttgagcg tcctgatata ttat 404

<210> 489
<211> 495
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 489

tatacatact caagctcgca caggagtgtg aggtgatact gagtattctt ttcaacaatg 60

actggccttc aattagtggg gattctgagg aagatgaata tggctccacg actggaaatg 120

aaagcaaagc gacgctgatg catgttccaa aagaacttgc tgaaattgac aacatggaga 180

acacgttcac caaactaact ctatcagcac tgcgtagctt ggaagaaatt atgggtagaa 240

gctcaactgt tagcattttc tcattgccta ctttgcataa ctaggctttg caactgcaag 300

aggattggaa aataaaatga ctgcactagc gactgcaacc aaataggtcc tcaggataac 360

atagatcttc tcgtgtttat cttcacatct atcttaatgt ttattagaan agaaatagac 420

acagaattta gacatgagtn gccatttata caagaggatc catctccctg tttaatggta 480

gatttcatat gaaac 495

<210> 490
<211> 357

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 490

actcatttta tatatagctt aaggtgtgtt tggtttgtat tttcattttt tgttttcatt 60

tcctgttntc agnttctgac actactagga ataaggttt ttacatcaat tatttaagac 120

tttcaacatc ggttattaac cgatgttgaa agtcccgatg ttgaaagtaa tatcgttaac 180

atctgttttt caaaatcgat ggtaactaat aaatacaaca tttggtattt aaatagccaa 240

tgttacatga taagaatttt gaanaaagaa atttataaat ttacatatca acatcgcgtt 300

atttaaaaac cgatgttaac tagcactaaa agtcaatgtt aactgtcact aacaaca 357

<210> 491
<211> 364
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 491

tgtaatcgat tacacaagtc ttgtaatcga ttaccagagt atattttcag aanataattt 60

ccaagagtca catctattca aatggtttat gaatggccat caaaggtcta tttatatgtg 120

acttggaaac acgaattatg agagagattt cattgcccaa aaagttttat cctctcataa 180

gattaagaga gtttttctga attgaaatgt cttatcctct caaaaagata ccttggtcaa 240

acacttgcat attcgataag gaattttgat tgatcttcat tgtataatct atctctttca 300

agggagatat cttcttctct tcttcttatt tctggaaaaa agggattaag agaccgacgg 360

tctc 364

<210> 492
<211> 442
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 492

ntntattgta atcttgagat tcaggacagc actctgattt ctgaaatatt tgggataaaa 60

atggtcattg accagtccct tttccatgac ttaaccaaat tacccagtga cggtgtacca 120

tttgaaggta cactgaatga cgactgaaaa tttgatttct ctgcccatga tgcccgccag 180

ttggtttgca ccaacaatgc ggatatgacc ggacgtcttc ttgccgggtc attggctttt 240

gaaagccgca tccttcacta tttaattgtg cgtattttgc ttccacggtc ttccaacctt 300

gcccaggttt ctgaggaaga tctaattatc atgtgggcct ttcatacagg gtgtcaactt 360

gactgggcac acttagtcag atatcgcatg cataaggcat tgcgaataaa tgctccatta 420

ccatatccac agcttgtcac tc 442

<210> 493
<211> 417
<212> DNA
<213> Glycine max

<400> 493

taacatcata tgaagccatg gataagagct tgtatgagga gatgatgagg ggaaggagaa 60

cgagagaatg agcacgaaat tttgtgcctc acatgaggtc tgaactttga agcgttattc 120

ccaaatgatc aaagttaaaa aaatgcacac gcatgacctc tatttatagc ctaagtgtca 180

cacaaaattg gagggaaatt tgaaattcta ttcaaaattt acttgaattt gaaattgaat 240

ttgtggagca aaattttgga gccaaaattt cactaattat gattagggga atttagctat 300

ggttcagccc actaatacaa gatcaagtcc aagattctcc actaagtgtg tttaggtgtc 360

atgagacatg taaagcatga aggacatgcg caaagtgtga ctatatgata tgacaat 417

<210> 494
<211> 416
<212> DNA
<213> Glycine max

<400> 494

tagcttgaac tatatgagat ttgaatctaa ttttacttgg atcaacaata taatatatat 60

ttaatttata gttgaaaata cggaaaaaca agaattttga tctattgata acatcatatt 120

tacctccatc gcaatgttat aatacgttct agaacatgct catattggtt tcgtaatagt 180

tgatattgat ttactcatag agctgaatat aagaacaatt gtcggtttta aagtacgtga 240

tattctttat aaaataaaac ggtggttata gttaatggaa ataataaaat taagaaatgt 300

actttattaa gctcgcgaat caatagctgt atttaaaaca atatgtctat tacttgttgc 360

ataacttgcc acgtctgtct tctaactgta cttgaatatc taatgacgga tatagt 416

<210> 495
<211> 318
<212> DNA
<213> Glycine max

<400> 495

gtttttgccc aaatggagac actggatgtc tgcctgtctc aagtcagcta gcatttctat 60

tcttatcaat ggcagtccta caaaggatat tgctcctact agaggtttga ggcaagggga 120

tcctttagcc cccttactct ttaatatagt tggagaaggc atcacaggat tgatgaggga 180

agcagttcag aagaacttat atataagcta tatggctgga aagaaaaagg aacccattaa 240

tattttgcag tatgcggatg acacagtttt tgtgggtgag gctgagtggg agaatgttat 300

tgttttgagg ctatgctc 318

<210> 496
<211> 433
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 496

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atattttgtg taggtaactg ttacacgtca attcttgtcc ccaaagatta tggattagag 120

attttaattt aggattccta taaataatat tataaagtta gaaacattaa aacaattgat 180

ttcagaaatt aatgtgaaag agattatgcc aaaattttgt tctggaacct ggataagatt 240

gctatatttt aaagtaaatt atattgtaaa ataatatcat ataaaggtaa ttttttattt 300

ggtaacatga aaactntata tgcaagtcaa aatccaaatt taaacatctt gtttctcaaa 360

taataataaa ctatattcca attttattaa ggggataccc ttctgggata tatatatata 420

tatatatata tat 433

<210> 497
<211> 362
<212> DNA
<213> Glycine max

<400> 497

ctgcctttgc cctgatatat cttgaggact catggtcact atgaatgaca aagtccttgg 60

gataaaggta gtgttgccat cgtttcaaag cccgtactaa cgcatacaac ttcttatcat 120

aaggtgaata gttaacggta tgaccactta acatttcact aaaataagca atcggatggc 180

cttcttgcat caacacaggc ccaattccca catttgaagc atcacactca atctccaaag 240

attcttgaaa gtttggcaac gcaagtatgg cggcattagt tagctcttgc ttaagaacat 300

tgaaagcttc ttcttggttc tctccccatt tgaaaccaac aatttttcttg aacacttcat 360

tg 362

<210> 498
<211> 225
<212> DNA
<213> Glycine max

<400> 498

agcttttcac tcggatgtcc gattccggag cataatatat cgagacgctc gaaattgagc 60

aacggaagct cttgagaaat tcaaatggtc ataactttcc acatggatgt ctgattaaga 120

cgcataatat atcaagatgt tcgaaattga acaacgaaag ctctcgagaa attcaaatag 180

tcataacttt tcactcggag ggtccgatca tgcgcataat atatc 225

<210> 499
<211> 484
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 499

ngctataata ttagttaaaa aatagtttat gaaatttatc acatattatt tttataaaat 60

aatcatacaa acattcatgt cataagataa aatacttaca aataaatctc aaacatatat 120

aatttttgtct ttataattaa taatttatgc tattgattta tgaaagtttg tgtatatgta 180

acctaactta atcttaaatt catcaattac aactatattt gataagacat ttcagttaat 240

ttttaatttt tttcactagc taaaaaattt gtttgactat ttagaaaaca agtttttttt 300

aatagtttct aacatttttt caaactattt gaagtaacat tntttaaaac cttagatttg 360

aaattctaac tttntatatt ttttttcatt gttatactta atatatttat ccaattntct 420

agttaccatt ttttaagaga tcataattgt attattngtc aatcatttta tctttttcaa 480

ctac 484

<210> 500
<211> 471
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 500

gtatggctcg aaacatgcac cgaggcagag gtacaagaag tttaatgagt ttatgagcaa 60

ctcaggattc aaaagatgtg acatggacca ttgctgctat gttaaaaaat atactaatag 120

ttatgttatc cttgctgtgt atgttgatga catgttgatt gcaggatcta gtatggcaga 180

aattaacagg ttgaagcagc agttggcaga taactttgaa atgaaggatc ttggtccagc 240

taaacaaatc cttggtatga gaattcttag aaacagatca gaaggaattn tgaagctgtc 300

tcaggagaaa tatatacaca agttgcttga caggttttac cttggagatt ctaagaccag 360

gaataccccct ttgggatctc atttgaaagt ttcaaagaag caatcttttg agacagatga 420

agaanaatgg tacatgtcaa gagtaccata tgcatcagca agtgggagtt t 471

<210> 501
<211> 363
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 501

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ggccttgatt ttcttagggt ccacttggac tccatttcta ccaactacaa accctaagag 120

aactatatta tctacacaaa aggtacctga aagaacctgc ctgagatgtc ctaagtgatc 180

atctagactc ctactataca ccacaatatc atcaaaataa ataactacaa atctaccaat 240

gaaatcccttt aagacatgat gcataagcct catanaggtg cttggtgcat tactgtgccc 300

aanaggcatc actagtcatt catacaaacc aaacttggtc ttgaaagcgg gtttccactc 360

atc 363

<210> 502

<211> 453
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 502

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catagttgtt gtttaggcgg ttatcgttat caaaattcta gaatgctttg taaagatgtt 120

catcaagtcc aagtctgtgc ctatgcattg tagtcgaaat gaattcaaga tagtcaattg 180

acccatttcc gtcaacatca gcctgaggaa aaaatataca tgtcttgcaa attgaaacaa 240

ttaggaacaa agcanaaatg catgacaaca aaaaatagta taaagatata ggaaatatca 300

tagtttaatc acaacattaa aaaaggctnt agctagagcc tacataataa taattataat 360

aataataata ataacaacga agcanacatg cattacaaca naacaaaatt aagaaataat 420

aaatatcagt gttaactcct attgtcacaa cat 453

<210> 503
<211> 385
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 503

tgtcctcggt gacgaanaca atagaataag cctcttcgag cttttcacag gcgtcaacga 60

ttcgaagaat gaagggtctg tgtttggagg tggcgatgag gtggaggaca acctcggtgt 120

cataggtggt gttgaagatg gagccgttgt cttcgaggtt ggttcggagg gtcttatagt 180

tgacgaggtt gccgttgtgg gccacgccga ctgagccgaa gcggtaaccg gcgacaaagg 240

gctggacgtt tttgagcatg gataggacgg cggtggagta tcggacgtgg ccgatggaga 300

tgctgccggg gagctggtcg agttttgatt ggttgaagac ttcggagacg aggccaacgc 360

cggtgatgga ttggaggacg ttgtt 385

<210> 504
<211> 296
<212> DNA
<213> Glycine max

<400> 504

agcttgagga gcttgcttta gcccatatag agctttattg agtctaaaaa cacgatgtgg 60

aagagtgtta ctctcaaacc ctgcggggtg ctctacatag actctctctt gcattagtcc 120

attgaggaat tcacttttac atccatttga agagtctcat atgtatgagc agcaatgacc 180

tatagtgtat gcctccggtg acaacaagag tgaagttatg tatatcatac ctcctttata 240

aaacctttgg aacaaccttg cctgttgtac atactaactt cctataaagc tatgtc 296

<210> 505
<211> 470
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 505

agctataggg tagaatttag atccatggac taagtatgag tctgcttatc tttgtacata 60

ttaaattgag attntattat ttttttgggc cttatattca gggattcaca gtgtagggag 120

ggtatcctag taatatagga tttttcagcc tttgtatttt agggcaccta gactagtttt 180

tgtattatgg gtagttttat aatttcacat gcattaagtg tattatttga tgtgtgtgtt 240

gngagagaaa tttaattgaa ttgcaagaag ctcaatccaa ttaaatttta gaccagccta 300

agggggaagt gagcatttgt ttgttacacc tcattatcac atcatatagt cacactttgt 360

gtttgtcctt catgctttac atgtctcatg gcacctaagc acacttagtg gagaatcttg 420

gatttgatct tagattagtg cgctgaatca tagctgaact cactaatcat 470

<210> 506
<211> 455
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 506

tcattctaca ncctgaaaag aggatgagat agttgcacga aagagaaagc ttcctaacta 60

aaattttcat gcaagtggac cttcttctag taattctgac ttaccgcagc cttttatccc 120

tcttcaattc ccacctagag caattccaaa caaaaaaaat ggaagaagca gaaaaggaga 180

tcttggagac cttcagaaaa gtagaggtga acatacctct gctagatgcc atcaagcaga 240

ttccaagata tgccaagttt ctaaaggagc tgtgcaccca caaaaggaag ctcanaggca 300

atgaaaggat tagcatgggc agaaatgtgt cagcattgat aggtaaattt gttcctcaca 360

ttcctgagaa atgtaaggac ccaggtactt tntgtatacc ttgcattatt gngaacaata 420

aatttgagaa tgacatgcta gatctaggag catca 455

<210> 507
<211> 439
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 507

tatcccctaa tgcacctatt ccattcctcc catggtcatc atcaccataa acagctataa 60

cctctctcca gccaaagtag ttaacaaagt ctgctattgc agtcatttca taaatgtcac 120

taaaagcagt tctaataaag aatgggaatt gaagtgaaga aagagtaggg tcagtggctg 180

taaatgatag tagaggaact tggagctcgt tcgctatatg agatatgaca tgagctgttg 240

tagacgtctg gngaccgatt atagccacag tttgtgttgc catgagctgc aaggctatta 300

cacacaattt atgtaaacca agagtaataa tctgccaaac tntgaagtaa cttgtctaat 360

aganaaaaag atgcttttaa agttttaaca cataaaaaag atgggaatat tgtgaaggac 420

gtaccctctg caatgctca 439

<210> 508
<211> 493
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 508

tccatgaatn tcttggtacc agacctagca attgtaccca agttgctcac catatctgaa 60

aaaaaaaaca taacaaaaat gaattagaga ctaaccaggt aaacaaaaaa attggtccac 120

aaatatctca ataaaagaac atctcaacct accagctttg gtcatgccaa taccattgtc 180

aacaatggtt agcatattgt tagtcttgtc aggaataata tgaatgaaca actatggcta 240

agtatcgagc ttgctcttgt ccgtcaaact ctcaaatcta gtcttgtcca aagcctanaa 300

ttttacatac aaccacataa ttaattaatc tttcaaaaca aatcaactca agaagaagac 360

caatattaac acaaccacac atcacactaa aaaaattcag tggcagggta caacatttca 420

atcataattc atctcccaac gtaaccaatt cactcctaca aaataaatta gatgtcacta 480

attcactatt cac 493

<210> 509
<211> 436
<212> DNA
<213> Glycine max

<400> 509

gtaacctcta agatcatatc atccacaaag aagaggtggg aaacttaggc atctcctccc 60

ttcccaaatg agaaaggttt ccatcaacta ttgtgaatag aatccaaaat cagatgagca 120

agtctctgca tgtagagcac aaaaaggaga ggaaataagg ggtctccatg acaaaggccg 180

ctggacaatt tgaaggaatc gataagagat ctattccagc tgatggagat gtttgtccaa 240

ttgatgcaac gagagattag ggagaacatc cgagaaggaa gaccaaggtt ttggagggta 300

tcgatggtga aatcccattc aatatgatca aaagcctttt gaaggtcgag cttcaagatc 360

atgtagcaag gcttactagt attatgctct agagaatgaa caagctattg gatgataaca 420

taattgtcca taacac 436

<210> 510
<211> 486
<212> DNA
<213> Glycine max

<400> 510

tcttagtctc agctgatgaa gatgaattct tggctacttc atgcactcct ctaatgacaa 60

tagcatcact tctggcacta aattgttggg agtttgaacc catcttctca attaaatttc 120

tggcttcagc aagggtcatg tctccaaggg ctccaccact ggtagcatct atcatacttc 180

tctccatgtt actgagtcct tcataaaaat attcgaggag aagctgctca taaatctggt 240

ggtaagggca actggcacat agtttgttaa atatctccca gtattcatat aagctctctc 300

cactgagttg tctaatgcct gaaatatctt ttctgatggt cgtggtcctg gaagcacgga 360

aatatttttc taagaatact ctcttgaggt catcccaaca cgtgatggac cttggagcaa 420

ggtaatatag ccagtcctct gccactccct ctaaagaatg acgaaaggcc ttcagaaata 480

tgtgat 486

<210> 511
<211> 457
<212> DNA
<213> Glycine max

<400> 511

ctacagcaca tgccactatt cttcaagttc ttaaaggata tgttaacaag gaaacacaag 60

tatattcatc acgaaaacat tgtcgtggaa tgaaattgta tcgttgtgat tcaaaagatc 120

cttccaccta agcataaaga ccttgggagt gtaaccattc cttgttcaat tggagaagtc 180

actatgggaa aggctcttat tgatttggga gccagtatta atttaatgcc actctccatg 240

tgcataaggt tgggagagtt ggagatcatg cccactaaga tgactttaca acttgctgac 300

cgctccatta ccagaccata tggagtaatt gaagatgtgc tggtcagagt aaaacaattt 360

atcttcttga tagactctgt ggtaatggat atctgtgaag atattgacat tcctgtaata 420

ttggaaggcc attcatcgta aactgtgagt tgatagt 457

<210> 512
<211> 200
<212> DNA
<213> Glycine max

<400> 512

tcagtgcttt cacacacaag ggtctactaa tttggttgct attccgttgg agggtattac 60

gggggttgct gatcttgatg agagaaagtt agttgcatat tttgacagca agattgttcc 120

tgtgcccaag gctgagggaa ctgagtacgt agcttcaaag caaaagcctc catttggacc 180

aacgttcatt ggagcagctt 200

<210> 513
<211> 455
<212> DNA
<213> Glycine max

<400> 513

agctttgagc caattcaaac gacaataact ttttactcgg atgtctgatt gagtcccgta 60

atatatcgag accgtcgaaa ttgaatattg aagctctaag ccaagtaaaa cgacaataac 120

gttttactcg gatgtctgat tgagtcccgt catataccga gacgctcgaa attgaatgtt 180

gaatctccga gccaattcaa acgacaataa ctttttactt ggatgtctga ttgagtcccg 240

caatatatcc agaccctcga aattgaatgt tgaagctctg agccaattca aacgacaata 300

acctttttac tcggatgtct gattgaatcc ccgtatataa cgagacgctc gaaattgaat 360

ggtgaagctc ttgaccaatt caaacgacaa taacttttta ctcggatgtt tgattgagtc 420

cccgcatata tcgagaccct cgaaattgaa tggtg 455

<210> 514
<211> 229
<212> DNA
<213> Glycine max

<400> 514

acaccataca ctactcaagc ttgaaattga acaacggaag ctctcgagaa attcaaatgg 60

tcataacttt tcacacggat gtccggctca ggcttataat atatcgagac gctcgaaatt 120

aaacatcgaa aactctcgcg aaattcaaat ggtcataaat tttcatacgg atgtccgatt 180

cgggcgcatc atatgtcgag aagcttgaaa ttgaacaacc gaaactctt 229

<210> 515
<211> 631
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 515

agcttgcatt gcgttggagt atacatccac cttttaagta tttgacgaag agaaatattg 60

tgaaatagaa acaaacttat acaaataatc agttcccaga tttctaaaga ttggacaaaa 120

aaggattaaa aataaaaaaa ataaaacaaa aaacattggt tagatttttt taacgcgtac 180

attattttat atatcatttg ggtaaaaaaa ttatatttgt attatttggg taatttttt 240

tgtattaaat aggcactatt agaaaatatg ctgttcacat ctgttattta tgacgttcta 300

cattggttat taaccgatgt tgaaagatta tagttaacac cggcttttta aaaccggtgg 360

taatgtaaaa ttgacacatc ggtatttaac aaccgatgta tataataaga ttacaccaaa 420

aacatatgaa tgtgatagtt acatcggtnt tatacaaaat gatgtaactt tacataaaag 480

aggttttata aaataatgta acgatacgta acatggtttg ataaaccgag gtacttcaaa 540

gtacattatt tataaaaacc gaatggatag gatttttaa aaacttttt tttacaaaaa 600

accaaataac ccggatttaa accacccccc c 631

<210> 516
<211> 201
<212> DNA
<213> Glycine max

<400> 516

tcggtattct atttcgagcg ttccgataaa ttatgggact caatttgaca tccgagtaag 60

aagttattgt cgtttgaatt tgctcagagc tttggcattc catttcgagc ttctcgatgt 120

attacgagac tcaatcggac atccgagtga aaacttattg tcgttcgaat ttgctcaaag 180

cttctacatt caattttgag c 201

<210> 517
<211> 207
<212> DNA
<213> Glycine max

<400> 517

taacaaaagg catgcgaagt gggtggaatt cctagagcaa tttccttatg ttatcaaaca 60

taaaaaggga aaaggtaata ttgtagccga tgctctttct cggcttcatg cattactttc 120

tatgcttgaa acaaaattga ttggtcttga atgtttgaaa agcatgtatg aaaatgatga 180

aacttttaga gaaatttta aaaattg 207

<210> 518
<211> 477
<212> DNA
<213> Glycine max

<400> 518

agcttgaagg tgtgtagccc accatctttt tatattagaa tactgggaat gtgtctacta 60

tcattggcat catttttct ctggcattga ggagccactt gagctgccaa gtctctccac 120

ctttgggcgt attcttttga aagatttgtg ccccctttt gcacatgttc tatagttgct 180

cctatccgaa gacattatac tgacactggc taacgaaagc aaccactaag tccttccaag 240

aatggactcg ggaaggttcc aagttagtgt accaagtaat agctacccca gtaagacttt 300

cttggaagga atgtattagc aattcctcat cttttgcgga tgcccccgtc ttccgataat 360

acatctttag atgggtcttg gggcaaggta gccccttgta cttgtcacag tccacaccct 420

gaacttggga ggggtgatga tattgtgtac taggaacaac tcttctaagt tagcaaa 477

<210> 519
<211> 206
<212> DNA
<213> Glycine max

<400> 519

agcttgataa tggaagacac atgaacagct cttgcaataa cattcatggg gctccgaaaa 60

atggtgagaa tggaggattg cctttgaggg cctcacttat gcaatcatga aacacaactc 120

ccaactcgaa agtggaggac acatgaccag ccctaagcaa taacattcat gtggctccca 180

aaaaaggtga aaatggagga ttgcct 206

<210> 520
<211> 449
<212> DNA
<213> Glycine max

<400> 520

aagcttgcca accatggaag ccctaaatct tcccactttt tgggggggc cattcttgga 60

tggccttgat tttctcaggg tccacttgga tcccatttct accaactaca aaccctaaga 120

aaactatatt atttacacaa aaagtacact tctgtatatt tgcatagagg gtgtttttc 180

taaggactga aaaaacttgc ctgagatgtc ctaagcgatc atctaggctc ctactgtaca 240

ctaaaatatc atcaaaataa acaactacaa atctacctat gaaatccctt aagacatgat 300

gcataagcct cataaaggtg cttggggcaa tagtgagccc caaaagcatc actaacccctt 360

catacaaacc agacttggtc ttgaaagcgg gtttccactc atcacccttt ttcatctgat 420

ttggcgatcc ccctttaag atcaatttt 449

<210> 521
<211> 240
<212> DNA
<213> Glycine max

<400> 521

gggatcttaa gtgaccgcgg ctgcagcttt taacattaaa tggtataact tttactcgga 60

ggccggaatt aggcgcataa tatatcgaga cgctcggaat tgaacaatgg aagctcttga 120

gcaattcaaa tgggcataac tttttactcg gatgtccgaa tcaagcgcat aatatatcga 180

gacgctcgaa attgaacaat ggaggcaccc aagaaattaa atgggcaaaa acgttttact 240

<210> 522
<211> 205
<212> DNA
<213> Glycine max

<400> 522

ctttgatgta acatttggag aggttaatga aacaacgtat tatgatgcgc tccatgagag 60

gttggatcaa atggagaata gagaccatat gaattgctca agagcttcca ttgttcaatt 120

tcgagcgtct agatatataa tgcgcctcaa tcggacctcc gagttaaaag ttatgaccat 180

ttgaaatgct caagagcttc cattg 205

<210> 523
<211> 485
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 523

agctntgaaa tccaaagatc taatccaagg tatatgtttc ataaagggga ttcccttact 60

tgtgctattc gagtgcaacc tattctttta tatcctattc gtgtgtaggg aaacttaagc 120

tttttgtgtc ttctttaaat aaagatatgg tgggagaaac cccaactagc ggttttgtgg 180

taatttctaa tgggggggttg aattggcctg tggaaatttc tggtagaaca ttaatgattg 240

atctaatttg ttggcctttg agccaaattg atggtattct gggtatggac tgggtatctt 300

ccaaccatgt cttgttaagc tgctttgata aaactatggc ggttgatggc tctagagtga 360

gtaaggatat atatggagaa gccagcttca tgatgaatca agattgattc aaagaagttc 420

tgatgatgac aaaggtgatg acaaaaagct caacgaccag aacaattaat gatacaaaga 480

tgatg 485

<210> 524
<211> 424
<212> DNA

<213> Glycine max

<400> 524

tatttcactc aagccagccc catagaactt tggcataaga gacttggcca ttgtcatatt 60

caaagaatgt tgaacatgaa gaagaaagac atgaccagaa gtctaatggg gttttctcgc 120

caaattgcaa tgcttggcag tttggtaaac aaaatagaat gccatttccc aaatcaactt 180

ggagagcctc tcaaaagatg caactaattc acactaatgt ggcagaacct caaagaacac 240

catcactaca agggagttca tactttattc ttttcataga tgattttaca agaatgtgtt 300

ggatttttt cttaaaattc aggcatgaag tggctagagt atttataaag gttaaagaag 360

atggtggaaa ctccaagtgg ctgcaagatt caagttctaa gaaccgataa tgggaaggaa 420

tata 424

<210> 525
<211> 449
<212> DNA
<213> Glycine max

<400> 525

agctttttgt tgcgttaaat ttcttaaatt ttatcacaaa ttcaaaacct taagccaccg 60

ggtcaacaat agaatctttt tattgctttt tttctaaagt tggcacaaaa aaacagatgt 120

tcaattatgt gggtagataa ttccaccaac aaaattattt gttaaatgta actcaatctc 180

tcacagtagc gtaagatcat attatattta tatgtggaaa aacaatttat ttaataaaag 240

aaattatatt taacttttat cgcatgtaaa actttattaa attaacgacg aatatgccat 300

tgcaacggaa ttaatctatg accaaatgat ttgaaagata tctatgattt ctgatttagg 360

ttaattaaaa aaggaaccaa ttcatatttt taattattta taacttatat taactaaggg 420

aataaaaatt tcaattctat tctcatttg 449

<210> 526
<211> 204
<212> DNA
<213> Glycine max

<400> 526

cttggaaaat atgctgagga gtgcgttatc tgcgataatt gatgaaatgt attcaacttt 60

cataaaggac agacatatcc ttaatggaat tctgatcctt aatgaagtgg ttgaggaaac 120

tttgaagaga aagaagccag ttatggtttt caaagcggat ttctaaaagg cctatgattc 180

tgtatcttgg tctttttgg atta 204

<210> 527
<211> 212
<212> DNA
<213> Glycine max

<400> 527

tcaagctttt ggaatataag ctgaggagag tgttatctgc gataattgat gaaaggtctt 60

caactttcat aaaggacaga catatcctta atggaattct gatccttaat gaggtggttg 120

aggaaacttt gaagagaaag aagcctgttc tggttttcaa agtggatttc caaaaggcct 180

atgattctgt atcttggtct tttttggatt ac 212

<210> 528
<211> 201
<212> DNA
<213> Glycine max

<400> 528

tgtgaccatt tgaataactc aagagcttcc attgttcaat tttgagcgtc tcgatatatt 60

atgcgcctta atcggacctc cgagtgaaaa gttatgacca tttgaataac tcaagagctt 120

ccattgttca atttcgagcg tctcgatatc ttatgtgcct gaatctgacc tccgagtgaa 180

aagttatgac catttgaatt t 201

<210> 529
<211> 583
<212> DNA
<213> Glycine max

<400> 529

tcacttcaat tggtgcatgc taatatctgg ggaccatcaa gtacccctag ctttggtgga 60

agaagatatt tttccctctt cgttgatgac tacacctgaa tgatgtgggt gtacttcatc 120

caacaaaaat ctgatgcatt ctctagcttc aaggagtaca aggccttagt ggaaaagcaa 180

agtgggcatt ccctcaaaat cttgagaaca aatcgtgggg gagaattcaa tgggcacata 240

ttcatcaatt tttgcaatga tcatggcatc aagaaggagc tgactgttcg tcacactcca 300

caacagaatg gtgtcgctga aaggaaaaat agaaccattg tggaaatggc ttgattgatg 360

ctacaacaca agaacctgcc aaagaatcta tgggcgaaag ctgttagcat agcagtatac 420

attctcaacc gttctccaac taaagaaatc ttaaatttga cgccatatga agcatggttc 480

aacagaaaac caacagttga tctttttaaa gttttgggat gtgttgctta ttcgcacttc 540

ccaaggagaa ccgattaaag ctttttgaaa aaggagaaaa atg 583

<210> 530
<211> 375
<212> DNA
<213> Glycine max

<400> 530

tcaacattca attttgagcg tctcgttata ttacgggact ctatcagaca ttcgagtgag 60

gagttattga cgatcggatt ggctcaaaga ctcaacattc aatgtccagc gtatcgatgt 120

gttactggac tcaatcacac atccgagtaa gaagttattg tcgatcgaat ttgctcataa 180

cttcaacatt caatttcgag cgcctcgctc tattacgggc ctcagtcaga catccgagta 240

aaaagttatt gtcgatcgaa ctggctcaaa gcttaaacat tcaatttcga gcgtctcgat 300

ctatcacgag tgtctttcgc acatccgagg ccagaggaat tgtccccaga attggcgtac 360

atgctgacat tcaac 375

<210> 531
<211> 450
<212> DNA
<213> Glycine max

<400> 531

agcttagagc caattcaaac gacaataact ttttactcag atgtctgatt gaggcccgtc 60

atatatcgag acgctcgaaa ttgaatgttg aagctctgag ccaattcaaa cgaccataac 120

tttttactcg gatgtctgat tgagtcccgc catatatcga gacgctcaaa attgaatgtt 180

gaagctcaga gccaattcaa acgacaataa ctttttactc ggatgtctga ttgagtcccg 240

tcatatatcg agacgctcga aattgaatgt tgaagctctg agccaattca aacgacaata 300

actttttact cggatgtctg attgagtcct cgaatatatc gagacgctcg aaattgaatg 360

ttgaagctct gaaccaattc aaacgacaat aacttttttac tcggatgtct gattgagccc 420

cgtcatatat cgagacgctc gaaattggaa 450

<210> 532
<211> 571
<212> DNA
<213> Glycine max

<400> 532

agcttatggt aaaactaaca gcaatggaaa gtacagtttc actgttgaag gctttgacta 60

tgtgaaaaat ggagcctcag actgcaagga taaactccat gctccttcta aggattcacg 120

ctgtttcata cccaccaagc ttaatgaggg aaccaaactg aaggtgaagt ccaaggataa 180

aaatgaaggt gcgctcagag cttaaccatt tgcttatgct cctgaaaagc catatgattg 240

cgaaaagtcc aatcccaagc ctttccctac ttcttatgac aaaccatatt attagaactc 300

taccccaccc cctttaccct taccgcaccc acaccctcct tactactata agtcaccacc 360

tccaccacca tcaacatact attacaaatc tcctcccca ccttcttatt actacaagag 420

cccttcttca ccatcaccat caccttctcc atattactat aaatctcccc cgccaccatc 480

accatcacca cctttaccct actactatta aatctcccct cctccccaca aagatccata 540

ccatcctcct tactactaca aggcaccctc c 571

<210> 533
<211> 586
<212> DNA
<213> Glycine max

<400> 533

tgatgatgtt attaaaggct ttgcactacc tctggcagta acagtgacaa agatgatcat 60

aagtacgttt acaacttgac atcaaatttt acttgagatt ttataatttc tgatacttgg 120

ttcacttgga cataacagtg gggagcaatt gatggaagat gaatctcaaa ttgatctaag 180

gagaaggaag aaacttgttc ttgatggtga tttggaaaga caaatcaaag atctccatga 240

gaagtaggtt tgaccagatc aaacttttgt ctgaactttg gagcatgatt taaattagag 300

ccttgtcaaa aagaaattca gtctttttta tttcattttg tttacatcat tggtacaaac 360

attcttaaaa ggagtgagca agatagatca attcatagct tttcaatatt ttgttgaata 420

tcattatttg tactgtattt caattcatag cttttcttgt actaatttaa cccgagttta 480

ataaattcca aaaattaaaa aaaaaatctc catattctac atcggttcaa ttataaacga 540

tgtagaacat atcctcattc tacatcggtt aggcaataaa cgatgt 586

<210> 534
<211> 367
<212> DNA
<213> Glycine max

<400> 534

ctaagctctt actcggatgt ccgattgagt cccgtagata tatcgagatg ctttttttga 60

aaatagtagc tcctagcaaa ttcgaaccat aataactttt tactcggatg tccgattgtg 120

ccccgtagta tatcgtgacg ctcgaaattg aaaacataag gtctgagcaa attcaaacgt 180

caataacttt gtactcagat gtccaattga gtcccgtaat atatcgagat gctccaaatt 240

gaaaatagta ggttcttgca aattcaaacc ataataactt tttactcgga tgtctgattg 300

agtcccgtac tatatcgaga cgctcgaaat ggaaaaatga ggctctgagc aaattcaagc 360

gacttta 367

<210> 535
<211> 644
<212> DNA
<213> Glycine max

<400> 535

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aaaactaaat taatattgaa gtctttatga aaatttaaaa cattctcatt taaccttaat 120

ttttattaaa ataaagtcta tcgaatgaaa tatttttat ccctactatt tttttctagt 180

tccttctccg tttcaaacta tatattatga tagttttaat tattggattt ttaaattttg 240

taggtgtgat tgttgaactt atgtgttata ttgcaaattt taaatcatat tgaactttag 300

cctatgtgat aatgataata ataatacaat tcttcctgat ttttgctttc actcaaacta 360

aattttgatt ggattgaatt acagatttta tcaaattcaa cccagatacc cacctatatg 420

attgatgaat gttgacaaga tgggtctaac tattttaaat atgtaatgaa tattagttcc 480

tcttttactt gagtgctaaa gtccggatca gaggaaaatg attacatatg accctggatg 540

tcagtatcta gatatattaa caaattatat aaaacagcag gacataattt ccattaaaaa 600

atatatgttt tattaaatta agcagatacc atagctttaa ccca 644

<210> 536
<211> 470
<212> DNA
<213> Glycine max

<400> 536

tgacaggttt aggtgcaggt gctgctactg gtggaggcac ttgaatttgg ttgccagacc 60

tcaaggtgat ggcactcaca tttttcggat tctgcacagt ctgtgaagga aatttgtcaa 120

aattttggga ctgagcttgg ttcaactgag tagccatctg cccatctgat ttgtcagact 180

ctgaatggag gctcttggct cttgctgaaa ttgcatattc tggaaggtca ttttccttac 240

taactcctct aaagaaggtt gaggaggagc ctcagttgct tgttgtcttt gttgtgaccg 300

gtgttgttgc tgctactgta ttggaggggg aacatatggc ttgctttgac ccccaccatt 360

ttaaaaaaga gggacacatt gttgttgttg tggaagacat ttccctctca aatttggatg 420

attccttcaa cctggattgg atctatttct tgaaaggcca taattattct 470

<210> 537
<211> 555
<212> DNA
<213> Glycine max

<400> 537

gggttaaagt ctcacgattg tcacatgctc atgcaataat tgttagtcgt ggctatacga 60

gacatcttgc caaacaaagt caggttagcc ataactcgcc cgtgcttttc cttccatgct 120

atatgtagca aagtcattga tcctgtcaag tttgatgagc tggaaaatga ggccgcaatt 180

atactgtgcc agttggagat gtattttccc cctgctttct ttgacattat gattcacttt 240

attgtgcatc tggtcagaga aatcaaatgt tgtggtcctg ttcatacaca taattcaaat 300

tcattaatat gtaatgcata tattggatga aagctttgaa aatggaactt atggcagttc 360

atcttaaatt gttgcaggta ctcttacttc ttcggatact gttcattctt ccaagcaggt 420

actcttcctt cttcagatat tgttccttct tcctagtgtc taattcttga ctcattttgt 480

atggtgtact atatgatgat gtaaatggga atatggtttc taaacagttt ttatacccgt 540

ttttgttta tgttc 555

<210> 538
<211> 369
<212> DNA
<213> Glycine max

<400> 538

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aaagttatga ccatttggat ttctcgagag ctttcgtagt ccaattttga gcatctcgat 120

atattaactc cccgaaccag acatcggggt gaaaagttat gaccacttga attctcgaga 180

gcttccggtg cttaatttcg agcttctcga tatgttatgc gattatatcg aacatccgac 240

ggagacgcta tgatagattt aaattctcga gagcttccgc tgatcaaata ctagcgtcaa 300

gatatgttgt gcgtctgaat cggacatctc agggaaaagt tctgaccatt tgactttctc 360

gagagcttc 369

<210> 539
<211> 337
<212> DNA
<213> Glycine max

<400> 539

agcttgagat tgatcaacgg aaagtctcga gaaatacaaa tggtcataat tttcactcac 60

aagtctgatt caggcgccaa acatatcgag acgcttaaaa ttgaacaacg gaagctatcg 120

agaaattcaa atggccataa catttcactc ggatgtctga ttaagccaca taatatatcg 180

agacgcttga aattgaacaa cggaagctgt caagaaattc aaatgctcat aacttttcac 240

tcggatgtcc gattcaggcg cataatatgt ttagacgctc gaaattgatc aacggaagct 300

ctagagaagt caaggggtca ttatttttca cacggat 337

<210> 540
<211> 353
<212> DNA
<213> Glycine max

<400> 540

gaaagacagt gaagtgtctt aagactgaca atggcttgaa attctgtaaa ggtgaaggca 60

ttgcaagaca gtgtgttgta cactatactc tatagtagaa tggagtagtt gaaaaaatga 120

acagaacctc gttagaaagg gccagatgca tactatccaa tataaggttg aataggagtt 180

ttggggctaa ggtagttagc acaacatgtt atctcatgaa ttgctcaccg tccactggca 240

tagatttcag gacccctatt gaggtatgat ctaacaaact tacttaatat tcaatgttga 300

agatggtttg atttcccaca tactatcatg taaataaagg taagctagag ccc 353

<210> 541
<211> 624
<212> DNA
<213> Glycine max

<400> 541

acctacagaa actaagctta ttcagctgcc ctgctcgacc aagcatatcc accacacaag 60

cataatgctc taactttggc tttacgccat acaaactctg catttgacca agatatttta 120

atccttctgt tactaagcca gcatggttac aggcaattag cactcccaga aatgtaaaag 180

aatccggtct gcatccttta ttttgcatta atccaaacag ctcaatagcc ttcagcacat 240

gtccatggat accatatcct gcaattataa cattccatac tgcttcatcc ttctcattta 300

ccctgtcaaa aatgttccga gattgttcca agcatccaca tttagcatac atgtctttta 360

atgcacaagt aacaaagtta tcctcagaaa gacgaggttt cattgcaaag gagtgaactt 420

ctttccccag ccgcaatgca tccacattta atctcggtat tatattgtat tatttgaagc 480

tattgaaagg aaaaattgga aaaaagatag taccttttgta gtaagaggtt gtaaaagcaa 540

aaagcatctg aagagtccgc attgaaatgg agacagacta cgagcaacga caccaaagca 600

ggaggaaaaa ttgcatacca aaaa 624

<210> 542
<211> 380
<212> DNA
<213> Glycine max

<400> 542

agcttttatc aatattaaaa catcttactc ttatcaaagc acatgtaact tataagtctt 60

gaataactct attaccaatt aagcaagatt gtttgcacag aagaaaatca acagataata 120

accatataac agcaaacttg ccatgggttg acaaattcag gaggaccagt ttgactgcct 180

ccactacttt gaggatcaga aggattattt ggcattccga ttgacgagat gcttctctgg 240

gaatgagctg cactatggtc taacttaaag gtgctgctgc tccagaaatc ttctgatcca 300

tccaccttag tcactgtttg accttgagtc cttagtcctt tagatgcttc atccattgaa 360

ataatccctg gagttttttt 380

<210> 543
<211> 490
<212> DNA
<213> Glycine max

<400> 543

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acccgatgcg atatatggtg agctatggcg gctcctatac tttcctatgc gtatgcttcc 120

accagcgaga tcaatcccat cagtggcctt gtttatgaca ttctgatgct tgagtcttct 180

accacctttc gtgagctatc cacacgcctt gggagcgcgc agtgggttcc ttaataattc 240

tcgcgacaat gggaccatca atgacaccgg ccggcaaact cgattgcctg cctgttagaa 300

tcgtacacct ttgatgtgca ctggtacgga taaacaggga tgccttattt agtatataaa 360

atatataaac gcgcatgaaa acactcttgg ttgctggaga aatagcttgc ctcttagaga 420

gtgccaatta tctaggacat tgagctcagg ccccttgctt gtcttccttc gggccggctg 480

aatagactac 490

<210> 544
<211> 551
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 544

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tacattgcct tgactttgca tccaacttgg atctctcatc ctttggaaca tgcataaaag 120

ccttgcagcc gaaaactctt aagtggtcat acttcacatt cttgcccaac cagattttgt 180

tcggcgcctc actattcaaa gcaataacag gactaagatt gataacatgc accgccgtgt 240

atagtgcctt accccagaag tgcttgggta actttgcttc agagagcata catctcactc 300

tctcaattaa tgtcttattc atcctctccg ccaaaccatt tagttgagga gttttctcat 360

gagcaatgtc atgcttcttg cagtagacat caaatggtcc ctaatactca ccgccattgt 420

caatacgaat gcgnttcagc ttcttgcttg attgcctctt aactaagaca tgaaactcct 480

tgaacttctt aagaacttgg tcatttgtct tttaagcata tacccaaagt ttcctggaat 540

agtcatcaat g 551

<210> 545
<211> 487
<212> DNA
<213> Glycine max

<400> 545

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ctcgcttggt tggaaagaca caaataagaa gaagggagga tcatcaacaa tcaatctcaa 120

tgttacaact caaagaactc aaaataagtt cgatgaggag cttaagaaag caaggagcta 180

tgaaattaag tgcttcaagt gtttgggaaa aagtcacata gtttctcaat gttcaactaa 240

aaagactatg ttacttaagg aggatagaga aataattagt gaatcttctt caaaatcttt 300

cccatctagc gatgaagaag agcatcaaga ggaaagaaag ttagaacgag atttgttcac 360

gattagaagg atgttgggta gccaagcagt tgaattggat gatagtcaaa gagaaaagat 420

ttttcatgcg aggtgcctta tccaaaggaa gttatgctct ttgatcattg atggtgggag 480

tttcact 487

<210> 546
<211> 381
<212> DNA
<213> Glycine max

<400> 546

ctggtgagca ggtcactcat aatgtgaaca ttcctgttga cttttaaaag gagaactaca 60

aatggttctt ccttgaccag taacccccaa tccaaggtac atgaattgag tttaattact 120

atccactttc agtataatta ttatcttaca ctctccattt atactgttaa tcaatcagaa 180

atcatatatg aaaacaactt ttaagtaatt ttatataaaa gttaacaaac ttattatatg 240

taccatacat aaactgctta ctcataaatt actattttta ttaagaaatg ttttagcttt 300

gttaattata tataagttct gtgtattttt gccaacatta tcttgctata ctagtagaat 360

gtttaatatg ttaaccaaat t 381

<210> 547
<211> 363
<212> DNA
<213> Glycine max

<400> 547

gacacgggct tcttctcctt ttgctagttg tgggttaaaa agacaattgt gcaaaatccc 60

ccaaaattta acaaaacaat catcctcaat gtccacatct ggaagttgaa aaaagagttt 120

caaattaatg ttacaaatct tccataacta atgagggaca caaagtgagt aaaggttgaa 180

agaaatataa ttctagtcca agatgtatta attatcatgt atgtacccta gctttcttcg 240

ggcagtaagt gataaatacc gcaaggtaaa ttgtctcaat caccccaccg aatgcattga 300

tggtgataaa aagcgtttct ccggtcttca cataggcata aaagatccaa agcattgcac 360

tga 363

<210> 548
<211> 621
<212> DNA
<213> Glycine max

<400> 548

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gctcaagagc ttcaatcatg tgctcttgat aaattccacc acctcttgta ataggtatgc 120

atttccctgt gcaagttacc attttagaaa caacagtact ctgtaaaaac aactagaaaa 180

gcttttcagc atattttgat gcatatatta ataaacttca acccaatcat atgaaataga 240

cagcagtaaa gcatcacagt aagtattaac cttccgattc aaacattgtt agcctagtga 300

agtgaaatgg gtttaattca atgctactga actatagaca aagacaacac acaaaaggac 360

ttcatccaaa tcaccacaat gtaatacatt cattgaagaa aggccttgat agttgataaa 420

cagatttgtt atattcaatg acatttttgc caattctggt tttctttttt ctttttttga 480

ttcagaatta aattttggga gtcgaaagga tactaaagtg ctttagctgc aaatttcctt 540

ttcaacaact tttaagcaac agatctgttg tgttaaagta ttgtcccaag atgaaaagaa 600

acaagattga ggatctatgt c 621

<210> 549
<211> 627
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 549

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gataatttac gagtttgata tatatagata tttattataa atattaaatt ttcaatatta 120

ttaattaatc aaaaattatt ttaaaacaat gttaacaaga tattataaaa gttaataaat 180

ttatcttgtg taaaaattta taaatagatg gccttgtaaa aaattaaaac aaacatttta 240

caattagtgc atatgatgtt tattcataat attttgttta attgaaaatt atatttttaa 300

tatatcatat taataaaata aatgtatatt agtaataata aaaaaattat tatttaaata 360

tgttatttaa atttaaaaat ttacttacaa ttaaatacct tactatttta aatagttttt 420

attaatgtca ataacaaaaa attcaatgta aaattatttt atataaaatt tatgtaaaat 480

acattgataa tgtaaaatta ttttatattg ttatcataat cttattaatt ttctcaataa 540

caactttaaa aatcatattc aagttgatgt tcaacangtt aacatgacaa tgtaatttat 600

ttttatattt acaatgcata ataatta 627

<210> 550
<211> 627
<212> DNA
<213> Glycine max

<400> 550

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agaagaacgt ggcatttacc tggggtgaaa aacaagagca agccttttct ttgctcaaag 120

aaaagcttac taaggcacct gttctagctc ttcctaactt ttctaaaact tttgagctag 180

aatgtgatgc ctctggagtg ggagttggag ctgtattgtt accaggtggg caccctattg 240

cttattttag tgaaaaactt tatagtgcca ccctcaacta ccccacctat gataaagagc 300

tttatgcctt aataagagcc ctccaaactt gggaacatta ccttgtttcc aaggaatttg 360

tcatttatag tgatcatcaa tcacttaagt acattagagg gcaaagcaag ttaaacaaga 420

gacatgcaaa atgggtagag tacctagagc aatttccata tgttatcaaa tacaaaaagg 480

gaacaacaaa tgtggtagtt gatgccctct ctaggagaca cgcattgttt tgctccctag 540

gagcccaaat tttaggattt gataatatta gggacttgta tgctttaaat gaacatttct 600

cttccattta cgagagttgt gggaaaa 627

<210> 551
<211> 427
<212> DNA
<213> Glycine max

<400> 551

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aagtttttgt cattcgactt ttcatagagc ttctgttttc aatttcgagc gtcacgatat 120

attaaagggc tcaatcgcac attcgagtta aaagttattg tcgtttgatt tttctcagag 180

cttccgtttt caattaccag cgtctcgata tcctacgaga cacaatcgaa catccggctt 240

aaaagctatt gtcgtttgaa ttggctcaga gcttccgtgt tcaattacca tcgtctcgat 300

ttattaccgt actcaatcgg acatccgaat tgtgagttat tgtcactaga cttttcatag 360

aaatttcgtt ttcaatttcg agcgaataga tatattagag ggctcgatcg gacatgcgac 420

ttaaagg 427

<210> 552
<211> 488
<212> DNA
<213> Glycine max

<400> 552

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ggatggcctt gattttctca aggtccactt ggaccccatt tctaccaact acaaacccta 120

agaaaactat attatctaca caaaaagtac acttctctat atttgcatag agggtgtttt 180

tcctaaggac tgaaagaact tgcctgagat gtcctaagtg atcatctagg ctcctactgt 240

acactaaaat atcatcaaaa taaacaacta caaatctacc tatgaaatcc cttaagacat 300

gatgcataag cctcataaag gtgcttggtg cattagtgag cccaaaaggc atcactagcc 360

attcatacaa accaaacttg gtcttgaaag cggttttcca ctcatcaccc tttttcatcc 420

tgatttggtg atacccactt ttaagatcaa tttttgaaaa gatattggca ccatgcaact 480

catcaagc 488

<210> 553
<211> 498
<212> DNA
<213> Glycine max

<400> 553

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tgctgcccaa gtttcatggt cttgcaggtg aagatcctca taagcatctt aaggagttcc 120

atattgtttg ttccaccatg aagccccctg atgtccagga agatcatatc tttctaaagg 180

cttttcctca ttctctggag ggagtggcaa aagattggct ttactacctt gctcccaagt 240

ccattttcag ctgggatgac cttaagaggg tgttcttgga gaaattcttc cctgcatcca 300

ggaccattgc catcagaaaa gacatttcag gcattaggca acttagtgga gaaagcctgt 360

ataagtactg ggaaagattc aagaaattat gtgcaagctg ttctcaccac cagatttctg 420

agcaactcct tcttcaatat ttctatgagg gacttatcac ctggagagga gtattattga 480

tgctgccagt ggtggagc 498

<210> 554
<211> 486
<212> DNA
<213> Glycine max

<400> 554

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taattaaaca caagtagagt ggttcaaaat tttaagtaaa attattttat tattttgaac 120

ataatttttt taataggttt acacttataa tataaaatca cttatacttt gatgtaggaa 180

agaagcttga caaacaaagc taattgaagc aagcaagaaa taaaataaat tattgaaaaa 240

atcaattgtg caaaagacat ttgaaatggt agcatctttt aatattttat attagttttc 300

ttacaagtta tataaaataa ctcatttttt attttgtgat tatttttata tgatatatga 360

aaggttggtg aaatttataa agacattatg cattatatta tattatttaa tttgtttttt 420

actatataaa ttttaataga aaaaagattt aatatctggt gaatgacaaa aaaattaagg 480

taaaga 486

<210> 555
<211> 305
<212> DNA
<213> Glycine max

<400> 555

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tcagaacttc attggaagag gtgaggttgg gatggtttac tagggcattc tacctgatgg 120

ctcaatggtt gcaatgaaac ggcttgaata atcaaattct caaagagatg ctgtgttcta 180

aagcgaggag gacattgtta agcaccttga agcaccgtaa tctggtgcca ttaaaaggaa 240

gttgcaccat tggaagaacc aatttgggaa attatatatt gtgatggttt ttaaagatat 300

ttaac 305

<210> 556
<211> 366
<212> DNA
<213> Glycine max

<400> 556

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atagagacgc tcgaaaatga acaacggaag ctctcgagaa attcaaatgg tcataacttt 120

tcacactgac gtacgattca tgcttataat atatggatat gctcagaaat aaacatcgga 180

agctctcgag atattcaaat ggtcataact tttcacatgg atgttcgatt cgtgtgcata 240

atatgtcaag aggctcaaaa ttgaacaacg gaaggtcttg agaaattcaa atgttcataa 300

cttttcacac gaatgtccga atcatgctta taatatatcg atacgctcga aattaaacaa 360

cggaac 366

<210> 557
<211> 438
<212> DNA
<213> Glycine max

<400> 557

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tcatgatcat ttgaatttct cgagagtttc cgatgtttaa tttcgagcgt attgatatat 180

tataaccctg aatcggacct cagtgtgaca agttatgacc atttgaattt gacgagagct 240

tccgttgttc aatttcgaat atcactatat gtgatgcgcc taaattggac atccggggga 300

aaagctatga ccatttgaat ttctcaagag cttccgttgc tcaatattga gcgtctcgat 360

acgtgatttg cctgaatcgg ccatccgtgt gaaaaagtat aaccatttga atttctcaag 420

agcttccgtt gttcaatt 438

<210> 558
<211> 456
<212> DNA
<213> Glycine max

<400> 558

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taataaatac ttattcatat tctcaaatct tgtatcatat ccttccattc attatatttt 180

ttaaaaataa aattatctgt caacaatgtc ataccataat ggttatctaa tctaaactat 240

ttaacctggc aaaacgataa tttttgttat tatgatgaac aagaattata aattataaaa 300

tcttagtcat ataatgaaaa ttaaaaaaat acatataatt ttgtaagtga ttattcaacc 360

agtaataaaa attttaggtt aattatttat ataaaattaa attagtcatt tttattctta 420

tataagatga tgatttacat taagatggag tcaatg 456

<210> 559
<211> 473
<212> DNA
<213> Glycine max

<400> 559

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cacttttagc cagggctgtg gctaatagga ctgatgcttg ttttataaag gttattggaa 120

gtgagctact tcagaaatat gttggtgagg gggctatgat gggtcgtgaa ctattttagg 180

taaaatgcac aagactccgt cctctagctt ttttttatca ttgtttcgat gaaaataaat 240

cattcgacta aaattttctg atttttagat ggctcggtca aagaaggcat gcattgtgtt 300

ttttgatgaa attgatgcaa ttggaggagc tcgatttgat gatggttgtg gaggtgacaa 360

tgaggttcac cgcaccatgc ttgaaattga gaatcacctt gatgggtttg atgctagggg 420

aaacaataaa tttttgatgg caactaacag ggtggttgaa tttattgtga gag 473

<210> 560
<211> 533
<212> DNA
<213> Glycine max

<400> 560

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gcgatggtag ctttgttcca cgatatgatg caccaagaaa tcgaagtgta tgtggacgat 120

atgatttcta agtccaaaac caaagaagag catctaatca acttacggaa gttgttcgag 180

aggttgcgaa agtaccagct aaggttgaac ccagccaagt gcactttcga ggtcaaatcg 240

ggaaaactgt tgggtttcat cgtaagccaa aaagggatag aggttgaccc cgaaaaagtt 300

aaagccatcc tcgaaatgcc gaagccatgc actaaaaaga aagtctgggg tttcttgggg 360

cgcttgaact acatcaccag gttcatatca cagctcacgg ctacctgcaa gccgttattc 420

aagcttttgc gcaaggatca gtccgttcgt tggaatggtg attgtcaaga ggtgtttgga 480

aagatcaaac aatgtctcat gaacccccctg gtactaatgc caccggtggg tgg 533

<210> 561
<211> 473
<212> DNA
<213> Glycine max

<400> 561

agcttgtcag tttattccca aaaacctgcc tagtccaaga atatggcttt caattgaatg 60

acaatagtct ctaaatcaat tcattggcgt atcacttcac tcacttgaat tacaacatga 120

tagatactta actgataaat catatatatg tgatatgagt aattaattaa aactatatat 180

atataggaca aagatatatt attgattaaa tttttaaaaa acaaaatatt gttagtgatt 240

atttttttaa atgaatatat gtaacataat tagaattgac agtaaactgt atggtaaaaa 300

acacagttat aatattaaga aaaaaattta atcaaatctc ctattttaaa tataactatg 360

cttattataa taaaacatta aaataccata attggatttg gatgtcctaa aacaactggc 420

actaatcctt tttaaaaaaa acttataact caaattgata aaagcttatc aat 473

<210> 562
<211> 568
<212> DNA
<213> Glycine max

<400> 562

tatgaaaata agagaaagaa actttcaaaa taaatttgta tattaaacaa attatttttg 60

gtcaccttgt taaataaata tttattttag tcaaattaat ttataagtta gtcgaataaa 120

cttttataat ctaattaact attagagcaa tttggcaatc atacccatgg ttaaagaagt 180

tatttaacca gtaaaaaaaa cttttaggaa ttaaatttac ttaaaatatt tataaaacat 240

atatactttt ttagggtaaa cgtatgtact taaaatatat cctttattca attttgttag 300

acattttagt aatttatttg tttcatttta attgtgattt tataatattg atgatgtatt 360

aaatattttt ttcttaatat atccattatc ggtcatcatt aagtgagaaa acaaaaaaaa 420

gtataaataa aagatagtcc aattaatata aaagaaaaaa atattataaa aattgcataa 480

taattttaat aaaatctata atataattac atatctaaat ttctgtacca aaatttgtcc 540

acaaataaaa tggagggatt ttatatta 568

<210> 563
<211> 497
<212> DNA
<213> Glycine max

<400> 563

atttacattt tcaaagatta catattgggg aatctaacat aacagacaat cgattgtaca 60

aaacaatgat aggagtaaaa tctagtaaca tcataattta aactcactgc gacggataaa 120

tgacaatcac catactcaag agcctcatgg ataatgataa gatctttcct accctaatct 180

aaaaaaatta gacgattaaa caatttatgt ttggtgacta catagtggca ctaatatgta 240

aatgcaaaaa tgctgacctg gccatgttca ttgaaagtat cgagtccaac aattccaagg 300

tccagatctc cagataacaa ttttcttgtg atgtatttgg gcctctaaaa ccaaactatg 360

agtttggatt gctgcagtaa tgcaagagaa ttggtttatg gtcatgtaga gatatagtac 420

attgatggaa gccaagggaa aaaatagaac gcacatgagg aagcaactca cttaacttat 480

ttctgctttt tggatca 497

<210> 564
<211> 342
<212> DNA
<213> Glycine max

<400> 564

agctttgtat ggtagaaggt gtaggacacc tctatgttgg ctaaagccct gagaagacct 60

caccttagga cttgaagtgg tacaacaaac caccgagaaa gtcaagttga tccaagaaag 120

gatgaggact gctcagagta ggtagaaaag ttatcaggat aagaggagga aagacttgga 180

attcgaggtt ggtgatcatg tattcttgag agtcactctg tggactgggg ttggtcgagc 240

attgaaatcc caaaaactaa cacctcgcct catcggtcct ttccaaattc ttaaaagagt 300

cggtcctgtg gcataccaaa atgcattatc cccatcacat tc 342

<210> 565
<211> 582
<212> DNA
<213> Glycine max

<400> 565

ttgttgacaa cactgtggct gcagcattca atgctgacct tgtccaacct ccatcaccct 60

tgctgcccaa attactttga tctctaagta catcatgatg taagctccat tggagcttgt 120

aggcctagga tcttcttcat caatggattc ctttgcttct tggaagatga atggcagtgg 180

aacggataaa ggaagagaga gaggagacgc cacttcaaag agaagatgag tttagaaaaa 240

gcccaccacc ataggaggcc atggataaga gctttgagga agaaggagat gaatgaaggg 300

agagggagag aagagcacga aattttgtgc tctaaatgag ctctgaaatc tgaagtttaa 360

tattcaaatg atcaaagttg aaaaaaatgc acacacatga cctctattta tagcctaagt 420

gtcacaaaat tggagggaaa ttcaaatttc acttgaattt gaaattgaat ttgtggagcc 480

aaaaattcac ttaatatgat tagtgaaatt taattatgtt tcaaccccac taatccaaga 540

tcaattccaa gattctccac taagtgtgct taagtggcat ga 582

<210> 566

<211> 539
<212> DNA
<213> Glycine max

<400> 566

tgctatgtac ccctacgcca aactagtatc atagaagaaa tatgatatgg gagaagagcg 60

gcgtaaaacc ggtaaaaaat aagtcaacaa ggtattgcat gcgaacttta tcatagaggt 120

ccgattctct acttggcttg ccaacatcat cataatcaaa aaggccaacg cctaatggca 180

aatattcatc gactacactg atttgaatag ggcatgccct aaagacgcat acccctttgcc 240

caacattcat agactagtcg atgggacatc cgagttccag gagcttagct tcctagatgc 300

ttactatgga tacaaccaat tcaaaatgca tgctctaaac aaggagaaaa tgacattcat 360

cactaaagat gccaacttta actgccagga caagccaact ttagtggagt tgggtatgtt 420

aaagtaagtt aatgacaaaa aactcccttа ctgagcatca tcccatgagg gaacatgttt 480

cctcaccaac ccaatgagtg gtgctacaag tatatacaaa tatgggacaa aacttttgt 539

<210> 567
<211> 314
<212> DNA
<213> Glycine max

<400> 567

gcatgcaagc ttgtaatcga ttacacaaat cttgtactct attaccagag gagaatttca 60

gaaaataatt tccaagagtc acatctgttg ccatcaaagg tctatttata tgtgacatag 120

aacacgaatt tgcgaagagt ttttgagaac acaaaggtct tatcctctcc aaaaaagaaa 180

aattatctta tcctcttaaa aattccttgg ccaataccct tgcaattcaa taaggaatta 240

ttttgagtgc tccattgttc aatctatctc tttcaagaga gaattcctct tctcttcatc 300

ctatttccaa aaag 314

<210> 568
<211> 446
<212> DNA
<213> Glycine max

<400> 568

agctgtgaga caactcaact ttcataactt tggactcaaa tgtctgatta cggaccataa 60

tatatcaaga cgctaaaaat tgaacacgga agctcgggcc caattcaaac tgccataact 120

tttgacttag atgtctgatt gtggaccata ttcgaactgc catgattggt gattctgatg 180

tttgactacc gcccataata tatcaagact cttgaaattg attacaaaag ctcctcacaa 240

attaaactac cataactttt gattggatgt ctgattgtgg ccgataatat atcaagatgc 300

taagaattga acacggaagc tcctagaaaa ttcaaactac cataactttt gacttgaata 360

tctgattgcg gaccataata tatcaagact cttgaaattg atttcgaaag ctatgagcat 420

attcaaaact ttcataactt ctgact 446

<210> 569
<211> 437
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 569

agctntcctt cattctcttt caagttaaca ttttgaataa ttttttatcat ttacaaatta 60

tttattttga agtaataatt tttgtggtta gaatgaaatt tgaacctgaa gtttaagtgt 120

agtaattttt ggaattagat tttttatttt gaaattatta ctaataatta tttataagcc 180

tctttgttca tggtttttct gccttagaaa tttttacatg tgacccttcc tgtttttgga 240

gttaaagaat tattcgtaaa ttatttaatt ggagtaataa tttttttgtt agaatgaagt 300

ttgaatgtgt agtttaagtt taatagagca agacaataga ttnttttatt tttatcattc 360

acaaattatt tattttaagt aataatattt tttgttacaa taaaattgta agctgaagtt 420

taagtgtatt atatttt 437

<210> 570
<211> 383
<212> DNA
<213> Glycine max

<400> 570

tatatggcct aggatgtggg tttgtgacta aattcaattt aaacacaagt cttgcacttg 60

ccacattggt acaactccct ccatcaatga tcaccatgca aactttgcca ttgatcaaac 120

atctaatgtg gaaaaagttt tgtctttaac ttttctccat agacttcaat taatgggcaa 180

gtaaccgtct aatcatcaac aaatctccct ccggtggttt ctacacttcc tcctcatcat 240

cctcactctc tttttccttt tcaacttccg actcactaat gtactctcca tctctaagaa 300

tcatggcttt cttgttaggg cactcatgtg cataatgtcc caagccttgg caccgaaagc 360

acttcacata ccaacttttt ttt 383

<210> 571
<211> 444
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 571

gcttgcttct atagtacata cacaatatac atcatcacaa tgacattntt aacatcaaca 60

aaatgtcatc tccaggtcat tgtcaacatc aacatcatct catctcaatg tcattctcaa 120

catcaacatt atctcatctc aatgtcattc caacatcaac atcattttat ctcaatgtca 180

ttctcaacat caacatcatc tcatctcaat gacattatca acaacaacaa catcatctat 240

atcaacataa tcattaataa caacatgatc tcgtatcaat attatcataa acaccaacat 300

cgtttgtatc aattattatt aatatcatct tcaatatcaa catcattctc tatcaacatt 360

atcataaaca tcaacgtcac ctcatatcaa ttaatgtcat tgtcataccc taatttcgtc 420

cggcgacctt tgcttgatga catg 444

<210> 572
<211> 438
<212> DNA
<213> Glycine max

<400> 572

tagacaatta catatcctcc ttctttgata cagataattc aaaatacttt gtttcatggt 60

ctgcccaatg aagaccctta tgctcactta gctacctata tagagatatg caatactatt 120

aagttggcgg gtgtgcctac tgatgcaatc cagttgagtc tgttctcatt ttctttatat 180

ggagaagcta agagatggct tgattctttt aaaggaaaca gtctgaagtc atgggatgaa 240

gtggtagaaa agttcttaaa gaagtacttc cctgaattga agactgcaga aggcaaagtt 300

gccatctctt ccttccacca gtttctagat gaatcgttga gtgaggcact catggttttt 360

cagaaccaat acagctcaac atattcatag atgggttgag accacaatct aagcagctct 420

tggatgcttc agctgggg 438

<210> 573
<211> 326
<212> DNA
<213> Glycine max

<400> 573

tttagccaat tcagacaaca ataacttttt actcggatgt cttattgagt cccggaatat 60

atcgagacgc tcgaaattga atgttgaacc tctgagctaa ctcaaacgac aataactttt 120

tactcggatg tctgaatgag tcccgtgata tatcgagacg ctcgaaattg aatgttgaaa 180

ctctgagcca attcaaacga caataaattt ttaatcggat gtgtgattga gtcccggaat 240

atatagagac gcctcgaaat gaatgtggaa cctctgagcc cattcaaccg ccattacctt 300

ttactttgaa ggttggatgg ggcccc 326

<210> 574
<211> 430
<212> DNA
<213> Glycine max

<400> 574

agcttgtagg gttaaagtct cacaattgtt acgtgctcat gcaaaaattg tcagtcgcgg 60

ctatacgaga catcttgcca aacatcgtca ggttagccat aactcgactg tgctttttct 120

tccatgctat atgaagcaaa gtcattgatc ctgtcaagat tgatgagctg gaaaatgagg 180

ccgtaattat actatgccag ttggagatgt attttccccc tgctttcttt gacatcatga 240

ttctcttgat tgtgcatctg gtcatagaaa tcaaatgttg tggtcctgtt tatctaccgt 300

ggatgtaccc agttgagcga ttcatgaaga tcttaaaagg atatacaaag aatctatatc 360

atccataacc atctattgtt gagagggaca ttgcagaaca agccattgaa ttttggtcac 420

aacacattca 430

<210> 575
<211> 419
<212> DNA
<213> Glycine max

<400> 575

tagcttatcc agaagcactt ttagaaatag aaatttagac aaaaaaaagt ttctccataa 60

gttagaaatg atcttataga gaagttatat gacagagttc ctataaatga gcttattcat 120

aagctaattt tagcttatac agaagcttat ttcattcttt tcttcttata ttttcctctc 180

ctcctagaag cgcttatggg gaagtttatc caaataggcc ctttatattt cattgttctt 240

tctcatttcc ctgagtcatt gctgctgaaa gcaactttga catctctccc agcaggaata 300

tgatcgacta acctctagac tcaaccccga tggtaaatca aagcacatct agtcgagaat 360

tttacacccc attgtgtaca gtcaccaaaa cttacacctt ttagtgttgt aatttatga 419

<210> 576
<211> 408
<212> DNA
<213> Glycine max

<400> 576

ttggagtttc caagtgccaa atcgtcttct tcttttgtcc agtcttcttc tggcttcaat 60

tcattagtgg gctttccttc tgtgtccagc atcttgggat gttcccagcc tttgatgaca 120

gctttccagg ttctgctatc cagtgatttg aggaaggcca ccatccttgc tttccagtat 180

tcatagctgg ttccatccac aatgggtggt ctgttcactg gtccttcttc tttctccatg 240

ttcatcacaa tttatctccc tagatctcac tcagtgaatt agagtgcccg ctctgatacc 300

aattgaaatt ctgatactga ggccagatgt cgtaccggat gtcacgacat cacgcttcag 360

aacatgcaga ttatatttga ctgtctgaca gattaaacaa gttaataa 408

<210> 577
<211> 430
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 577

agcttgaacc ttacagaccc tattctagtg atcttacaag acttgttgtt tccaagtagg 60

aatgaaccac caacttgttc atcaagctcc tcaaaccaag acttgtttgg ggtcatatag 120

aatgaacacc cagagtccaa gatccattct gtctcagagt tttcatgaga caccattaaa 180

gcctcagctg actcataacc atcttcaact agagcagcat ttctaggctc tttagattga 240

tcttacttgc ttcctttcta tctatcagga caaaatctcc tagtatgacc ttctcttttg 300

cagtggtaac atctaatgtt tggtacatta gatccagatc gagtttgtga cttggatctt 360

tttccttctg tcttatcatc cttcgtatac tatcttacac gaactgagag ttcctacnca 420

tgtacataag 430

<210> 578
<211> 573
<212> DNA
<213> Glycine max

<400> 578

tctttgagaa aacttccttg agaagctaga gcttagctac acacacccct ctcataacta 60

agctcacctc cttgagaagc ttccttaaga agattcctta agaagctaga gcttaactac 120

acatacctct ataatagcta agctcacctc cttgagatga gaagctagag cttagctaca 180

caccccctat aatagctaag ctcaccccca tgacaaaaaa catgaaaata acaaaaaaaa 240

gtccttatta caaagacaac tcaaaatgcc ccgaaataca aggctaaaac cctatactac 300

tagaatggcc aaaatacaag gcctagacga aggaataacc tattctaata tttacaaaga 360

taagcgggct catacttagc ccatgggctc gaaatctacc ctaaggctca tgagaaccct 420

agggcctctt cttggatctc tagcccaatc tacttggagt cttttagcca atgcccttgc 480

ggggtaggat tgcgtcaacc ctcacgactt tatctgcgta gggacattgt gtatcatgcc 540

gccaacatga tacaccttta ctaaggccac caa 573

<210> 579
<211> 412
<212> DNA
<213> Glycine max

<400> 579

ttcttttgga tttgattgga atttctgact tgaaagaatt ccttggttgc tttgacacac 60

aacactcaac acacaattgt tttggtatct caatttgggg aagaccatga gccattttct 120

tacttttcaa attacttaaa ctcctgaaat ttaaatgacc aaacctgtga tgctacatcc 180

agctttcatc acttatagaa gcagccaagc attgaaattc tgcagtctga attccaatct 240

tgaatgctct atttcttgac aaaggggcct ctataatcaa cctcctattt ctatcaaata 300

tctttatttg attggcctcc atctgcattg agtagccctt ttctagcaac tgtctcaaac 360

tcagcaaatt attcttcata ttgggaacat atagcacatc attgataaat ga 412

<210> 580
<211> 462
<212> DNA
<213> Glycine max

<400> 580

tggacttcct gtgttttggg aacctctcct tcctcaagtg tacccaaacc tcatcacctg 60

gttcaagcat gactttcttt ctgcttttgt tggcttgcct tgcatagctc gcatttttct 120

tttcaatttg ggccttcact tgctcatgca acttcttcac atactcagct ttagcctgtg 180

catccttatg cttaaacata gcaatgttag gcataggcaa ccaatcaaga ggagtcaaag 240

gattaaatcc atacactatc tcaaatggtg aacaattagt tgtgctatgg acagcccgat 300

tataagcaaa ctcaacatga ggcaaacagg cttcccaaga tttaagattt ttctttaaaa 360

cagtcctaag cagcgtgcct aaagtcctat tgactacctc agcttgacca tcaccttgtg 420

ggtgacaagt agtagaaaac aacaatttag tactaatctt ac 462

<210> 581
<211> 425
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 581

tagagtcacc tgaagctgca gcttcctggc ctttaggtaa aaagactcgt gatcgctatg 60

gatgacaaac tctntgggta ataggtcatg ctgccagagt tgtagagccc taaccaaagc 120

atgcaactcc ttaaataaga gaagaggaaa ggcagaggct cctaactttt gactaaaata 180

agctatcgga tgtgcctgtt gggataaaac agccccaatg cccatatttg acgcatcaca 240

ctcaatttga aatgatgttg cgagattaag cataacaaga atgggtgcat tatttaacct 300

atggttgagg gcagcagagg cctcttatta gttgttaccc cattcgaaac ccacattctt 360

cttaacaact tcacgtagag gagcagccaa tgtactaaca tccttatcca atctgctata 420

gaaac 425

<210> 582

<211> 217
<212> DNA
<213> Glycine max

<400> 582

tatactgcaa acatctacaa taaaccttct caacctcagc agcttaatca accactacag 60

aacaaatatg acctttcag caacaagtac aattctaggt ggaggaatca ttcaaacctt 120

atatggtcga atcccttcca acaacgacaa caacaacaac caccttattt ttataaagtt 180

gctggcccaa gcaaaacata ttttcctcca ccaatcc 217

<210> 583
<211> 438
<212> DNA
<213> Glycine max

<400> 583

agcttgaatc ggacatctgt gtgaatagtt atgaccattt gaatttatca agagcttccg 60

ttgttctatt tcgagcgtct ctatatgtga tgcgccataa tttaacatcc gtgtgaaaag 120

ttgtgaccat ttgaatttct caagagcttc cgttgttcaa tttcgagcct ctcgacatct 180

tatgcgcccg aatcgaacat ccgtgtgaaa agttatgacc atttgaattt ctcgagagct 240

tccgatgttt aatttcgagc gtatcgatat attatatgcc ttaatcggac ctcaatgtga 300

aaagttatga ccattttaat tgcccgagag cttccgttgt tcattttcga gcgtctctat 360

atgtgatgtg ccttaatcta acatccgtgt gaagagttat gaccatttga atttctcaag 420

agctttcctt gtttagtt 438

<210> 584
<211> 540
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 584

acctttccaa catttggtcc atgaatggca gatgaaaatg acatcattca acttgcggta 60

gtcaataaaa attcgccacc cagtgattgt ccgtgtagga ataagatcat tcttatcatt 120

acagatcatc ttcatatcgc ctttctttgg caccacctgg accaaactca cccaagtgct 180

atcagagttg gataaattag tcttgcttca agcaacttga ggacttttt gcacacctcc 240

tccttcatag atggntgagt ctcctctatg gatgtctatc cagtctgaat tcaccttcca 300

tcattatgct atgcatgaaa taggatggac taatcccctt aagatcaaat atgtgtcatc 360

ctattgttgt cttgtgcttc ttaagaacct ccaccaatag tgcttcctca attgaagaca 420

acgtattatt gataaccact agtttaacat catctgcttc ctgggagaca tacttaaggt 480

gaggaggtag aacccttaac tcaaccttaa gtttttctgt aagagtgcct ttttttagct 540

<210> 585
<211> 437
<212> DNA
<213> Glycine max

<400> 585

agcttcggct ttgtcctcaa tgcttcatgt agacttgccc aaaatcgcga agtgaacctc 60

ggatccctgt cagatacaat actggaagga attccatgca accttactac ttctttgata 120

tacaacatcc actagcttct ccattctata cttcatattc actagaataa aatgagcaga 180

tttggtaagt cgatctacta tgacccatac agcatcatgt cctcgactag acttaggtaa 240

actagataca aaatccatgg atatgctctc ccatttccat tccggaattg ccaagggctt 300

caattctcct tatggtcgat gatgctccgc cttagccttt tgacatgtca aacaccttgc 360

tacatattca gctacatctt tcttcatgcc atgccaccat aaacttctct tcaaatcttg 420

gtacatctta gtcattc 437

<210> 586
<211> 478
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 586

cccttcatga tgaatcaaga ttgattcaaa gatgttttga tgataacaaa ggggatgaaa 60

aaaagctcaa aggtcaattc atgataatca aagaatgagt tcaagatgtt caaagatgtt 120

taagatgatc aagatgatca agattgaata aaaaacactt caagaatcaa gaatcaagat 180

tcaaggttca agcttccaag aatcaatatc aagattcaag actcaatatt caagaatcaa 240

gagaagactt aaatgagata agtatgaaaa ggttttttca aaaacttagt agcacatgga 300

tgttttctca aaaaatgttt accaaagagt ttttactctc tggtaatcga ttactagaat 360

attgtaatcg attaccagta gcaaaaaatg attttgaaaa agttttcaca tgaatttaca 420

acgttccaat tgatttcaaa aagttgtaat cgattacaat gttntggtaa tcgattac 478

<210> 587
<211> 334
<212> DNA
<213> Glycine max

<400> 587

ttgctatcca acaatgttgc ttcatgcttt aggatttcta tacattggtt ctctgataaa 60

taccttgtgt tgtcttcagg agctcatata aagagtgtat gcacacaagc cggtatgtat 120

gctatccgtg cccggaggaa gactgtaaca aacacagact tgctttatgc accaaataaa 180

gtcatctaag gataccagaa catcactgca actcccaagt atatggtcta caactgaggt 240

atttttcat ctttttccga gaccatagca gctttatctt tattttcccc tggaaattga 300

agggcatgcg attctatcta attaactctc tgtt 334

<210> 588
<211> 447
<212> DNA
<213> Glycine max

<400> 588

agcttgaagg acatgcacaa agtgtgacta tatgatgtgg ctatggcgtg tagcaagcaa 60

atgctcacct ccccttagg ctggaccaaa ctttaattgg gttgggcttc tcccaattca 120

attaaattta tctcccaaca cacatcaaat agggcactta atgcatgtga aattacaaaa 180

ctacccctaa tccagaaact agtctaggtg ccctataata caagagctaa aaaatcctac 240

attactaggg taccctccct acactatgga gccctaaata caagtcccaa aaataatgaa 300

atcctaatct aatatgtaca aagataagtg gtctcatact tagcccatgg acccaatctt 360

cttggagtct tctatccaat acccttgagg gatagtgatg tagctccatg tggagcttgt 420

agaccttgga tcttcttcat caatgga 447

<210> 589
<211> 333
<212> DNA

<213> Glycine max

<400> 589

attgcacaac ggaagctctc gagaaattta aatggtcata acttttcaga atggaagtcc 60

gattcacgcg cataatatat cgagaaactt gaaattgaac aacggaagtt gatgagaaat 120

tcaaacggtc ataacttatc acactaaagg tctattcagg cgcataatat atcgtgacgc 180

tcgaaattga acattggaag ctctcgacaa atgctaatgg tcattacttt tctaatggac 240

attcgattca tgcgcataat atatcgacac gcttgaaatt gaacaacgga cgcctcttat 300

aagttcaaat gcgtatagct ttttacaacg aag 333

<210> 590
<211> 447
<212> DNA
<213> Glycine max

<400> 590

agcttgtaat tgaatacctt aatgataacc aactatcctg tttcacagtt cttaaaacat 60

aaccaagaac aatttaacat attacaacac ctcataatcc attataacat gttatcaaat 120

acaattttaa gcataaaaaa tcaactttgt tcatacaact ataagtacac aaagattaca 180

aaaatattaa tgttgcttct tattctatta cttttattaa taaaaattaa ttactttaaa 240

atcatataaa taataagatc taattaattg ataatataat ttttagtcac taataaatgc 300

atatgaaact cactcttttt cttcttctca aaatcacctg ctaatatata tatttttggg 360

gtttctattc tacattaaaa catagtaccc tatttatact aatcactgac tattatgctc 420

atatagtgaa cccaatttat attaatc 447

<210> 591
<211> 433
<212> DNA
<213> Glycine max

<400> 591

agcttaccac ctttcccatg atgcagtcac cagattgcga acttcccttt aaactcatgt 60

gtgatgcctc taactatgca cttggggttg ttttgtcaca gagagttaat aaactatccc 120

atgtcattgc ctatgcttca cgcactttag atgcaaccca agttaactac accaacacta 180

agaaggagct tttatctatt gtttttgctt tagagaaatc cagatcttat tttctttgct 240

ctcgtattat tgtctttact gaccatgcag ctttgaggta cttattgaag aagccttatg 300

ctaaacctag attgataagg tggatgcttc ttcttcagga gtttgatatt aagattaaag 360

acaggagtgg tgcagagaac ttggttgttg atcatttgag ctagattgag gaacttattg 420

atttctttcc tat 433

<210> 592
<211> 430
<212> DNA
<213> Glycine max

<400> 592

tgtttacccc atgttgaatt tgcttacaat agagttgttc ataatgccac taattgttct 60

ccttttgaag ttgtttatgg ttttaaccca ctaactcctc ttgatctttt gcctatgcct 120

aatgtttctg tttttaagca taaagaaggt caagcaaagg cggactatgt gaagaagctt 180

catgagagag tcaaagatca aattgagagg aaaaataaaa gctatgctaa acaagccaac 240

aaagggagaa agaaggttgt cttctaaccc ggagattggg tttgggtgca catgagaaaa 300

gaaaggtttc caggacaaat aaaatctaag cttcaaccaa ggggagatgg accatttcaa 360

gtgcttgaaa gaatcaatga caatgcttac aaagttgagc tgcccggtga gtataatgtt 420

aattccacct 430

<210> 593
<211> 422
<212> DNA
<213> Glycine max

<400> 593

agcttatgtc tggtcgagta tacatctaag catatataac tctcccaaca acttatgcat 60

atggaattgc ttccattttt ttcgttccaa ttcatttcta agacattgtg cgagactaaa 120

tttgtctcct ttctgaattg gaatgggtga tgttgagcac ttttccatcc tgaatctctc 180

tagtacttta ttgatatatg atttctgaga caaccctaac aatccttgtg atctatttct 240

gaatattttt atccctatca cataacttgc ctcacccata tcttgcattt taaagatgct 300

agagagaaac ttcttagtct catgaagtag accaagatca ttagttgcaa gcaaggtatc 360

atcaacatgt agaattagaa aaataacctt actcccactg accttcaaat atatacactg 420

at 422

<210> 594
<211> 229
<212> DNA
<213> Glycine max

<400> 594

tttcactctg atgtccgatt caggcgcaga atatatcgag aagttcgaaa atgaacaaag 60

gaagctcttg agcactatca atgatcataa cttttaactc ggatgtccga tttacgcgca 120

taatatatcc acacatatca aattgaacaa tggaagctct tgagaaattc aaacggtcat 180

aactatttac tcggagggcc gagtcagtct cactatatat tgagaccct 229

<210> 595
<211> 374
<212> DNA
<213> Glycine max

<400> 595

agctttcatt gttcaatttc tagcgactct atatcttatg cgcctgaatc tgacctgcga 60

gtgaaaagtt ttgaccattt gaatttctcg agagcttccg ttgaccaata ttgagcgcat 120

cgatatatta tacgcctgta tcggacctcc gagtgaaaga ctatgagcat atgaaatgct 180

ctagagcgtc cattgttcaa tattgagcga ctcgatttat tatgcgcccg aatcggacct 240

tctacgtgaa ggttatgacc attggaatcc ctcgagagcg tcgggtgctc aatttcgagc 300

gtctggatat attatgcgcc tgaacatgac ttccgtgtga aaacttctga ccatttgtat 360

ttctcgagag cttg 374

<210> 596
<211> 443
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 596

agctntacta ttcaaagaat agccaagaaa tataccttca tatgattttg catcaaactt 60

gcccaagttg tctttcccat tatttatcac aaagcattta catcaacaaa tatgaagatg 120

ggaaatattt ggttttcttc ctttgtatag ttcatatggt gttttcttta agacaggtat 180

aattaatgct tattcattat atagcatgca atattaacag cttcagccca aaaatattta 240

ggaagatttg tatcattaag taaagttcta gctaattctt ctaatatcta ttttcctctc 300

aactactcca ttttgttgag aggttctagg tgtagaaaaa ttatgttcta taccattttc 360

atcacaaaat aattcataat atttattctc agattctcct ccatgatcac ttctaatgga 420

tgcaatgttg agattnttct tat 443

<210> 597
<211> 525
<212> DNA
<213> Glycine max

<400> 597

ttgagcaaat tgaaatgaca ataactttat acacggatgt ccggttgagt cccgtaagat 60

atcgagacgc tcaaaattta gatccgaagc tctgagaaaa ttgaattgac aataacttta 120

tacacggatg tccggttgag tcctgtaata tatcgagacg ctgcaaattg aaaacggaag 180

ctcgtaggaa attcaaacga caataacttt ttactcggat gttcgattga atcgggtaat 240

atatcgagac gctcaaaatt gagactagaa gctctgagca aattgaaatg acaataactt 300

tatacacgga tgtccggttg agtcccgtaa tatatcgaga cgctccaaat tgagaacgga 360

aactcttagg aaattcaaac gacaataact ctttactcgg atgcccgaca gagtgtcgta 420

atatatcgag agacgctcca tattgaaaac ggaagctcgt atcaaattca aacgacaata 480

acttttttact cggatgtctg attgagtccc gtaatatatc gagac 525

<210> 598
<211> 491
<212> DNA
<213> Glycine max

<400> 598

ctataaaact aagcttatgc tgcaacattt acatagacct cctcaacctc agcagcaaaa 60

tcaaccacag cagaacaatt atgacctctc cagcaacaga tacaaccctg gatgaaggaa 120

tcaccctaac ctcaaatggt ccagccctca gcaacaacaa cagcagcctg ctccttcctt 180

ccaaaatgct gctggcccaa gcagaccata cattcctcca ccaatccaac aacagcaaca 240

acctcagaaa cagccaacag ttgaggcccc tccacaacct tccctcgaag aacttgtgag 300

gaaaatgact atgcagaaca tgcagtttca gcaagagacc agagcttcca ttcagagctt 360

gactaatcag atgggacaat tagctacaca attgaatcaa caacagtccc agaattctga 420

caagctacct tctcaagctg tccaaaatcc caaaaatgtc agtgccattt cattgaggtc 480

gggaaagcag t 491

<210> 599
<211> 428
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 599

agcttgtcta aggcgcagaa gcatcagcaa aatgtttaca taattntgct tgacagttcc 60

agcatcagca tattcctaac atgacatgac atcatgcaca tgtcaatagt ggacttcaaa 120

aatagcttac caagaaaata tacttacatg aagtcatgaa caatactatt atcaaatgct 180

cccacttgat ttgagttgga aaaataggcg caaccacatt acaaataaaa tattatagaa 240

gtcacatgag attcctttgt aaagacaaac catacctgaa actgtgcacg tgaatcagcc 300

tctagtttgg aatagaaatc acgttcctcc atagaaaaat caacttttt cagctctata 360

tacttaggcg gcaaggaaat aataggttcc ccgtcaagaa gtgtacctac agagaatgat 420

catcacat 428

<210> 600
<211> 453
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 600

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tataaaagac cgcctgatga tacttcatcc ccctttggat tatctgaaag tgaagaatct 120

ggagcggggg aaaacaaaat aaaagaaaaa gctgtgaatg gaagtgactt tgctatggcc 180

gcagataagg ctggggcttc tgtgtttcaa atgaggaaga ataagatatc aactgatgaa 240

tctggagata gtgtgcatag acaaggaaga agtggaagga atttatcatt agtaaggcca 300

gacctccctt ctgggaggga gaagtcagag aatgtaccaa caatgaagcc agtacaagac 360

atgaagccta atgataagag taaaacgtaa gctggattta ttnttagatc tagttcatcc 420

tttctacttc tattttccaa aactgtcctc ata 453

<210> 601
<211> 439
<212> DNA
<213> Glycine max

<400> 601

gagctttgac tgacccctca cacttatact cctaacacgt cccgctaact aataaatcat 60

catttggcaa gtacccatcc ttcttaattt ttgaatgaag atcatgacgt atatgcccca 120

ggggctcata ttgagagcgt gggttatcac caactacgaa tacttgcact gtatcgacaa 180

cttctatcca actacaacct gcctgctttt ttaaccccat gtccttcatt ctcatcctaa 240

cgatcgctgc ttctttccat ttccctactg aagcatacat atttgaaagt aatgaatagg 300

tgcctgcatt ctgtggatca attttcaaaa ttatctctgc tacaagcttc ccaatatcag 360

catttccatg cacattacat gcagcaagga gcgctcacca gacagtcaat ggcacctctt 420

ccccaagccc ctgaatgat 439

<210> 602
<211> 473
<212> DNA
<213> Glycine max

<400> 602

ttgagaaaat tcaacaacaa taaattttta ctcggatgtc tgattgagtc atgtaatatt 60

tcaagacgct cgaaattgaa taccgaagct ctgagcaaat tcaaaccaca attacttttt 120

actcggatgt ctgaatgagt cccgtaatat atcgacacgc tcgaaaatga atgtttatgc 180

tctgagcaaa ttcaaacgac aataactttt tactcggatg tctgattaag tctcgtaata 240

tatcgagacg ctcgaaattg aatactaaag ctctgagcaa attcaaacga caataacttt 300

ttactcggtt gtctgagtga gtcccgtaat atatcgagac gctcaaaatt gaatgtttat 360

gctctgagca aattcaaacg acaataactc tttactcgga cgtgtgactg agtcccctaa 420

tatatcgcca cgctcgaaat agagtcttga tgctctgagc aaaatcaaac gac 473

<210> 603
<211> 437
<212> DNA
<213> Glycine max

<400> 603

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ttctcctttt gaagttgttt atggttttaa cccactaact cctcttgatc ttttgcctat 120

gcctaatgtt tctgttttta agcataaaga aggtcaagca aaggcggact atgtgaagaa 180

gcttcatgag agagtcaaag atcaaattga gaggaaaaat aaaagctatg ctaaacaagc 240

caacaaaggg agaaagaagg ttgtcttcga acccagagat tgggtttggg tgcacatgag 300

aaaagaaagg tttccggaac aaaggaaatc aaagcttcaa ccaaggggat atggaccatt 360

tcaagtgctt gaaagaatca atgacaatgc ttacaaagtt gagctgcccg gcgagtataa 420

tattagttcc accttca 437

<210> 604
<211> 322
<212> DNA
<213> Glycine max

<400> 604

tctacattca atttcgagcg tctcgatatg ttacgggact caatgataca tcccagtaaa 60

aagttgttgt cgcttgaatt ggctcacagc ttcaacattc aatttcgagc gtctcgttct 120

attacgaggc tcaatcagac atccgagtaa aaagttattg tcgtttgaat tggctgacag 180

cttcaacatt caatgtcgag cgtctcgata tgttactgga ctcgatccga catgcgagca 240

aaaagttatt gtcgtttgaa ttgtctcaaa gcttcgacat tcaatgacga gcctctcgat 300

atattacggg actcaatcag ac 322

<210> 605
<211> 378
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 605

tcgaatgtct gattgagccc cgaacatatc gagacgctcn gaaatgaatg gtgaaccttt 60

gagctaattc aaacgacaat aacatttttc tcggatgtct ggatgagtcc cgtagcataa 120

tcagacgctc gaaattgaat ggtgaacctc ttagctaatt caaacgacaa taacttttt 180

cacggatgtc tgatagagtc ccgtaacata tcgagacgct cgaaattgaa tggtgaagct 240

ctgagccaat tcaaacgaca ataactttnt tctcggatgt ctgatagagt cccgtaatat 300

atcgagacgc tcgaaattga atgttgaaac tcttagccaa ttcaaacaac aataactttt 360

tactcggatg tctgattg 378

<210> 606
<211> 366
<212> DNA
<213> Glycine max

<400> 606

ggaatgaatt tgttttctag caaaacaaat tattatacct atagttcata ttgctaaatg 60

gaccaatcta agttttgtgc ttttatttgt tttttgctta gctagtctct tcttaagtaa 120

tctcccttgt ttttcttgaa caataggtgg cagaacgtaa caatgatcct caattggcag 180

acttcattga gagcgagttc ttgtatgagc aggtaaaact tgcagttgaa ttcatagtat 240

ggttggattt cataagatat aagactcctt gaccattgta tgtaatacaa tactctgaac 300

tctttacgtt ctaaaataat tggtgtcttt tacacggatc aagaaaataa taataaataa 360

atgaat 366

<210> 607
<211> 467
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 607

gcaagcttat gcgttagctg actcanatct tgattcagag tcttcaaagt atgtgatctg 60

tctcttggag gaagctctta gatgcccttt agatggtctt cggaaaggac aagtgagtgc 120

taagttttgg attaaacatt ttatgctgat atcagtgctg aagtaatgta tttatatttg 180

ttattctttt aaattgtagg cactgaataa tctagggagt gtctatgtag actgtgataa 240

actggacctt gctgctgact gctacatgaa tgcactcaac atcaagcata cacgagcaca 300

tcaggggttg gcacgtgtat atcatcttaa aaatctccgg aaagcagcat atgatgagat 360

gacaaagcta atagaaaagg ctcggagtaa tgcatcagct tatgagaaac gttcagaata 420

ttgcgaccgt gacatggcaa agagtgatct tagtatggca tcacaat 467

<210> 608
<211> 407
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 608

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aacctttata ctttataaaa tatgcaaata tagtcttctt tttctaagaa ttcatcatgg 120

tttattagag ttaaaaaaaa aaagagtaaa tgcatatata ttctaaagct tgaaaatcac 180

attattaata aaattacaag atttcaatta caattatgtt cggtgagata tttcagtaag 240

tttctagtat tttttattag ctgaaaaaat tatttgacta ttcgataaat aaaccatntt 300

taatagttct taacattttt tgaaacatta tttagaataa tatttttaa aacgttaatg 360

tttaactttt tatatnnttt tattnttatc tttgatatat ttattca 407

<210> 609
<211> 390
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 609

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aagttcttat taaccctcta gcatatattt tttattctca tccataaaaa aataagaata 120

gcttgatgta tatatactat taattaagaa tttttattat ttatactaat tatatgcaat 180

tacttacaaa agttactttt tgacagaata tctcatatat tgaatctagt tggaacgatt 240

caaaacacaa cttaaatatg ttttcaaatt atattgagat tgacttttaa aattaaaatc 300

atcaaattaa ttttatgcca aaaaaattag tgagatggaa caagtcataa ttactctgaa 360

aaagagtnga actttatagt tttaactttt 390

<210> 610
<211> 355
<212> DNA
<213> Glycine max

<400> 610

tttaggggta tttgactaat gagggtttat gggtagttta ttaattaggg tttagtgtta 60

cttaaccaat tagggtttat gggtatttga aaaattaagc tttagtgtta cttcaccagt 120

tagggtttag gattatgaga caatttataa ttacttgatt gatcactatt taggggtatt 180

tgaaatttgg gattcatagg ttacttgata aattggagtt tatgtgcgtt tatctaacta 240

gggttatgaa tacttgacta ttagggttt agttttactt gatcgataat taagggttat 300

cgtacttgag taattaacgt ctttgggtac ttgacaaatt atgatttatg attac 355

<210> 611
<211> 310
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 611

aacacacttc aatcaaaatg ggtttggccc taggtgcaca agatatggaa tggaacaact 60

tgatgtgagg atactttctt acatggtaag ctngaaaaaa aatccatatg actcatgcag 120

aaagttntct cccaaaaggt gaagaaaggc aggtatgctt gctaaaaatg tcactttatg 180

gccttaagca atcacctcgc tagtggtaca aaagggttga tactttcatt tttaataatg 240

gctttaaaag gtgcgagtat gatggttatg tttacttgan ngacaatgag catgatgcta 300

ttgtctactt 310

<210> 612
<211> 446
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 612

agatggacca tttcatgtgc ttgaaagaat ctttgaaaat gcttacaaag ttgagctgcc 60

cggtgagtat aatgttagtt ccaccttcaa tgtctctgat ttatctcttt ttgatgcaga 120

aggagaatcc gattngagga caaatccttc tcaagaggga gagaatgatg aggacatgac 180

caagagcaag ggcaaggatc cacttgaagg acttggagga cctatgacaa gggctagagc 240

aaggaaagcc aaggaagctc ttcaacaagt gttgtccata ctgtttgatt acaagcccaa 300

gtttcaagga gaaaagtcca aggttgtgag ttgtatcatg gcccanatgg aggaggacta 360

aatgacacca ctttgtttca attttagagt gtttagtttg gctaaataat ggcccaatcc 420

ttgtaaagtt ggctaaccaa aaatat 446

<210> 613
<211> 382
<212> DNA
<213> Glycine max

<400> 613

tctttgtttc agatgaggca gatgagtttg tagctacctc atgctgtgag ttttaagcca 60

tcttctcaat caagtttctg gcttcagtag gagtcatgtc tccaagggct ccaccaccgg 120

cagcatctat catacttctc tccatattac tgagtccttc ataaaaatat tggagaagaa 180

gctgctccga aatctgatgg tgagggcaac tggcacatag ttttttaaat ctctcccagt 240

attcatatat gctctctcca ctgagttgtc taatacctga gatatccttc ctgatggccg 300

aggtcctgga agcatggaaa tttttttttct aaaaatactc tcttaaggtt atcccagctc 360

gtgatgaacc ttggagcaag gt 382

<210> 614
<211> 209
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 614

agaagatggt gagaggacta ccctctatta accaccttga tcaactctgt gaaggatgtt 60

tattggcaag caatttagaa tgagttttcc agaggagtca aacgcaagag ctaagaagcc 120

acttgagcta atacatgctg acgttngtgg gccaatcaag ccaagctcac taagtaaaaa 180

taactatttc gggcttttca ttaatgatt 209

<210> 615
<211> 397
<212> DNA

<213> Glycine max

<400> 615

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cttatcaccc atatcggcaa ttaaagaaag cttttaatgg aagccaagag aatgaaagta 120

caccaaaaag ccttaggctg aaataaagtt tatgattggg taaaggacat cgtaagtatc 180

tttgggaaga acccaaagaa ggaatcattt gagaagaaca tatggaagaa aaggtcaata 240

ttctttgatc tttcatactg gtctgatcta gatgtacgac aatgtataga cataatgcat 300

gtcatgaaaa atgtttgtga tagtttaatt ggcaccatta acattaaaga caagacaaag 360

gatggtttga aatgtcatca atatttgatt gacatgg 397

<210> 616
<211> 355
<212> DNA
<213> Glycine max

<400> 616

ttacatgtca aattcttgtt cccaccacat tatgagtttt taagtttaat gggcagcatg 60

ttgatatact gaaagattca atgttccaaa tgaataataa tcaagtggcc tagtgcatct 120

gaatttttga taatcaaatc aatgcataag ccctttaagc atgttttgat gtcctagaaa 180

tagtagattt ttaacatttg agcaagaaaa tcaaaacata cagtcatcac tcctgttgct 240

gcactgacac cagcttcacc aaacatagca gttgctgctt cagtgacaag agcagttgcc 300

ccaatattga ccaccctgca tacaacaaaa tactagcatg agaaacattc tatac 355

<210> 617
<211> 354
<212> DNA
<213> Glycine max

<400> 617

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aaaagttatg accatttgaa tttctcgaga gcttccgttg ttcaattacg accgtctcta 120

tatattatgc gccttaatcg gacctccgag tgaaaagtta tgaccatttg aattggtcaa 180

gagcttccat tgttcaattt cgagcgtctc gatatattat gcgcccgaat cggacatccg 240

agtgaaaagt tatgaccatt tcaatttctt gagagcttcc gttgttaaat ttcgagcgtc 300

tcgatatatt atgtgcctga atcggacctt cgagttaaaa gttatgacca tttg 354

<210> 618
<211> 347
<212> DNA
<213> Glycine max

<400> 618

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cgtaggcaca agggtgtggc cgaacctgta taaatttgag tttgcacttt cttttccctt 120

aatctccttt atttattatt gctttatatt catattcaaa ttgttttatt tgaatcaata 180

tttaagaaga ttgtcattaa gggaattcat aacttgaata aaaagtgaaa tacattttta 240

attggggaag tagtttggaa tatcttaatt caaccccccc cccttcttaa gatatctgag 300

gccgcttgtc taacaagtgg tatcacagct ttattcttgt ataaagt 347

<210> 619
<211> 395
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 619

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attcgctgcc caagcatcat ggtcttgcag gtgaagatcc tcataagcat cttaaggagt 120

tccatattgt ttgttccacc atgaagcccc ctgatgtcca ggaagatcat atctttctaa 180

aggcttttcc tcattctctg gagggagtgg caaaagattg gctttactac cttgctccca 240

agtccatttt cagctgggat gaccttaaga gggtgttctt ggagaaattc ttccctgcat 300

ccaggaccat tgccatcaga aaagacattt caggcatcan gcaacttagt ggagaaagcc 360

tgtataagta ctgggaaaga ttcaagaaat tatgt 395

<210> 620
<211> 473
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 620

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attgaagtta ctaagatgtg gagagccatg aaagaagcaa agcaactagt ggaagggaat 120

gagaggaaac aatatgccaa agtatttgat tatgcacatg aattattgat gagcaatcct 180

ggatcaacag ttaaaatcaa cacagtgcca agtccagaag gtccaccaca attttagagg 240

ctatatattt gtcttgctgg ctgtaagaag gggtttggtg ctggatgtaa accattcata 300

ggtctagatg gatgtttact aaagagtgca tttggaggaa acttgctttc ttgctgtggg 360

cttgatgaca ataaccacat ctttgttatt gcttatgctg ntgnggacat tgagaacaaa 420

gacaattgga aatggtttta actttgntgc atgaagatct tggggattac ata 473

<210> 621
<211> 307
<212> DNA
<213> Glycine max

<400> 621

agcttccatt ggttgaattt gagcacctcg atatatatgc gcctgattct aatctccgag 60

tgaaaagtta cgaccatttg aattcctcca gagcttccat tgttgaattt cgagcgtctc 120

gatatattat gcacaagaat cggacctctg agtgaaaagt tatgaccatt tcaatttctc 180

gagagcttcc gttgctcaat ttctagcacc tcgatatatt atgcgcctga atcggacctc 240

caagttaaaa gctatgacca tttgagattc tcgagagctt ccgttgttca atctggagcg 300

tctcgat 307

<210> 622
<211> 363
<212> DNA
<213> Glycine max

<400> 622

tgttgaatta ccgaaaggaa ataaggtagt tgtagcataa tggatatttc ataacaaatt 60

ggacgaaaat ggtgaggttg tgagaaacaa ggcaatatta gtctctaaag gtgactcaca 120

ataggaaggt ataaactaca tagaaacttt tgcacatatt gcacgtttag aagcaatacg 180

catcttactt tcatttgcaa cctatagtaa tatgaagttg tattaaatgg atctaaaaaa 240

cacattttta aatggattaa tccaagaaga agtttctatt gaacaatctc ctggatttca 300

aagtgaaacc cttcttcaac atgtttttaa actcaacaaa gcatcatatg gacttaaaca 360

agc 363

<210> 623
<211> 442
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 623

gcttgctaac ccatggaagc tcctaatatc tcccacactn tntaggttgt gccattcttg 60

gatggccttg attntcttag ggtccacttg gaccccattt ctaccaacta caaaacctaa 120

gaaaactata ttatctatac aaaaggtaca cttctctata ttttcataga gggtgttntt 180

cctaaggact gaaagaactt gtctgagatg tcctaagtga tcatctagcc tcctactata 240

cactaaaata tcatcaaaat aaaaaactac aaatctacct atgaaatccc ttaagacatg 300

atgcataagc ctcataaagg tgcttggtgc attagtgagc ccaaaaggca tcactagcca 360

ttcatacaaa ccanacttgg tcttgaaagc agntttccac tcatcaccct ttttcatcct 420

gatttggtga taaccacttt ta 442

<210> 624
<211> 463
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 624

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aattatgacc tttcaagcaa tagatacaat ccaggttgga ggaatcatcc aaatctgaga 120

tagacaagtc ctccacaaca acatcagcct gtccctcctt tccaaaatgc tactggtcca 180

agcaagccat atgttcctcc tccaatgcaa caacaacagt agcagtcaca acaaagacaa 240

caagcaactg aggctcctcc tcaaccttcc ttagaggatt tagtgaggca aatgaccatc 300

cagaatatgc aatttcagca agagacaaga gcctccattc agagtctgac aaattagatg 360

gggcagatgg ctactcagtt gaaccaagct caatcccaaa attctgacaa attgccttca 420

caaactatgc agaatccgaa aaatatgagt gccatcacct tga 463

<210> 625
<211> 360
<212> DNA
<213> Glycine max

<400> 625

tcagaattca atttcgagcg tctcaatata ttacgggact caatcatata ttcgtgcaaa 60

aagttattgt cgtttgaatt agctcagagc ttcagaattc aatttcgatc atctcgatat 120

attacgagac tcaatcagac atctgagtaa aaaagttatt gtcgtttgaa ttagctcaga 180

gcttcaaaat tcaatttcga tcgtcttgat atattacagg actcaatcag acatctgagt 240

aaaaaagtta tggtcgtttg aatatgctga gagcttcaac attcaatttc gagcgtctcg 300

atgtattacg ggaatcaatc agacatccga gtaaaaagtt attgccgttg gaattagctc 360

<210> 626
<211> 430
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 626

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atacatcgag acgctcgaaa ttgaatgttg aagctctcag caaattcaaa cgataataac 120

tttttactcg gatgtttgat tgagtcccgt aatacatcga gacgctcgaa attgaatgtt 180

gaagctctca gcaaattcaa acgacaataa ctttttttact cagatgtctg atagagtccc 240

gtaatatatc gagatgatcg aaattgaatt ctgaagctct gagctaatcc aaacgacaat 300

aacttttttgc tcggatgtct gattgagtcc cgttatctat tgagacgctc gaaattgaat 360

tctgaacctc agagctaatt caaacgacga ataactttta ctcggatgtg tgattgagtc 420

ccgtaataca 430

<210> 627
<211> 388
<212> DNA
<213> Glycine max

<400> 627

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ataccattat ttcctttaga tttaaggaaa atactgttta tcggtgtatg tatctgaagg 120

tcagtgggag taaggttatt ttctaatttt gtatattgat gatatcttgc ttacaactaa 180

cgatcttggt cttcttcgtg agactaagaa atttctctct agaaactttg aagtgaaaga 240

tatgggtgag gtaagctatg tgatagggat aaaaatattc cataatagat cacaaggatt 300

gttaggttta tctcagacag tatatatatc gataaagtgc tagagagatt caagatggaa 360

aggtgtttaa cattgcctac tctaattt 388

<210> 628
<211> 449
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 628

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cattgttatc atttatttct ccatcattga ggtgccactt gagctgccag gtctctccac 120

ctttgggtgt attctttgaa acatttgtgc ccctttttgc acatgttctg tagttgcatc 180

ctatctggag ccatatcaga attgtactga cactgcctaa cgaaagcaac tattaggtcc 240

ttccaagaat ggactcggga aggttccaag ttagtgtacc aggtaacagc taccccagta 300

agactttctt gggagaaatg tatcagtagt tcctcatctt ttgcgtatgc ccccaccttc 360

cgacaataca tctttagatg gttcttgggg aaagtagtcc ccttgtactt gtcaaagtcc 420

ggcaccttga acttgggagg ggtaatgat 449

<210> 629
<211> 358
<212> DNA
<213> Glycine max

<400> 629

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aagttattgt cgtttgaatt agctcagagc ttcaacattc aattttgaga gtctcgttat 120

attacgggac acaatcagac atccgagtaa aaagttattg tcttttggat tggctcagag 180

atttaacatt caatttcgag cgtctcgata tatgacggga ctcaatcaga catccgagta 240

aaaagttatt gtcgtttgaa tttgctcaga gcttcaacat tcaatttcga gcgtctcgat 300

atatgacggg actcaatcag acatcccgag taaaagttat tgtcgtttga attagctc 358

<210> 630
<211> 435
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 630

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atatatcgag acgctcgaaa ttgaatgtgg aagctctgag ccaattcaaa cgacaataac 120

tttttactcg gatgtctgat tgacgccccg aatatatcga cacgctcgaa attgaatgtt 180

gaagctctga gcaaattcaa acgacaataa ctttttactc ggatgtctga ttgagtcctg 240

tcatatatcg agacgctcga aatngaatgt tgaagctctg agccaattca aacgacaata 300

actttttact cggatgtctg attgagtccc gtaatatatc gagacgctca aaattgaatg 360

ttgaagctct gagccaantc aaacgacaat aactntttac tcggatgtct gattgagtcc 420

cgtcatatat cgaga 435

<210> 631
<211> 435
<212> DNA
<213> Glycine max

<400> 631

agcttgtatt tctctcccat ggttgatata atatctatga tggtatcaaa gctcttcctt 60

tgaagagccc tgctgcgcta cttatattct tcctctcgat tatcatatcc ttcattctta 120

catcatgagt gaacaacaac aagatcaatc acttaatgta cacagtcctt attaccttta 180

tctgggagaa aatccagcga tagctttggt ttcttcggtt cttgattcat ccaattataa 240

ttcatggagt cgatctatgc ttattgcatt aagtgcaaag aacaaatctg agtttgtcga 300

tggttttatt caaagacctg catcagatca tgcacttcat gcagcttgga agaggtgaat 360

aatatggtga tttcgtggtt ggttcattca atctctcttt caattaggca aacatactat 420

ggatggataa tgcac 435

<210> 632
<211> 461
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 632

agcttatgct acanacatct acaatagacc tcctcatcct cagcggctat ataagccaca 60

acagaacaat tatgacctct ncagcaacag gtacaaatcc gggtggagga atcatccaac 120

cttagatggt cgaatccttc acaacagtag caacaacaat aacaggctta ttttagaatg 180

ttgctggccc aagcagacca tacgttcctc caccaatcca gcagcaacaa cagcaacagc 240

cccagaaaca acaaatagtt aaggctcctc cgcaaccttc ctttgaagaa ctngggaggc 300

aaatgactat gcaaaacatg tagtttcaac aagagaccag agcctccatt cagagcttaa 360

ctaatcagat ggaacaattg gccacacagt taaatcaaca acagtcccag aattctgaca 420

gaataccttc tcaatctgtc cagaatccca caaatgtgag t 461

<210> 633
<211> 300
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 633

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atatcaaact gctccaaatt gaaaatggaa gctcgtagca aatttaaacg agaataactt 120

tttactcaaa tgtgcgattg agtcacgtaa tatatcgaga cgctctaaat tgaaaacgga 180

agctcatagc aaatgtaaac cgtaataacc tttaactcgg atgtccgatt gagtcctgtg 240

atatattgag acgctcaaat atgaaaacag aagctctgcg caaattctaa caacaataac 300

<210> 634
<211> 399
<212> DNA
<213> Glycine max

<400> 634

ctaagcttaa gaaaaagatg gcctcagcaa attccttatt tccagtaagg aattctatca 60

atagacctcc aatctttaat ggagagggtt accactactg gaaaacccga atgcaaattt 120

ttatcgaggc aatagatcta aatatctggg aagccattga ataaggcct tatataccca 180

ccacagtaga aagagtttca atagatggta gttcatcaag tgaaagcata accatagaaa 240

aacctagaga tagatggtct gaagaggata gaaaacgagt acaatacaac ctaaaagcca 300

aaaacataat aacatctgcc ctaggaatgg atgaatattt cagagtttca aattgcaaga 360

gtgctaagga aatgtgggac actcttcgat taacacatg 399

<210> 635
<211> 234
<212> DNA
<213> Glycine max

<400> 635

tctcatgatg aaaaatcacc attgaaggac ctcattgaag atcaaagatc cagcctccat 60

agaagctcca caagcaagct tccatcaagt tatgaccatt tgaatttctc gagatcttcc 120

gtggttcaat ttcgggcgtc tccatatgtc atgtgcctga atcggacctc cgtaagaaaa 180

tatatgacca tttgaacttc tctagagctt tcgttgttta atttcgagct tctc 234

<210> 636
<211> 389
<212> DNA
<213> Glycine max

<400> 636

tttctcagtc gtctgtaagg atgattgtgt gttagaaagc gacgatccct actgtagact 60

gtttttctgc catgtttaag ttgtatgtaa cttgtatttt cttcacagat ggggcatgca 120

tgatgaccct taacactgta accgctgaga ttcccatatg ctggaaagtc attaatggta 180

caaaaaagca ttgcacgcat ttcaaaggtc tccttgtgaa acacatcaaa cactacaacc 240

ccctcgtccc acaactttct cagatcttca accaacagac ttagataaac atcaatgtca 300

tttcctggct gtcttgggct cgatatcatc atagacaaca tcatgtattt tcgcttcatg 360

cataaccaag gaggcaaatt gtaaattac 389

<210> 637
<211> 482

<212> DNA
<213> Glycine max

<400> 637

ttaagcacct gagctgcagc tatgctgaaa cattataata gacctctcta gcagcaaaac 60

catctacaat agaataatca tgacctttca agcaatagat acaatccagg ttggaggaat 120

catccaaatc taggatggac aagtcctcca caacaacaac agtctatccc tccttttcag 180

aatgctgctg gtccaagcaa gccatatgtt cctcctccaa tgcagcaata gcagcaacaa 240

caacaaagac aacaagcaac tgaggcccct cctcaacctt ccttaaaaga gttagtgagg 300

caaatgacca tccagaatat gcaatttcag caagagacaa gagcctccat tcaaagtctg 360

acaaatcaga tagggcagat ggctacttag atgaatcaag ctcaatccca aaattctgac 420

aaattgcctt cacaaactgt gcagaatcca aaaaatgtga gtgccatcac cttgaggtct 480

gg 482

<210> 638
<211> 372
<212> DNA
<213> Glycine max

<400> 638

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catacaaaga tgatttactt tatgaggcat gtgaaaaggg aaaaaaatta aaaaactctt 120

ttttcaagaa aaaacattgt ttccacctca agaccttaca tattgatctg tttagtccaa 180

ccaaaagaca tctatcaggg gaaaaaaggt attgactcat cagagccgat gactactcta 240

aatggacatg ggttaacttc ctagcctaga agaatgaatc ttttagtgtc ttctttaaat 300

tttgtaaaag aattcaaaat gaaaagaatt atgcattacc ttaatcaaaa gtgatcatat 360

gggagaattt ga 372

<210> 639
<211> 370
<212> DNA
<213> Glycine max

<400> 639

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ttgtaataat gtgtccaacg agacagcttg gcaagcactc attgtagctg gaacatactt 120

agcttcacat gttgataaag ccactatgga ttgcttctta gaactccatg atattggtgt 180

tgcaccatac atgaatatgt aacctatagt actctttctg tcatctctgt ctcctcccca 240

atccgcatca gtatatccca ctaattcctc tgagttgttg ttgtctttat ttggaaatag 300

aattccagta ttgatggtcc cttttatgaa ccttagaatc ctcttagcag ttaggagatg 360

aggaattctg 370

<210> 640
<211> 369
<212> DNA
<213> Glycine max

<400> 640

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aagctctcga gaaattcaaa tggtcataac ttttcactcg catgtccgat tcaggcgcat 120

aacatatcga gacgcttgaa attgaacaac tgattttctc gagaaattca aatggtcata 180

acttttaact cgcatgtccg attcaggcgc ataacatatc gagacgctcg aaattgaaca 240

acggatgttc tcgagaaatt caaatggtca taacttttca ctctcatgtg cgattcaggc 300

gcataactta tcgagacgct cgaaattgaa caacggaagc tctcgagata ttcaaatagt 360

cataacttt 369

<210> 641
<211> 311
<212> DNA
<213> Glycine max

<400> 641

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agtttactta caacaatagc taccaagcca gtattggtat ggctcctttt gaagctttat 120

atggacgaaa gtgcaaaact cctaattgtt ggtatgatga tggagaagca gtacttcttg 180

gacctgaaat gctacaacag attaacgaac aagtgaagtt gatttgagag aagataaagg 240

catctcacga taggcaggag agctattatg atagaaggag gaagccacta tattctcagg 300

aaggagaaca t 311

<210> 642
<211> 321
<212> DNA
<213> Glycine max

<400> 642

tctcgatata caatagggct taatcggaca tccgagttat tagatattgt cgttagattt 60

ttctcagagc ttccattttc aattacgagc gcctcgatat tcaacgggac tcaatcggac 120

atccgagtca aaagttattg tcggttgaat ttacttagaa gttctgtttt caatttcgag 180

cgtctcgaaa tattataggg ctcaatcgga catccgaatt aaaagttatt gtcgtttgaa 240

tatacttaga gcttttgtat tcaattacga gcgtctcgat attctacagg acacaatcgg 300

acatccgagt caaagatatt g 321

<210> 643
<211> 433
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 643

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gtaattcgaa ctttaattat cttttaattc gttcctaaag atagatcgcc aaatctgttg 120

ctaactgcac attaatctgt taaagatata acagatttat gtgtccagta ttttcgggca 180

agatgtcctg gacatcgtat ccgacatcgt ggatcctgca gcttcaattc ttcatttgac 240

attntatctt gccttgtgca ttgtgcagcc caatctgatt ccttgacata acgttggaca 300

tcatgtgcag caactctagc tttccttcat tatctaagtg cttatggttt aacaaaattt 360

tagccaatct tttaaaactc agtaaagcta agcactaaca atctcccccc ttggcanatt 420

tgtctaaaca tac 433

<210> 644
<211> 445
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 644

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gcagaacaat tatgaccttt ccagcaacag atacaaccct ggatggagga atcaccctaa 120

cctcagatgg tccagccctc agcaacaaca gcagcctgct ccttccttcc aaaatgctgc 180

tggcccaagc agaccataca ttcctccacc aatccaacaa caacaacaac cccagaaaca 240

gccaacagtt gaggcccctc cacaaccttc cctcgaagaa cttgtgaggc aaatgactat 300

gcagaacatg cagtttcagc aagagaccag agcctccatt cagagcttaa ccaatcagat 360

gggacaatta gctactcaat tgaatcaaca acagtcccag aattctgaca agctgccttc 420

tcaagctgtc caaaacccca aaaat 445

<210> 645
<211> 437
<212> DNA
<213> Glycine max

<400> 645

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actattataa gttgtaagct tttggagaag caaagttgtt gaagttatgg aaggtaatgg 120

tagaaggagg aggcgccact tcagcagaat ccatgcattc tcttgtggaa aagcttcatt 180

caaaggggag cattcactca taggcggtcc tggattctca aggatagtgt actgcaacga 240

agcggaacgc ggtgagggga gtcttgtgag ctatggtgac aattatgtga gtactactaa 300

gtatacagtg gccactttcc ttcccaagtc cttgtttgag caattcagga gggttgccaa 360

tttttacttc cttatctgtg caattctgtc tttattcccg gtttctcctt actcggctgt 420

cagcaatgtt gttcctc 437

<210> 646
<211> 459
<212> DNA
<213> Glycine max

<400> 646

tagagcctcg ggtagttcat taaatatttg tttcatttca tccaagctca tattgtccaa 60

aacggagggt ctaggggcaa ccctcacaat ttcaccacct tttggttcct gaactcgtgc 120

gtcggcttta atgactagtt ctgaattaga gtttgcacca cattttatta taaatggtga 180

ggtcgagcca gtattaaatt ggagtacatt ccactgtgta acgtcagttt cagatccaga 240

gcccagatct gttgatggca tgcgatcatg agatatatct tgaatggggt catcttcttc 300

aggaattgac tgtatcataa caaaataaag gattcaggca tcaaagaaaa tcaatccaaa 360

ttaattttca tcagttgagt cctttagcat attataaaat tgttaccaac ttggacaacg 420

gatgaaagaa gttaagcata caatacacaa tacttcgca 459

<210> 647
<211> 397
<212> DNA
<213> Glycine max

<400> 647

actcagctgg gaaattatgt tctaatatga ctatctttga tctaagctat tataaagctt 60

gttgcaagct cgtaatttat aattgaaagt tattaacttg acttattgaa atataaatgt 120

ttgaataaaa tatatactgg aataattgat ttaaataaaa taattaaatc ttataaacat 180

attcatatga tattcttata taatttttaa ctttttttatg tcaattagta aaatataata 240

cacatatcat ctatcgataa caatatcttg atgtaatgct gaaataataa aataaatatc 300

gttaatatta taatggataa acattgtaat ataaaaatat ccgcataata ttaatataat 360

aaatcacaca tacattatta tctatcatta ttaatat 397

<210> 648
<211> 464
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 648

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attgagacac tcgaaataga atacagaagc tgtaagcaaa ttctaacgtc aataactttt 120

tactcgaatg tccgaatgag tcacgtaata tatcgagaca ctcgaaattc aatacagaat 180

ctctgagcaa attctaacga caataacttt taactcagat gtctgatcga gtcccaaaat 240

atatacagac gctcgaaatt gaatacagaa gctctgagca aattcaaacg atgataagtt 300

ttaacttaga tgtccgatcg agtcccacaa tatatcaaga tgctagaaat tgaatacaga 360

agctgtgagc aaattctaat gacaataatt ttttacttgg atgtccaatt gagtcgtgta 420

atatttcgag acgctcgana ttgaatagag aagctctgag gaaa 464

<210> 649
<211> 267
<212> DNA
<213> Glycine max

<400> 649

acttttatgc tgaacaaatg atggcttgaa tgtgaaaagc atgttgaaat gagaaacttt 60

gaaaatttta aaattggaaa aatttcagaa aatggtttct ttagacatga aggctttctt 120

tttaaaaaaa acaaattgtg tgtgcctaaa tgttctacta aaaatttgct tgtttgtgaa 180

gcacatgagg aggtttaatg gggcattttg gggtccaaaa gactctataa acattacaag 240

aacagtttta ttggcctcat atgaaaa 267

<210> 650
<211> 465
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 650

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tcttaagaag ggggttgaat taagatacta caaactattt ccccaattaa aattctattt 120

caatttcaat gcaagttaca agttcccttg aaaatgaact cttaaataat gattcaaata 180

gaacaatatg aatataaatg taaagcaata acaaataaaa gagtttaagg gaagagaaag 240

tgcaaactta gatttatact ggtttggtca cacccttgtg cctacgtcca gtccccaagc 300

aaccggcttg agagtttcaa tatcttgtaa aattccttta caatttctga acacacaagg 360

acaatacttc ctttgtgttc agatttcttt acaacaagag accctcggtc tctcaatccc 420

ctttgagaat ttagaaagaa gagaagaata aatctctctt gaaag 465

<210> 651
<211> 405
<212> DNA
<213> Glycine max

<400> 651

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gcaaaaaaat tatgacctct ccagcaacag atacaaccct ggatggagga atcaccctaa 120

tctcagatgg tctagccctc aacaacaaca acagcagcct gctccttcct tccaaaatgt 180

tgctggccca agcagaccat acattcctcc accaatccaa caacaacaac agccccagaa 240

acaacaaaca gttgacgctc ctccgcaacc ttccctcgaa gaacttgtga ggcaaatgac 300

tatgcagaac atgcagtttc aacaagagac cagagcctcc attcagagct taactaatca 360

gatgggacaa ttggctacac aattaaatca acaacagtcc ctgaa 405

<210> 652
<211> 387
<212> DNA
<213> Glycine max

<400> 652

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aagaaaagct tactaaggca cctgttctag ctcttcctga cttttctaaa acttttgagc 180

tagaatgtga tgcctctgga gtgggagttg gagctgtatt gttcaaggtg ggcaccctat 240

tgcttatttt agtgaaaaac ttcatagtgc caccctcaac taccccacct atgataaaga 300

gctttatgcc ttaataagag ccctccaaac ttgggaacat taccttgttt ccaaggaatt 360

tgtcattcat agtgatcatc aatcact 387

<210> 653
<211> 386
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 653

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tatcttaggg atcaagtgaa caaagagaaa ctgaaagtgg agtactgcta cacatttgat 120

caacttgctg atattttaac caaacccctc aaaggggaga ggtttaaaat gttaaggggc 180

ataattggct tgatgaactt aggagatcag aattaaggga aggtgtgaga gtttaatttt 240

gttttgtgtg gggtagattt gtttgtgctt tgaatataag agagagtaac agaattttaa 300

aattctgtta taagtactag cctaagtgtg aagggttatt actctgtntt tgcttgtata 360

aaagggcata catacatctt aataaa 386

<210> 654
<211> 358
<212> DNA
<213> Glycine max

<400> 654

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acttggaccc tatttctacc acctacaaaa cctaagaaaa ctattttatc tacacataag 120

gtactcttct ctatatttgc atagagggtg tttttcctaa ggactgaaag aacttgcctg 180

agatgtccta agtgatcatc tacgctccta ctatacacta aaatatcatc aaaataaaca 240

actacaaatc tacctatgat atcccttaag acatgatgca taagcctcat aaagtgcttg 300

gtgcattatg gagcccaaaa ggcattacta tccttcttac aaaccacact tggtcttg 358

<210> 655
<211> 403
<212> DNA
<213> Glycine max

<400> 655

agcttgataa cccattcttc tttccttatt acatgatgca taagcctcat aaaggcgctt 60

ggtgcattag tgagcccaaa aggcatcact agccattcat acaaaccaaa cttggtcttg 120

aaagcggttt tccactcatc acccttttc atcctgattt ggtgataacc acttttaaga 180

tcaatttttg aaaaggtatt ggcaccatgc aactcatcaa gaaaatcatc aagtctagga 240

atggggtgcc tatactttac agtgatgttg ttgatggccc tgcaatctgt acacattctc 300

catgtaccat ccttttggg caccaacaac actggcacaa cacatgggct taggctctct 360

tggacccaac ccttctccaa caattcttta acctgagact cta 403

<210> 656
<211> 469
<212> DNA
<213> Glycine max

<400> 656

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ccatggctta ttccttatgc gcctgaatcg aacatccgag tgaaaagtta tgaccatttc 120

aatttctcga tatcttccgt tgttcaattt cgagcgtctc gatatgtgat gttcctgaat 180

cggacctccg tgtgaaaagt tatgagcatt tgaatttctc gagagcttac gttgttcaat 240

ttcgagagtc tcgacatgtg atgtgcctga atcggaccac cgcgtgtata gttatgacca 300

tttgaatttc tcgagagctt ctgtcgttca attgcgaggg tctcgatatg tgatgtgcct 360

gaatcgaaca tccgagtgaa atgttatgac aattctaatt tctcgagagc ttccactgtt 420

caatttcggg cgtctcgata tattatccgc ctgaatcgga catccgagt 469

<210> 657
<211> 336
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 657

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atggaaactc ccgagaaatt aaaatcgtca ttacttttca ctcggatgtc cgattcaggc 120

acttcagata tcgagacgct cgaaattgaa caacggaagc tctcgagaat ttaaaatggt 180

cattacttta cacatggagg tccgattcat aaacatcaca tgtcgagatg ctcgaaattg 240

aacaacggaa gctgaagaga atttcaaatg gtcataactt ttcacttgga tgtccgatnc 300

aggcgcatca tttatcgagg cattggttat tgaaaa 336

<210> 658
<211> 389
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 658

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aggtagttcc aaagaaaatc ggcctcaccg tgataaaaaa tgagaaggag gagttgattc 120

ctactcgagt gcagaacaat tggagagtat gcatcgacta taagaggctg aaccaggtta 180

ccaaaaagaa ccattttcca ctgcctttca ttgaccagat gcttgaacgc ctggcaggta 240

aatctcacta ctatttcctt aatggttttt ttggttatat gcaaatcact attactcctg 300

aggatcagga aaagaccaca ttcacctgcc ccttcggcac ttttgcctat aggaggatgt 360

ctttcggcct gtgcaatgcc cctggtacc 389

<210> 659
<211> 456
<212> DNA
<213> Glycine max

<400> 659

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tgttgcccaa gtttcatggt cttgcaggtg aagatcctca taagcatctt aaggagttcc 120

atattgtttg ttccaccatg aagccccctg atgtccagga agatcatatc tttctaaagg 180

cttttcctca ttctctagag ggagtggcaa aagattggtt atactacctt gctcccaggt 240

ccattttcag ctgggatgac cttaagaggg tgttcttgga gaaattattc cttgcatcta 300

ggaccacttc catcagaaaa gacattttag gcatcaggca acttagtgga gaaagcttgt 360

atgagtactg ggaaagattc aagaaattgt gtgcaagctg tcctcaccat cagatttctg 420

agcaactcct tcttcaatat ttctatgagg gactta 456

<210> 660
<211> 377
<212> DNA
<213> Glycine max

<400> 660

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cctaactaga tgattgagat gatgcatgtt tatgtgtgca gtcctacaat gccacaacca 120

agaatcatct ttcttactta ccaaacaact cagttcatga aacgatgcat gttcaatgtt 180

taacatatag atattaccta tccttttacc aatatggaca acctcactgg atatggcttc 240

actagtaagg caacaattct tgttgaattt gattttgaag cctttgtcac atagttggct 300

aatgctcagg aggttatgct ttagtctatc aacatataga acattctttg tttgtgtttt 360

gtactaattt ccaatat 377

<210> 661
<211> 447
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 661

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tgaaggtctc caagatctcc ttttccgctt cttccatttt ttttgtttgg aattgcttta 120

ggtgggaatg gaagagggat aggaggctgc tgtaagtcag aattactaga agaaggtcta 180

cctgcatgaa aatttttgtt aggaagctct ctcttttgtg caactatctc atcctctttt 240

tcaggtgtag aatgaagctt gacaggttca ngtgcaggtg ctgctactta tggaggcact 300

tgaatttggt tgccagacct caacgtgatg acactcacat tntttggatt ctgcacagtt 360

tgtgaaggca atttgtcaga attttatgac tgagcttgag tcatctgagt agccatttgt 420

cccatctgat ttgtcagact ctgaatg 447

<210> 662
<211> 393
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 662

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atgttgaaca acctccataa tttgaaataa cagataagcc aaatcatgtt tatagattga 120

aaaagacttt atatggtttg aaacaagccc caagggcatg gtatgaacgt ctaagtaaat 180

ttcttttaga aaaagatttt tctagaggaa aagtggatac cacactattc ataaagagaa 240

agtatgatga tattatgtta gttcaaatat atgttgatga tataatattt ggatccacta 300

acgattcatt gtgcaaggag ttctctcttg atatgcaaag cgaacttgag atgtcaatga 360

tgggagaact aaattacttc ctgtggttac aaa 393

<210> 663
<211> 395
<212> DNA
<213> Glycine max

<400> 663

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taatcgatta cacagtgcaa attttgaatt taaattttaa tagctgttgt aaatcagttt 120

tggccaccgg taatcgatta catcctctgg taatcgatta ccagagagta aatttgttga 180

aaaagacttt tttaacttaa aattcttggc caaacctttt gcaatttcaa ttggaattcc 240

cttcctattt aatatccttt ctaagactct atagactgtc ttgatcatcc atcttgaata 300

tctttaattt ctttgtcttg aataaagctt tgagacgcat gtgaaacttt ggcatcatca 360

aaacattcag ctttatcctt tgtctacaaa tttgg 395

<210> 664
<211> 446
<212> DNA
<213> Glycine max

<400> 664

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aagaatgtgt aagctgactt ctctctcatt tccttttata ttcccagatg aaatgtaggt 120

tccatggcta gttgtacttt cctatgcact tggatataat aaacgaagtt cggtaaccat 180

aaagataatt acaatttggt gagcctgcta aatgtttata agggaccgtg tagtggaaca 240

tctttggaga caggtgtgcg agggaaacaa actacttgct gactcaaatg atcaatgcag 300

atgtaatgcc gaagacattc tattggaaat ggaccgtatc ttacagcctg aaggagctgt 360

gatattccga gatcaagcca acatgttaat gcatgtgaac agaactgtga aatgaatgag 420

atggaatacc agaatggtgg atcatg 446

<210> 665
<211> 450
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 665

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aataaactct tcttggtagg aatatgaact ctatcatgca aaattgcatg gtcactggca 120

gccacatttt caattaagtc catggcttct ttaggtttct tcaacttaat ttttcctctt 180

gcataaacgt cgagtaactg ctttgattgc ggccgtaacc catcaatgaa gatgttcagc 240

tgtataggct ctgaaaaacc atgagtggga gttttccgca gcaagctacg gaatctttct 300

aatgcctcac tcaaagattc atcaggaaac tgatggaatg aagatgcagg tctttaaact 360

gttgcccttg aatgaatgca accatctctt ggcctcccca gataaagaaa atgaaaatag 420

gctgagccta atagcatatc caggtacatc 450

<210> 666
<211> 385
<212> DNA
<213> Glycine max

<400> 666

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ctacggaacg cagtcaaaca tccgagtaaa aagttattgt catttggatt tgctcaaaga 120

ttctgttttc aatttgaagc gtctcgatat attacaggac tcaattggac atccgagtta 180

aatgttattg ccgttttaat ttgttacgag cttccatttt caattacgag cgtctcaata 240

tattacggga ctcaatcgga tatcctagtt aaaagttatt gtcatttgaa tttgctcaga 300

gcatctattt tgaatttcga gtgtctcgac atactacggg actcaatcat acatccgagt 360

aacaagttat tgtcggttgg atttg 385

<210> 667
<211> 386
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 667

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aacactgtat ccttgaaaag caaaaaaagg tcagcttctc aagggcaggt aagactccta 120

aagttgaana gctagaattg gtgcacacaa atgtttgggg gccagcccca gtgaaatctg 180

ttggaaactc acgctattat gtcactttta tcaacgagtc taccagaaag gtatgggttt 240

attttcttaa aaataaatct gatgtgtttt ctgtgtttaa aaggtggaaa atagaagttg 300

aaaatcaaac aggtctaaag gttaaaagtc tgaaatctga caatggtagg gagtatgata 360

gtcaggagtt taaagacttc tgttca 386

<210> 668
<211> 362
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 668

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ttctgcaagg taagaacagg gattgcaaag attgagtgtg cagttcttcc ctcagacaac 120

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gcagaggcta gtgtcttccg catgaaagtt tttcaatccc cctataacca taaaggaaga 240

aaatgccacc atattgcata ttaacatcat tcattactat atcaaagata ctttnttgct 300

catctgcacc aaggaaagtt gaaaatattc ttaattactt aagatatata aataattgaa 360

tt 362

<210> 669
<211> 459
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 669

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tgtcttagcg tagttgatcc cttctacttg atgattatcg agtataacta accgggcttt 120

aaaaggttca attgtcccat ccaagtgata cttcatgcgg tacacccatt tgcacctgag 180

agctttcttt tcgggtggta gttgttgcat ggtccacgta cgatttcatt caagagcttg 240

aatctcagat tgcattgctt ctttcttgtg agcatctttc actacctcat gaaaatagag 300

tggttctttt tctgcaataa taattgcaag gaaatgtcta tgtggcaaag aaaatttttc 360

acaatttaca taatgcgaga taggatagga tgcacctgan aaaatgagat taagccgatg 420

aacgagtgat aggagataac ttcttaatca tgtgtatga 459

<210> 670
<211> 457
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 670

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tattatgtac acatatatga taagttatga atgtattgaa acgttattta ttaatttaat 120

tctcctcaag gaccgagatt atgtattttc ctatgcacat ttaacagaat atttgcaagt 180

attgattata cattgagact ctatgtagaa aaagatataa acacaatttt tataaaataa 240

aatttcataa aattcaactt tataagattt attcttagtt cctacaatgc atatatgcgt 300

gtttcagtgc tttttaactt tccttatatt tgcttcaaaa atatggtaga ttttagagat 360

atatgaactt agtccaccaa ttaaattata acttgtatgt gtccttattt ctcanatatt 420

atagtaatgc aacattctca aatactcaca tccttct 457

<210> 671
<211> 405
<212> DNA
<213> Glycine max

<400> 671

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cctcattcaa cttgtggggg cgcaccttct tgttgaacgc gttctttatc ctttgttgat 120

acaggcgcct atggctcatg ggcgtcaaac gcttaccttc aataaggttg agttggtcgt 180

agcgtgtttg agcccactct gattcttcta ggcccgattc tgctagtatc ctctgggaag 240

ggacctctac cttaaacggg agcactgctt ccatcccata aaccaaggag tacagtgttg 300

ccccagtaga atttcgtacc aaggttcggt acccatgcag ggcaaaaggc aacatttcat 360

gccaatcttt gtacgacact gtcataccct aatttcgtcc aagga 405

<210> 672
<211> 451
<212> DNA
<213> Glycine max

<400> 672

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taaaggagaa gagatgagag gaggcaccat ccactagaga ataagccatg aaaggagaag 120

cttcaccacc aagagagtgc cttggataag aatcttagag agcgccatcc actaaatgtg 180

cttaggtgtc atgaggcatg taaagcatga aggacatgca caaagtgtga ctatatgatg 240

tggcaatggg gtgtagcaag caaatgctca cctccccctc taaaatttaa ttggattgag 300

cttttcccaa ttcaattaaa tttatttccc aacacacata tcaaatattc acttaattcc 360

tatgaaatta cagaactacc cctaatacaa aaactagtct aggtgcccta aaatacaagg 420

gctgaaaaat cctacatttc tagggtaccc t 451

<210> 673
<211> 272
<212> DNA
<213> Glycine max

<400> 673

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ggggcaagta aattttcttc ccatcagacc ttggatgcaa gtgtgatcgt atccccatct 120

catctagatc ttgacgggta ttcaagtcat ccttcatctt gccttgaatg ttaaggagca 180

tcccaatcac attgtcacat acatttttct ccacatgcat aacatcaata caatgtctaa 240

cgtctagatt agaccagtcc gaaagatcaa ag 272

<210> 674
<211> 395
<212> DNA
<213> Glycine max

<400> 674

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aggccagctg tgatgagtga caaaaacaat gctgtcctgt tagatgcaaa accagccaac 120

tgaacaatgg tgggactata atacatcaca gtgttgattc ccacaaactg ctggaagatt 180

aagaggccca caccagcata taaacctctt ctcacagctg aagttcttaa aagtttgact 240

atgttgatct tctctgatga ttctgcttcc ttaatttcca tgtcaactga ttctttcaag 300

gcctgaattt cgccttcaac ttcatgtggt ggataaatct ttttcagaat cgattttgct 360

tcctcttcct taccctgtgg gaacaaaaat ggaac 395

<210> 675
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 675

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cgagcaaaat aggtggcgtc taatataatt taaattgtaa gttcaacatc aattttcaat 120

aaaaaaaacc aatgttaaca aattcatgtt aacgttaaca tcggttttat tcaataaacc 180

gatgttaact gatcatacgt taacatcggt tttcagaaaa ctgatgttaa cgaactaagg 240

ctaacatcgg ttttctgaaa acccgatgtt aactaattaa tgttaacatc ggtttttcca 300

gaaccgatgt taaagtcact ttgttaacat cgattntatt caaacccgat gttaaagtat 360

acacaatatt cacaattatg ccacgacgtt tatcttaaca ttggtttt 408

<210> 676
<211> 435
<212> DNA
<213> Glycine max

<400> 676

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atcgatcgcg gactgtaaca acattaagag acctgtaatc gacacatatg cgccatgttc 120

catccttttt cttcacgaga agaactggag acgaatatgg gctcgtgctt gatcttatta 180

agcctgcaga taagagttct gcgatttgcc tctcaatctc ggcctttga aagtgtgggt 240

acctataagc gcgtacgttg accggagctg ttgcagggag aagggtgata cgatggttta 300

cttcgcgtga gggaggcaag cttctgggtg gttggaaaag tttatcgtat cggagaagaa 360

ggtttgcgat tggtgtgata atacgtggag gatgtgtggc tgtacctgtg ggggtttcag 420

ataagagaca taagt 435

<210> 677
<211> 358
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 677

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aatatttta taactgttaa tttgtttatt aatttcaaaa attattttaa caaataaatt 120

aattcaaaca ttttgtatat tttaatgagg aaagtatatg attcgatatt atcattttag 180

tgatgtattc aagtttcttt gaaatatatg attagataac attattttat cacgtattca 240

cataatttaa ataaaaagtt acaataacgt gaggaatagt gaaattttgt tacgcaagat 300

aatgaaattt gatatattct tattaaattg atatagaatg aaatataana atttaaaa 358

<210> 678
<211> 434
<212> DNA
<213> Glycine max

<400> 678

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ctatttcaat tgaatgatta ataataaaaa atcaatattg attcgaatta taataatact 120

aacatttttt ttattagtag gaagtgaatt tatgtactag aaagttcaat aactcacgcg 180

cattattcaa taaagttaga ccgacttggt attataatac taacatgaac acttatttca 240

tctgcataac ttatcttaat aatttggtca tttaattttt atttttttaa gtacaaaggt 300

ctaaaatagt caatagtttg atgtatatat attattattg gacatagaat atcaaaattg 360

taaataatgt taaaactaat ttatatttga tatattaact aatttcacaa tagtttgaat 420

tatttttaa tatg 434

<210> 679
<211> 182
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 679

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tgattgttga tttgctttcc aactgattgt tgtaccaaac aaagtgaaca catattctgt 180

ta 182

<210> 680
<211> 506
<212> DNA
<213> Glycine max

<400> 680

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gattaatttt acttgcaaaa gcttatatgg aacaagctga gatgactaaa gcggtcctgg 120

atttgttctg ggggaaaaat gaatgtggag aaaaccaaga tattcttctc agaaaacatc 180

aactggcata taaaggagga tcttactgca aagattggtt ctcaatgtac tttggggaaa 240

tatcttggag tgccgatatt ccataaaaag gtgaagaaag aatcctttga gttccttcta 300

cataaagtta atcacatatt aagtggttgg aaaagtaaaa tgttatccat ggcgggtaga 360

ttaaatcttg caaagtatgt gaacaaagct cttccctcat atgtgatgca aattgtgaaa 420

attccggcct acatttgtgg tgaaatttat agaaatgtag agcattttta tttgggggat 480

gatgagaata cgacgagagt gcatat 506

<210> 681
<211> 169
<212> DNA
<213> Glycine max

<400> 681

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atgcaagttg aaagccttgg aggaaagagg tatgcctatg ttgttgggga tgatttctcc 120

agatttacct gggtcaactt tatcagagag aaatcagaca cctttgaag 169

<210> 682
<211> 620
<212> DNA
<213> Glycine max

<400> 682

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atgcttgata gatgaggaag aaagctttct tgtctctctt tcttgaatcc tttaaagtct 120

ccttttgtgc ttgggatagt gaagtctcat cttgcggctc cttataacct ttttcaacca 180

tttttcaaac atcatgtgct ccaagaagga ccttcatttc gatgctctaa ttgtcatatg 240

cgctcccctt tagaaatgaa acttggaagg atgccgctca attgcttgcc ataactatag 300

aggaatttct tatcaaaacc taagctctaa taccactttg ttggaaagga gataggaagt 360

atttgagaga aatggaggag gagagaatat ttgaaaaaag gctagttttt atcacttgag 420

atacgctttg ggcttgactc ctttttgtgt ctttggatgc tttacaaata acaacctctc 480

cccctattat aggcttcaat gagggattct aaatacctca agaaagatcc acacacctta 540

attgagagtt tacacatttt ttccaactac ttagttctac acacctcttt ccatgcaaat 600

attttttca cttatttcta 620

<210> 683
<211> 392
<212> DNA
<213> Glycine max

<400> 683

tgaaattgaa caacagaagc tcttgagaaa ctcaaatgtt catatacttg tcacacggaa 60

gtccgatgca ggcgcataat atattgagat gctcgaaatt gaacaacgaa tgctctcccg 120

aaattcaaat ggccataact tgtcacacag aagtccgatt caagtgcata atatatcgag 180

acactcgaaa ttggacaacc aaagctcttg ataaattcaa atggtcataa cttttcaaac 240

ggaagtctga ttcagccaca taatatatcg agaagcttga aattgaacaa cggaagctct 300

cgggaaacaa aaatggtcat aacttatcac acggacgttc gatttaggcg cataaaatat 360

ggagacgctt gaaattgaac agcgaatgct ct 392

<210> 684
<211> 176
<212> DNA
<213> Glycine max

<400> 684

agcttaagag cctacttttg tggcaaaaca atatagttgg aacaatccca taagagcttg 60

gaagctgcat agagatcaaa gtcctagact tatcagaaaa ccttctcaca agtagcatac 120

caaggagctt tggcaacatt tcaaatatcc aggagcttca actaagtgtc aataag 176

<210> 685

<211> 554
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 685

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aaagagtggt ggaatttgca ggaggatttt gcttgtagat cattgtatca agaacggtgt 120

caaaattctg aggagaatct agggagacaa agaacatagg aattgcaacc ttctgatgga 180

tttctaggtc gcccacaagg ttaacaagct caacaaaatc actgataagg cgctgaggaa 240

catagaacac ctcagaactg catattagga ggtttttatc gttgtcgctt ggttctttgt 300

aactgacttg aaagtgcgct ggcatcgtgc taacaacctt ctgtaccatt cttgcttgtt 360

gtgataacca atctgagtcc tcaccatttg ttaatataga agaccaagac tcggatacct 420

gaattcccag taatgtgtaa attgtcagag aaaagagcta tacgaccttc taagagctat 480

atgacctttt aagagttaaa gctatgctgt anaatatttt cagtgacatt gtcctgaatg 540

attgaatatg atct 554

<210> 686
<211> 609
<212> DNA
<213> Glycine max

<400> 686

tgaaggacat gcacaaagtg tgactatatg atgtggcaat ggtgtgtatt aagcaaatgc 60

tcacctcccc tctaaaattt aattggattg ggcttctacc aattcaatta aatttatttc 120

ccaccataca catcaaatat tcacttagtg cgtgtgaaat tacaaaacta cccctaatac 180

aaaaactagt cttggtgccc taaaatacaa ggactgaaaa atcccatatt tctagggtac 240

cctacctaca ttatggagcc ctaaatacaa ggaccaaaat taatgaaacc ttaatctaat 300

atgtacaaag ataagtgggc tcatacttag cccttgggcc cgaaatctat cctaaggctc 360

atgagaaccc tagggccttc tcttgcatct ttggcccaat cttcttggaa tcttctatcc 420

aatgcccttg cggggtagga ttgcatcact aatgtaccca accctagggt attttatgaa 480

taagagccta agagaaacct acctttagcc caaactagaa aaactattat tgcatgcctt 540

ccgaaattca tgcataagct aacatggtaa acacacgaaa aaatcgagtc aacgagagac 600

acaactttg 609

<210> 687
<211> 179
<212> DNA
<213> Glycine max

<400> 687

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aagagcctta gatatatgtt tgatcaaaga gagcttaaca tgaggcagag gagatggtta 120

gaggtcctta aggattacga attttagctt aactatcacc caggtaaagc caatgtagt 179

<210> 688
<211> 362
<212> DNA
<213> Glycine max

<400> 688

tgagcaaatt caaacgacaa taacttttga ctcgaatgtc ctattgtgtt ccgtaggata 60

tcgagacact agtaattgaa aacggaagct ctgagaaaaa tcaaatgaca ataacattta 120

actcggatgt ccgattgagc cctgtaatat atcgagacgc tcgaaattta aaacggaagc 180

tctaagaaaa gtcaaacgac aataactttt aactcggatg tccgattgag tcccgtaaga 240

tatcgagacg ctcgtaattg aaaacggaag ctctgagaaa aatcaaacga caataacttt 300

taactcgaat gtccgattga gccttgtaat atatctagac gctcgtaatt taaaacggaa 360

gc 362

<210> 689
<211> 533
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 689

attagtgtac catacaactg cagctccagc caagctatct tgtaaaaaag tgtatgaaca 60

actttgcatc cctagagtgt gcccccatct tgcgacaata catcttgaga tggttcttag 120

gacaagtcgt ccctttatac ttgtcaaaat caagcacttt gaattttggg gggatgacaa 180

catccggtac caagcaaaga tctgtcatgt ccacgaatgg atagtcacca aatccttcaa 240

cagctctcaa tctctcctcg aggagatcga gtttccttct ttcttcggcc gccgggggtg 300

gtccttctat ggacaagaat attggttgtg ctgtgaggtt gggctgaggc aacgtgttgg 360

gcaccggccc ctcgacgagg atcggagggt agaaatcgac atccncttgg gcatactctc 420

gatgatcttc atggaccgcg tttaggggag gatggtgcgc ggtagctagg atagatgggt 480

ctgcttcggc accccaacta acagcggcag cggtggccgt gttattctcc atg 533

<210> 690
<211> 439
<212> DNA
<213> Glycine max

<400> 690

tggcaagttt gtattgtaca aatggtccca gagtgcccct tttattatgt actcataaac 60

cagtatattc tcgaaccttt tattgcaagg tgcctgtgac gaatcttata caaaatcatg 120

atctctctct gaaattctgg aaggccttga cctgacctgt taagaattat tgattaaatt 180

tattatttat tatattataa ccaggtaaga actaagatca ttattaatat atatatatat 240

atatatattt agatatattg atatcttaaa gattggacga accataactc ccatatatga 300

aatgataaga ggttggtgag ataaatggag attttaagat gtgtattaaa acattgtact 360

aaaaaagaat aaccgaataa cagagtactc ggggacttta agattatttc tcatgcgaat 420

ttttttttatt tctctttta 439

<210> 691
<211> 627
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 691

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aagaaggagc tgaatgcttt ggaggctggt atctctgaca gaattctgaa tcaatttgaa 120

gtggagctca agaagtctct tcaggagcaa ttgtggcatg ctgctaatgc ctatgaatgt 180

atgctgaagc aaaaggctat agtgaaatgg ttaaaggaag gggacagaaa ttcagcttac 240

ttccacaagc tgataaatca tagaagaaga cataatgcta ttcaaggatt gatcattgat 300

ggggaatggg ttcaggaccc tagtagagtc aaaactgagg ccttcaatca tttcaaagat 360

agattttctg agcagaattt taatagacca accctggatg gtgtgcagct accttccctt 420

ggtcaaagtg agaatgaagc ccttgtggcc agattttctg atgctgatac agtttggtta 480

ccaaaagcca tcaagaatga taacaaagca gtaatttaaa ttaaattcat cttagctntt 540

ctattttatg atcactctcg attgctggaa tggtgaagga aatgggcttc tttatacgag 600

gaccctatac agctgcaatg tgacatc 627

<210> 692
<211> 175
<212> DNA
<213> Glycine max

<400> 692

ggcatgcaag cttcttctca acaggatgat aaaacctata tttctattca ttctcaccat 60

agccaatgaa gatacactgc cttgactttg catccaactt ggatctctta tcctttggaa 120

catgcacaaa agccttgcag tcaaaaactc ttaagtgact atacttcaca ttctt 175

<210> 693
<211> 632
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 693

agcttcaagt tgctcggata gcaacttgtt ttgggccaac aaagtgttct atgatgaaag 60

cttcaacagg cttcttttgg ttgggatgtg tgctctatca cacaagattg aatggtcact 120

agcaaccata ttgtcaatca attccatggc ttcttcaggg gccttcaatt ttatttttcc 180

cctgcagaag catctaaaag ctgcttggat tgtggcctta acccgtcaat gaaaatattg 240

agcaggattg gttctaaaaa tccatgagta ggcgtctttc ttagtaaccc acaaaatctt 300

tccaaagcct cactcaagga ctcgtttgga aattgataaa aggatgagat ggcagctttt 360

ccttcagcag tcttggactc taggaagtat ttcttcaaga atttttcaac cacttcatcc 420

taagtcttaa gactgttacc tttaaatgaa tggagccatc tttttgtctc tccaaacata 480

gaaaatgaaa acaagctcaa tctaacagca tcctcaggca tgccaaccag tctaacagtg 540

gtgcaaatct caatataagt ggctaaatat gcatatgggt cttcatttgg cagaccatga 600

aacaanatgt tctgaatcaa ctgaattaat ga 632

<210> 694
<211> 385
<212> DNA
<213> Glycine max

<400> 694

taaacattca atttcgagag tctcgttata ttacgggact cattcagaca tccgagtaaa 60

aagttattgg cgtatgaatt ggcttaaagc ataaacattc aactttgagc ctctcggtat 120

attacgggac tcaatcagac atccgagtaa aaagttattg tcgtttgaat ttgctcagag 180

gttcaacatt caatttcgag cgtctcgata tattacggga ctcaatcaga catccgagta 240

aaaagttatt gtcttttgag ttggctcaga ggctcaacat tcaagttcga gcggcccgat 300

atattacgtt aatgaagcgg acatcacgct aaaaagttat tgccgattga attcgctccc 360

aagatcaaca ttacattttc gagcg 385

<210> 695
<211> 651
<212> DNA
<213> Glycine max

<400> 695

ttagtgcctc ctcaccaggt ccataatgag catttgcaga tttattggca ttccaagtac 60

tagaattctt attagctaat acgtcaaaaa tatagttact tgtattaaga tcaccacact 120

gggcatacat ttgaattagg gagctttgga caaatgtttc taattcaaag cctgctacaa 180

ctatatgtgc atggatgggc attccatgat ccaaaaggtc atcaggagac aaaaaagcac 240

tgagaagatt aacaatagta atgtagttta caggcacacc ttcttctctc aacaaattga 300

aggcttcaat cgctgcatta ggttctttgt tatcagcatg tccacctatt agtgcattcc 360

aagtcacttc atctctgtca ggcataattt tgcacaccct ttgtgcagca gccatggaac 420

caaatttccc atacatggta accaatgcat tacctatgat caaattgtga tggagaccaa 480

gaagaatcac aaaggcatga acaatcttta atgtttctaa atatacatgc agataatgca 540

gtagtgaagg tacatagttt gtcggctttc ttgtttgaag catctcaatc aaaagttcta 600

agcacgtgga taatttccat tgtcacattg cttgccatat ggaattcatg a 651

<210> 696
<211> 330
<212> DNA
<213> Glycine max

<400> 696

gcctaagatc ctcttcatca atggattcct tatctttttt gaagatgaat ggcagcggta 60

tggagaatga atatagagaa gatactccac ttctatgaga aaatgaattt agaaaaagct 120

taccaccata ggaggtcttg gataagagcc tgtaggaaga acatgactga acggagaggg 180

agagaatagc acgaaatttt gtgctctaaa agagctctaa aatctgaagt cttattttca 240

aatgatcaaa gttggaaaaa atgaacacac cttaccttta tttattagcc tgactgtttc 300

acacaactgg agggaaattt taattttaat 330

<210> 697
<211> 490
<212> DNA
<213> Glycine max

<400> 697

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caccatatga aagtttgtag gtagcacttc ctccccatgc acatggacat ttcatgcagc 120

tgatttgcgg gccttggttt cattgcattg gaatcataaa ccaaggctgc aagaaggcca 180

tagagacatg aacctaaagg aatgttagtg atgaggatat tgtggttcac accaacactg 240

tttgggccaa atagctctga ggtaatagac actgctgcag aaaacacaaa gcctgaactc 300

agccctatca aggcagtgcc tatgtgtaat gcagctccac tgccagatat ggccagcaaa 360

atgaatgcaa ttggtgttag caccaagcct gctccaaacc atccagctct tgcaatgtgt 420

atcttcctgc attgtcatac aacattagat gaatttacgt gcaatgttgg tttcgtgaca 480

tgtcctccca 490

<210> 698
<211> 412
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 698

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aagaatccca ttgggtggtc catataaaca ttctcctcta attctccatt aagaaaggca 120

ttttttgcat tcatctgatg tagctccaag tcataatggg ctactaatgc tatgataatc 180

ctgaaagaat cctttattga gaccgatgaa aacgtctctt tataatcaat gccatctttc 240

ttagtaaatc ccttagcaac aagtctagcc ttgtaacatt taaggttgtc atgagagtca 300

catttagtct tgaagaccca cttacaaatc ttacaacttt ggtnattcta ccaggtgcca 360

aacaccatta tgttcccatg gaattatctc ttctttcatg ggatttaact ac 412

<210> 699
<211> 365
<212> DNA
<213> Glycine max

<400> 699

gcataatatt ataataatca cttccaaaaa ttgacaaaca taatttaaaa gaaatataat 60

aataaccata atattaatta acaatcataa tttgtttatc acaatagaaa ttatccaaaa 120

taaacattct atcaatttac ctaagtaaac attgtatcag tgtaccaatc attacaaatt 180

tatccaaatt ataataatta gtcataatct actataaata aaagataaac atatatcata 240

taccaagagt gtccgaccgc caaaattcga agaagtgaaa tatgagttaa catattttta 300

tataatattt agcatattgt tattataaat aattaaaaaa aaactaaata tcatgtcaac 360

aaaat 365

<210> 700
<211> 470
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 700

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gataaaggta gtgttgccat gttttcaaag cccgtactaa ggcatacaac tccttatcat 120

aagttgaata gttaagggta ggaccactta acttttcact aaaataagca attggatggc 180

cttcttgcat caacacagcc ccaatcccaa catttgaagc atcacactca atttcaaaag 240

atttttgaaa gtttggcaac gcaagtatgg gggcattagt tagctnttgc ttaagaacat 300

tgaaagcttc ttcttgtttc tctccccatt tgaaaccaac attnttcttg agcacttcat 360

tgagaggtgc tgtcaaatgt gctaaaatcc ttcacanatc gtctataaaa acttgctaag 420

ccatgaatac tcctcacctc ggtcacagac ttaagtgtag gccattcttg 470

<210> 701
<211> 458
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 701

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gaagtccgat tcaggcgcat aatataccga gacgctcgaa attgaacaac ggaagctctc 120

gagaaattca aatggtcata actgatcaca cgaaagtccg attccggcag atagtatacc 180

gagactcttg aaattgaaca acggaagctc tcgagaaatt ctaatgggca taacttttca 240

catggaactc cgattcaggc gcataatata tcgagacttt tgaaatataa caacggaagc 300

tctcgagaaa ttcaaatggt cataaaattt caaacgaaag tccgattcag gtgcataata 360

tatcgagagg ctggaaattg aacaacggaa gctgtcgaga aattcaaatg gtcataactt 420

atcacaccga agtccgattc aggcacataa tatatcga 458

<210> 702
<211> 437
<212> DNA
<213> Glycine max

<400> 702

gaagctcttg agaaattcaa atggtcataa cttatcacac ggaagtccaa ttcatgcgca 60

tagtatatgg agacgctcga aattgaacaa cgaaagctct cgagaaattc aaatggtcat 120

aacttgtcac acgaaagtcc gattcaggcg cataatatat cgagaagctc gaaattgaac 180

aacggaagat cttgagaaat tcaaatggtc ataacttgtc acacggaagt ccgattcagg 240

cgcataatat accgagacgc ttgaaattga acaacggaag ctctcgagaa attcaaatgg 300

tcataactta tgacacggag gtcctattca agcgcataat atatcgagac gctcgaaatt 360

gaacaacgga agctctcgag aaattcacat ggtcataact tatcacacgg aagtccgatt 420

caggcgcata ctatatc 437

<210> 703
<211> 456
<212> DNA
<213> Glycine max

<400> 703

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atttctcgag agcatccatt gtttaatttc aagcttctcg atatattatg cacctgaatc 120

agacttccgt ttgaaaagtt atgaccattt taatttctcg agagcttccg ttgttcaatt 180

tcgagcgtct tggtatatta tgcgcttgaa tcggacttcc gtgtgataag ttacgaccat 240

ttgaatttct cgagagcttt cgttgttcaa ttccgagctt ctcgatatac tatctgccgg 300

aatcgaacct ccgtgtgata agttatgacc atttgaattt ctcgagagct ctccgtggtc 360

aatttcgagc atctcggtat attatgcgcc tgaatcagac ttccgtgtga caagttatga 420

caattagaat ttctcgagag cttccgttgt tcaatt 456

<210> 704
<211> 447
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 704

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ataagagatt tcagatggac tttaatccta atcccacagc cgacctttc acgagatctc 120

tacttaaccc tttggttaaa tgatcagcca aattatgctg agttctcaca aactccactg 180

atatcacacc atgcatgatt aactcccgaa ccatgttgtg tctaacaccc aagtgtctag 240

acttcccatt atacacttga ctatatgcct tagccaaagt taatatgggg gaaccttatt 300

ccttttgtag gaattcagtt caacaagtaa caggctgtca acatagcctc accccanaat 360

ccttcactta nacccgaata ggataacatg gaattcacca tttctttcaa ggttttattc 420

ttcctttcag ctacaccatt ctggttt 447

<210> 705
<211> 409
<212> DNA
<213> Glycine max

<400> 705

ctcagcttaa cattcaattt cgagggtctc gatagattac tggactcaat cagacatccg 60

agtaaaaagt tattgtcgtt tgaatttgtt cagagcatca agattctatt tcgaacgtgt 120

cgatatatta tgggactcaa tcggacatcc gagaaaaacg ttattgtcgt ttgaatttgc 180

tcagagcttc ggctttcaat ttggagcgtg ttgatatatt acgagactca atcagacata 240

ccagtaaaaa gttattgtcg tttgaattgg ctgagagcat caacattcaa tttcgagcgt 300

ctcgatatat tacgggactc aatcagacat tcgagtaaaa aattattgtc gtttgaattg 360

ctcagagctt caacattcaa tttcgagggt ctcgatagat tactggact 409

<210> 706
<211> 435
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 706

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atatatcgag acgctctaaa ttgaatgttg aagctctgac caaattcaaa cgacgataaa 120

tttttactcg gatgtctgat tgagtcctgt aatatatcga gacgctcgaa attaaatgtt 180

gaagctctaa gcaaattcaa acgacaataa ctttttaact ggatgtgtga ttaagtcccg 240

taatacatcg agacgctcga aattgaatgt tgaagctctc agcatattca aacgacaata 300

actctttact cggatgtctg attagagtcc gtaatacatc gagactctcg aaattgaatg 360

ttgaagctct gaccaaattc aaacgacgat aacttttac tcggatgtct gaatgaagtc 420

cgtaatacat cgaga 435

<210> 707
<211> 478
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 707

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tcagatatct taagaagggg ggttgaatta agatattcca aactgtttcc cctaattaaa 120

aatctatttc acttttttact caagttatga attcccttaa tgacaatctt cttaaatatt 180

aattcaaatg aaacaatttg aatatgaata taaagcaata ataaataaag gagattaagg 240

gaagagaaaa tgcaaactca gttttatact ggttcggcca cacccttgtg cctacgtcca 300

gtccccaagc aacccgcttg agagttccac tatcttgtaa attcctttta caagttctaa 360

acacacaagg acaatccttc ctttgtgtnt agaattcctt tacaacaaga gactcacaat 420

ctcttaatcc cttagagaat gagaagaaga agaagaacaa atctctctag aaagagat 478

<210> 708
<211> 453
<212> DNA
<213> Glycine max

<400> 708

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gatattccaa actacttccc caattaaaaa tatatttcac tttttattca agttataaat 120

tcccttaaca atgaacttct taaatattga ttcagataaa acaatctgaa tatgaatata 180

aagcaataat aaacaaagga gattaaggga agagaaagtg caaactcaga tttatactgg 240

ttcggccaca cccttgtgcc tacgtccagt ccccaagcaa cccgcttgcg agatccacta 300

tcgttgaaat ttcttgtaca agatctaaac acacaaagac aatccttcct ttgtgttaga 360

attcctttac aaaagaaccc acggctctta atcctagaga atatgagaag aacagaatga 420

attatcctaa agagataaat tacagatgac act 453

<210> 709
<211> 457
<212> DNA
<213> Glycine max

<400> 709

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taaaaggtct cctactggcc ttaccattgt ccttgtttat gttgaagatt tggtgcttac 120

tgacactgat cttgctgaaa tctagcaact aaagcactcc ctggatgcaa aattcagtat 180

taaggacctt ggaatactca aatacttcct tggttatgaa gtagcccgat ccacctcagg 240

tattgccttg catcaaagaa aatattgcct tgatcttctt ctagacacta atctgcttgc 300

tgcaaaacct tctttcttac ctatggatcc tacactaaaa tttcacaaat cttctggtat 360

tcctttcttt gatcctactg tttacaagag gcttatggcg cgattattat atcttactca 420

cacaaagccc gatattagct atgctgttgg aaaattg 457

<210> 710
<211> 447
<212> DNA
<213> Glycine max

<400> 710

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gcagcctgga cccaagaatt tgcgcacttt tgtctatctg atttaagttt tagttcctct 120

tctggtatgc ttctttcatt atctggagaa gaatcatctg gaatggattt agatagcgag 180

tcaacaatca tccgcgcact atttatgcta gcatgaagag ttaggaactg ctctactgca 240

ggctgtgggt tttgttcctt atcagaatta cttagctctg catatacact gccaaaaaca 300

tcacaaaata agagtcagaa acaatctgtt atgctgtatt gcaggagggt gacacaatat 360

aatgcctacc atcccataga agaattgtgg aagacgtgga tgattaacat aatatatgcg 420

taaaccccag tctgtctgta tgattga 447

<210> 711
<211> 461
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 711

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gcaaagggtc cagtgcaaca atactcaagt tggtccaatg ccaaacgtgc actcttgcaa 120

gcaatgacac ttccatctga ccctttgaca gcaaaatttg gaggacaaac tatgttcaca 180

tcactagggc agctagttgt gttgcaaccc cttaagcctc cctgagcgat caccaacact 240

ggcagattga agccatcaac aaggctaaca tcatagaaat cttgtccttt atttgaagcc 300

aaagtgaatt ccactagaga aactggaggg gttccaccat taccattgca tggtacttga 360

cctgatccac agtcaccagt ggcacaagtg aatttcccat atgtgtctgt tgagcattga 420

gacttggccc agaatctgcc agaccatgga gctgtgacat c 461

<210> 712
<211> 426
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 712

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tagttgaaaa aatactggtg actgtccctg aaagatttga ggctactatt acagccttgg 120

agaatactaa ggatctgtca aaacttacct tggcagaact tgtaaatgct ttgcaatccc 180

aagagcaaag aagaagaatg agggctgatg attctgtgga aggagtattg caagctaaat 240

tgcaaattaa ccaaggagag aaaagcaagt ggaagaaata caacaagaag aatttcaata 300

cacaagaagc agcgggtaac actagcaaca aaagtggaga caacaacaaa ggatttcctc 360

cttgcaagca ctgtggcaga atgggtcatc ctcctttcaa atgttggaga agacccgatg 420

ttaagt 426

<210> 713
<211> 317
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 713

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tatgttatgc cctgtgggta tggaatacca caaaatacat gcttgcccta atgattggct 120

tttgcataaa catcaatttg ctgaantgcg cagctgcgct acatgtggag cgtcacgttt 180

caaagtgaag tatgatgaaa gcagtgtaga tggaggcaca tacgaagact tggcatgaca 240

agagtggtgg ggtcttccag taataccaac gtttaagcga ttgtttgcta atgcacatga 300

agcataattc ctcacat 317

<210> 714
<211> 380
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 714

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cttggacatc ttttagaaat gcttgctgaa ttaagacagg cagaaatcca gcgtctccac 120

tagggacaaa aacccattct ttgcagcata taatccaaaa aagcccatga gactgagtca 180

taggcctttt caaaatccac cttgaaaacc atagctggcc ttatgcttct acaagcttcc 240

tcaatcacct cattaagaac tagtatgcca tgcaggatgt gtctgttttt gatgaaagtt 300

gtctgcctct catcaataag accagatatc acttgtctca atctatttgc taataactta 360

gatatcaccn tgtacataca 380

<210> 715
<211> 394
<212> DNA
<213> Glycine max

<400> 715

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gaaccattat gaggcggata agatattatg ccctgtgggt atggaatacc acaaaataca 120

tgcttgccct aatgattgta ttttgtatag acatcaattt gctgaaatgc gcagctgccc 180

tacatgtgga gcgtcacgtt acaaagtgaa ggatgatgaa agcagtgttg atggaggcac 240

atacaaagat tgtccatcaa aagtgtgttg gtattttcca gtgataccaa ggattaggcg 300

atttgttgct tatgcacaag acgcaaaaca cctaacatgg catgctaatg ggaggattaa 360

agatggatcg ctcgtcatcc agctgattct tctc 394

<210> 716
<211> 466
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 716

tcctcgcaca tattagggaa gttgngagca agatgctggt catgtatatc tacaagaaca 60

acttctattt gatatcgaaa aagaaacaag cacaaagata cgtaatgttg aatcangaaa 120

agttatgtta aaagaacgac ttcgccataa aagggtactt cttatactcg atgatgtaaa 180

taaattgcat caattgaatg ttttgtgtgg aagtcgtgaa tggtttggtt cacggagtag 240

aataatcatc acaactagag atatgcatat acttagaggg agaagagttg acaaagtgtt 300

cagaatgaaa ggaatggatg aatatgaatc tattgagctt tttagttggc atgcatttaa 360

gcaagcaagt ccaagagaag atttattgaa ctttctagaa atgtagttgc ttattctgcg 420

ggattgcact agctcttgaa gtccttgggt cctatttgtt tgatat 466

<210> 717
<211> 457
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 717

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tttcttgctt ctccaacttg ggtttcaaca ttctatagtt gatcactcct tttttatcca 120

tcacacagtt gattcccttа ctactcgtgt atgtagatga catagtcatt gttggaaatt 180

ctatggatat gataacttca ttcaagcaga atttagataa tcaatttggg cattcttaag 240

ttctttcttg gtgctggtgt tctcagtgcc aaacctgcaa gcacccctтc tgaacctacc 300

tttgagactt cgccaagatg tcgctcctat acctgacttt cacacgccca gatatatccc 360

atgttgacca acaacttagt caattttcag ccctcccaac agtgagtcat tatcaataag 420

cccaacgcgt actttgngta tttgaaaagg aatccca 457

<210> 718
<211> 486
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 718

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catcctctaa atcactatta agaaaggcta tnttcacatt catttgttgt aactcaaggt 120

caaaatgagc aactaatgcc aagataatac gaagagaatc tttcttagat acaggagaaa 180

aagtctctat gtagtcgatt tcttcttttt gagtaaatcc cttagcattg agtcttgcct 240

tatatctctc aatgttgcct aatgaatccg ttttgatctt aaagacattt acagccaatg 300

gcctttgccc cattaagaaa ctctacaagg ctccaaactc cattactctg catgtaattc 360

atctcatcct tcttggcatc ataccataga tntgactctn tacaactatg gattgatcaa 420

acgtctcatg atcattntca gctgcaatat tatagtcaaa ttttgcaaat atacaatata 480

ataact 486

<210> 719
<211> 465
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 719

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acggatatgg ctcccgatcg gaaccagctn tagagcatga ccaagcgaga acatgagtcc 120

attaaagaat atgcccaaag gtggagagac ctcgcagccc aagtcgttcc gcccatgact 180

gagagtgaga tgatcacaat tatggtagat acgttgccta cgttctacta tgaaaagctg 240

atagggtaca tcccagctaa ctttgcggac ctcgtcttcg cccgagaaag gatcgagtcc 300

ggactaagaa aaggcaagtt tgaatatgcc tccaacgtta cccccaacaa caacagaaga 360

gccccagtgg tgggcacgaa gaanaaggaa ggagatactc acgcggtcac caccgcccca 420

acatggatga nagcgcccca naatatccaa aactcatacc agcac 465

<210> 720
<211> 448
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 720

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tggaaggcct ctcatcttat acatgacaat cttagacgag tcaatggggt gtatgctggg 120

gcaacatgac gaatccgaaa agaaagagcg cgctgtttac tacctaagta agaagttcac 180

aacctgtgaa atgaactact ccttgctcga aagaacgtgt tgtgctttag tatgggcatc 240

ccatcgtcta aggcagtaca tgctgagcca tactacctgg ttgatatcca agatggaccc 300

ggttaagaac atctttgaaa agccagctct cacgggacga atcgcccagt ggcaagtcct 360

gctatccgag tttgatatag tctacgtcac ccanaaggcg ataaaaggaa gcgccttagc 420

agaattattg gctcaacagc ctcttaac 448

<210> 721
<211> 420
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 721

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atattttgtg tgtaacctaa aacttcattc aaattatata aattctcaca agtggatcaa 120

cccagcaata tgacttgttt tttcaaattc tcactactag aaaaagcaga tttaacattg 180

gcgcattaac attgattttc tacaaaaccg atgttaacat aaatgcggtg acataattgt 240

aaataatgtg tatccgttaa catcagtttt gaagaagaaa accgatgtta acgtatgatc 300

agctaacatc ggtttgttga ataaaatcga tgttaacgtt cacatcaatt tgttaacatc 360

gggtttttat tgaaaaccga tgttgaactt acattntaaa ttatatntga cgcgacctat 420

<210> 722
<211> 449
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 722

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caatcatcaa atataaatgt ggattaaata ttaatcgatg tcaataatat gtttagtagg 120

ttatgtaact taatgtgaaa attttcaaaa attttaataa ttgcagcatt agtccaattc 180

aacttaatgt gataaataca ttggtcttca aatttcacct caataaatta tatgacttat 240

gtagaaaaat ctagcaaatg aatctagcaa aatcaaatat ataaatagaa aattacatta 300

gacgatgtta attaattctc cttcatcatg atcattacga ttagcatgaa cgtgattagc 360

ttcttcttct ccgacaacat taggagtgat ttgtatggac agaggactaa cataggtgtc 420

catgtatgaa tcatcatctt ctacattaa 449

<210> 723
<211> 350
<212> DNA
<213> Glycine max

<400> 723

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ctcttttgat cctgtcgaac actacacgca gactctgttt ctttccatta aaaaaccttc 120

ttccttcttt tgtgcttatt aacaaagact ttgctgtgca agataaatga gaatgatcta 180

ttcaagcatg actggaggag cagatcatga gttcaagtgc tgcagatata tcctagaaat 240

ggatactagc attccttgtc ggacttctca ctgagattat agccactctc atcaatcctg 300

cagatgagaa tattgctggg tataagcttc tggctgagct taaatacgtc 350

<210> 724
<211> 419
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 724

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actgtacagg gaaagctgag aaacggttct ttggcagcta taaaggtttt atcagctgaa 120

tcaagacaag ggatccggga gttcttgaca gaaatcaagg tgatctctag tatagagcat 180

gagaatctag tcaagttaca tggatgctgt gtggaagaca accacaggat tttggtatat 240

ggctatcttg agaacaacag cctagcacaa acacttattg gtaagtgaac tactgccatg 300

tgatgtgagt atgctntgtt agaaaaacta tcttgataat gaattaatcc tcatgagttt 360

ataggttcag gccatagtag catccaatta agttggcctg taaggaggaa catttgcat 419

<210> 725
<211> 434
<212> DNA
<213> Glycine max

<400> 725

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attatgcgct tgaatcggac ctccgagaga aaagctcaga ccatcatgag cgctcaagag 120

cttccattaa tcaatttcga gggtctcgat atgttatgtt cctaactcag agctccgagg 180

caaaagttat gtccatatga atatgtcgag agctctcggt gtttaatttc gatcgtcttg 240

tatatgtgat gctcctgcat cgcacctccg agtgaaaagt tatgaccatt tgaataccta 300

gagagcgtcc gatcttcaat ttctagcgtc tctatatgtg atgcgcctga atcggacctc 360

ctaatgagaa gcaatgacca tctgaattta tcaagagctt ccgctgacaa attcgagcgc 420

ctctatatga gatg 434

<210> 726
<211> 448
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 726

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gcaacaaaat caaccacagc agaacaatta tgacctttcc agcaacagat acaaccctgg 120

atggaggaat catcctaacc tcagatggtc cagccctcag caacaacaac atcagcctgg 180

tccttccttc caaaatgctg ctggcccaag cagaccatac attcctccac caatccaaca 240

acatcaacaa ccccagaaac atccaacagt cgaggccccc ccacaacctt ccctcgaaga 300

acttgtgagg caaatgacta tgcagaacat gcagtttcaa caagagacca gagcctccat 360

tcagagctta accaatcaga tgggacaatt agctacccaa tngaatcaac aacagtccca 420

gaattctgac aagctgcctt ctcaagct 448

<210> 727
<211> 448
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 727

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ttagggatca acttgaaact tatgtgcttc aagtgagaag aaatgcttct ttttccactt 120

gtgaagatgt tcaaagtttg gctatgaaga tggttcaaac tgagaaacat ttggtatttc 180

cattggttta taaacttatt gagctagctt tgatattggc cggtgtcgac aacatccgtt 240

gaaagagctt tttcagcaat gaagattatc aagtctaaat tgcgcaataa gatcaacgat 300

gtgtggttca atgacttgat ggtatgttac accgagcggg agatattcaa gtcacttgat 360

gatattgata ttattcgaac atctaccgca cagaagtctc ggaaaggaca cttgcctcgt 420

aattntattt aacccgctat tgtaagat 448

<210> 728
<211> 475
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 728

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aggcaaatgc agctgatgat tgtgtatacc acaagtttag tgggagtaaa tactcattct 120

tagggttata tgtcaatgat atactgctta ctagcaacga tataagcttc ttacttgaga 180

ctaagaaatt tctgatgaaa gattctatga tgaaagatct tggggaaacc tcttttgtat 240

tatgaattta gatactaaga gatcactctc aaggtatcat aaggttgtca caagagagtt 300

atatcgataa gggcctagat agattcggca tgaaagatag taaaccagga gataccccga 360

tagctaaatg agacacnatt agtctcacac aatgtcccaa taatgacctt gaaagaatag 420

agatgcaaaa gattccttat gcatcagcag tatgaagtct aatgtacgct caagt 475

<210> 729
<211> 455
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 729

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gccaactaac taactatttc tgttaaagct gtttatactg ctaagagccc ccctcaagct 120

gggaatggat attcatcatt cccagcttgt tacaaaggtg ctgaaaggtg gctggtcgta 180

aagctttggt gaatatgtcc acaagttgca ttganggatg agaccggaag gagcttgacg 240

agacccgcag tgactttgtg gcggataata tgacaatcga tctcgatatg cttggtgcgt 300

tcatggaaaa cgggatttgt tgctatctga attgcagatt ggttatcaca atataaagtg 360

gctggctgaa taaatgctac accaatgtct tggagaatat acgttaacca ttgcagctca 420

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<210> 730
<211> 414
<212> DNA
<213> Glycine max

<400> 730

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tctgaagaag ctattctaaa tggccccaaa ttgtattctt gagtctttaa tgctcgtgct 120

gaccaagctt ctgttcctgg cctgtttatt ttcttcactg aaataatttg tgttctgtgc 180

tgacgagtgt gctgtaagaa actgactttg gcgatcttaa cctacctaat actctatttt 240

gaaaacagga aaaaccgagt ccatggatcc aaattcaaga attatggttc ctgaagatag 300

gcatggactc catgcaattg atattttgga ccctgacttg gtatgcttgt tttaaagttt 360

gttgaagtgc aatgcagata tccaagcaag ttattcatga atcctatata attc 414

<210> 731
<211> 440
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 731

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attataagat tgttttgaga gtgaaagatc gtaacaacta acactgatta aaaaaaaaaa 120

aaaaactaat tgtacctgta ttggagacat atccctttgc atataatcaa gaggggtcca 180

agaggcaagc ttttcacaag ttttagaacc canaatacag cctctaatag tgttccaata 240

gcgaggatcc tgaattctct tcctcaacca tggtgagtaa tcttgaagac gatactcctt 300

gtaaaccctt ccaggcactt ccacaccacc gcccttgcta gtcacaccaa aaccaaatat 360

tgtgaagccc atgagtgctg ctatgaggaa caacatgacc accaagtaca accatagtgc 420

acatgccaca tgaaaacatg 440

<210> 732
<211> 439
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 732

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ctaagctcac ctccttgaga tgagaagcta gaacttagct acacaccccc tataatagct 120

aagctcaccc ctatgacaaa aaacatgaaa atacaaaaaa aaattcctta ctacaaagac 180

tactcaaaat gccccgaaat acaaggctaa aaccctatac tactagaatg accaaaatac 240

aaggcccaaa cgaaggaaaa acctattcta atatttacaa agataagcgg gcttatactt 300

agcccatggg ctcgaaatct accctaaggc tcatgagaac cctagggcct tcccttggat 360

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cagcagagtt tgaccttca 439

<210> 733
<211> 436
<212> DNA
<213> Glycine max

<400> 733

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ctaagctcac caccttgaga tgagaagcta gagcttagct acacaccccc tataatagct 120

aagctcaccc tcatgaccaa atacatgaaa atacaaaaaa gtccctacta caaagactac 180

tcaaaatgcc tcaaaataca aggctaaaac cctatactac tagaatgacc aaaatacaag 240

gcccaaacga aggaaaaaca tattctaata tttacaaaga taagcgggct catacttagc 300

ccatgggctc gaaatctacc ctaaggctca tgagaaccct agggccttcc cttggatctc 360

tggcccaatc tacttggagt cttctatcca atgcccttgt gggttaggat tgcatcattc 420

cctccacctt ggaaag 436

<210> 734
<211> 309
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 734

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tttctcgaga gcttcctatg tttaatctgg agcgtctcga tatattatac ccctgaatcg 120

aacctcagct gtgaaagtta tgaccatttg aatttcttta gagcatccga tgttcattnt 180

tgagcgtctc tatatgtgat gaagcttaat cggacgtacg tgcgaaaagt tatgaccatt 240

tgaatttcta gagagcttac ggtgttgaat atcgagcgtc gcgacatatt atgcgcccga 300

atcggacat 309

<210> 735
<211> 447
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 735

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agattctatg ttataacatt taaaatataa aactacatta tgaaaaatgc aatggtaagt 180

aaattaaata ctttttcttg agagattcat aactaataac gcgaagttga aatagacata 240

acgttttaag ttgaaattct attaatttac aattagtatt gtttgattga gtagaaagaa 300

aagtaaaaaa agattaataa aattaaatta aaatagaatg tacaaatata aattctgcat 360

tattttactg gttattattt tttttattct ctttttcttc aaacgaaacc ttagtattct 420

tataattgaa tgagtttttt atgtcca 447

<210> 736
<211> 171
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 736

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tgcaagttga aagccttgga ggaaaaaggt atgcctatgt tggtgtggat gatttctcca 120

gatttacctg ggtcaacttt atcagagaga aatcagacac ctttgaagta t 171

<210> 737
<211> 419
<212> DNA
<213> Glycine max

<400> 737

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ggtcataact tttcacacgg atgtccgatt cgggcgcata atatgtcgag aggctcgaaa 120

ttgaacaacg gaagctcttg agaaattcaa atggtcataa cttttcacac ggatgtccga 180

ttcaggagca tcacatatag agacgctcga aatttaaatg ggcataattt ttcacacgga 240

tgatcgattc aagcttataa tatattgata cactcgagat tatacatcgg aaactctcga 300

gaaattcaaa tgggcataac ttttcacacg gatgatcgat tcgagcgcat aatatgtcga 360

gaggctcgaa atcgaataac gtgagctctc gagaaattca aatggcgata catttatac 419

<210> 738
<211> 422
<212> DNA
<213> Glycine max

<400> 738

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ccaagagaag caatggaagt gagaggaagg ggagccaaag cgccaagaca accaatgatg 120

aaacggagca catcttccct agagagacaa cagtacctat cacggatagg agtgatggaa 180

gttgaggggc tccgattcat gttaagtggt agattgttgc tgctgttgcc aggagattca 240

ctattcttga gccacttgcc atagtagata actgagaatc gcttgctcat gcccttccat 300

ggctacgctc ttggaacaag cagacgcttc acaccttgtt tcatcatgtt cagcgcatct 360

atcaacctta atgagaggaa gtaaagtaag atattaaggg tggttttgtc aaattagaaa 420

aa 422

<210> 739
<211> 376
<212> DNA
<213> Glycine max

<400> 739

tggtctaacc tttcacatgg aggtccaatt caggctcata atatatcgag atgctcgaaa 60

ttgaacaatg gaagctcttg agcaattcaa atggtcataa ccttactctc ggaggtaaga 120

ttcatgcaca taagttaacg agacgctcga aattgaacaa cggaagctct cgagatattc 180

agatgatcat aacttttcac tcggaggtgc gattcaagcg catcatgaat agagacgctc 240

gaaattgaac aacggaagct ctcgagagat tcacatggac ataacatatc acatcgaggt 300

cagattcaag cacataatat atcgagacgc tcgtaattga acaacggatg ctgtcgagaa 360

atctaacggc ataact 376

<210> 740
<211> 455
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 740

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tattatgcgc cttaatcgga cctccgagtg aaaagttatg accatttgaa taactcaaga 120

gcttccattg ttcaatttcg agcgtctcga tatcttatgt gcctgaatct gacctccgtg 180

tgaaaagtta tgaccatttg aatttcttca gagccttccg ttgttcaatt tcgagcgtct 240

cgatatctta tgcgcctgaa tcggacctcc gagtgaaaag ttatgaccat ttgaataact 300

caagagcttc cattgttcaa ttacgagcgt ctcaataaat tatgtgcctg gatcgacctc 360

cgagtgaaag gttatgacca tttgaattgc tcaagagctt ccattggtca atttcgagcg 420

tctcgatata ttatgcgcct gaaccggacc tccga 455

<210> 741
<211> 367
<212> DNA
<213> Glycine max

<400> 741

tccattgttc aatttcgagt gtctcgatat attatgcgcc tgaatcggac ctccgaatga 60

aaagttatga ccatttgaat ttctcgagag ctacctttgt tcaatttcgt gcgtctcgat 120

atattttgcg cctgaatcgg acctccgagt gaaaagttat gaccatttga atttctcgag 180

agcttccgat gttcaatttc gagcgtcttg atatactatg cgactgaatc taacctccgt 240

gtgaaaagtt atgaccattt taatttctca agagcttccg ttgttcaatt ttgagcgtct 300

ctaactgtga tgcgcctaaa tcagacatcc gagttaaaag ttatgaccat ttgattttct 360

cgagaac 367

<210> 742
<211> 446
<212> DNA
<213> Glycine max

<400> 742

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gtgaagaaga atgtggcatt tacctggggt gaaaaacaag agcaagcctt tgctttgctc 120

aaagaaaagc ttactaaggc acctgttcta gctcttcctg acttttctaa aacttttgag 180

ctagaatgtg atgcctctgg agtgggagtt ggagctgtat tgtacaaggt gggcacccta 240

ttgcttattt tagtgaaaaa cttcatagtg ccaccctcaa ctaccccacc tatgataaag 300

agctttatgc cttaataaga gccctccaaa cttgggaaca ttaccttgtt tccaaggaat 360

ttgtcattca tagtgatcat caatcactta agtacattag agggcaaagc aagttaaaca 420

agaggcatgc aaaatgggta gagtac 446

<210> 743
<211> 451
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 743

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ccttaaaatg atcaccactt aagtaaaaca gaatcatttg ataagcaaga actacgtagg 120

tctgatttcc tcatcgcaat tgaggatacg tangagcaaa agccccgctt ttgtcgacca 180

ccccaagaga tcgttaatgt gccaatgcct taacgtttct ctcctttcaa aaacaagaga 240

tcgttaatgg tccaatgcct taacgcttct ctcctttcat aaacaagaga tcgttaatgg 300

tccaatgcct taacgtatct cttctttcan aaacaagaga tctttaatgg ttcaatgcct 360

taacgtctct ctccttcata aacaagagat cgtatatgtc caccgcctaa cgttctcatc 420

tttaaaatca aataccggta atggtcaaca c 451

<210> 744
<211> 470
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 744

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ctacctctca tattattgac aaattctatt tctataatat ataaaattgt atacttttta 120

tgtaagaaag aaaatatata aaaagaataa tttatcatta aaagtgggtt gtatattaat 180

tattataatt taattatgtt tatatgagaa actgttaaaa tgatatgtta aagtaaaaga 240

ctacggatat catttttta ctctaacaca actaatggtt ntagcacatg tttgtgtgta 300

gtcatttgct gtgttcagga tcgacccgtc agaaagtaaa atctaaaata aaaattgaga 360

gaggattttt tattctaaag aanataatga tagttgaagt cttttattta actgtgtgac 420

attgtttact ttaaaaaata atatatatca taatagacct aaagtttaag 470

<210> 745
<211> 445
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 745

agataaggct aatatctgca tattntnttc ctttctttct tgttttatat atgatcaaat 60

tatctaatct ataagattaa aagaatgatt aatttaatta taataataca cttattttca 120

acttatatct tttcaaaata tttccgttat taatattttt taatggcttt gtgatatatt 180

ttttcttttt tataaaatat atttataatt tcaaagtaat aaatattata aaatgaataa 240

tttagaaaga aggtaatatc attctaataa aatggtattt ctggcccttt tactcatctt 300

taattttgag cttaattctt atttaaatct atttaagaat gtaattatct aactatgttc 360

aattcaataa atgtaattcg caagtcatat ctaatggatg tattacggtc atatgatatg 420

ttttgatgga atatcatagt taaat 445

<210> 746
<211> 471
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 746

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cttggcctca tcatttctgg ttntggggtg gcagcagata aatccaaggt ggctacaatg 120

agttcctggc cagttccgaa agattcgaag agtttgaggg gatttttagg attgataggc 180

tactatagaa gatttgtcca aggctatggt aaaatagcaa agcctttgac tgaattactg 240

aaaaaggata gctttgtatg gacactagta gctactctag cttttgaaac tttaaaatct 300

gccatggtca gtttgccttt attagcagtt cctgattntt caaaaacctt tgttctggag 360

acaaatgctt ctagcanagg agtaggggct gctcttatgc aagagggcag gcctttggct 420

tttatgagca naggactctc ccctcgagca cagctgaagt cagtctatga a 471

<210> 747
<211> 452
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 747

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actaagctca cctccttgag aagcttcctt aagaagattc ctaaagaagc tagagcttag 120

ctacagatac ctctctaata gctaagctca cctccttgag atgagaagtt agagcttagc 180

tacacacccc ctataatagc taagctcacc cccatgacaa aaaacatgaa aataacaaaa 240

aaagtcctta ttataaagac aactcanaat gccccgaaat acaaggctaa aaccctatac 300

tactagaatg gccaaaatac aaggcctaga cgaaggaaaa acctattcta atatttacaa 360

agataagcgg gctcatactt agcccatggg ctcgaaatct accctaaggc tcatgagaac 420

cctagggcct ttccttggat ctctagccca at 452

<210> 748
<211> 433

<212> DNA
<213> Glycine max

<400> 748

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agatccatca tcagaatctt cctcagcatt agcttcttct ccaagttcaa tccctgaaaa 120

tgacatagat ctcttgccaa gaaaggatgc tcctccacct gcatatcaac attgtgaaac 180

attagtatta ggccactaca caacataata ttgcaccatt ggttggtgtt tttgtgatct 240

agaggagaga gtaccatggt actcttgagg tgcacatgaa gttataattg agtcgagtga 300

acgtggaggt tgatggtcat cttggtgagg tgttgtagca tgaaatttgc tgagaagata 360

gccatatcat tgctggctag cctatgcctg atgccactga tcttcaatgg ctgaatgata 420

ttctgatcac cat 433

<210> 749
<211> 360
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 749

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aagttattgt cgtatgaatt ggcttaaagc ttaaacattc aactttgacc gtctcgatat 120

attacgggac tcaatcagac atccgagtga aaagtaactg ccgtttgaat aggctcagag 180

gttcaaaact caatttcgag catctcgtta tatgactgga ctcaatcaga catccgagta 240

ataagttatt gtcgtgtgaa ttggctcaga gggtcaacat tcatttttga gcgtctcgat 300

atattatggg actcatatag acatccgagt aagaagttat tggcgcttga attggcacat 360

<210> 750
<211> 424
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 750

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atatatcgag acgctagaaa tggaatgttg aacctatgag cctattcaaa cgacaataac 120

tttttactcg gatgtctgat tgagtcccat aatatatcga gacgctcgaa attgaatgtt 180

gaacctctga gccaattcaa acgacaataa ccttttactc ggatgtccga ttgagtgact 240

taatatgtcg ggacgctcga aattgaatgt tgaacctctg agccaattca cacgacaata 300

acttttttact cggatgtctg attgagttcc gtcatatatc gagacgctcg aaattgaatg 360

ttgaacctct gagccaattc aaacgacaac taacttttac tcggatgtct gattgagtcc 420

cgta 424

<210> 751
<211> 395
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 751

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tcatcatgga acttgtctca aagaaatctt gtccttcana tgtgtgccca gcgcaaccag 120

cacgtccatg ttagcggatt ttcgcttcag tgcatgatat gaacctacat agaacctaat 180

agtaatagcc atagtaaaat gactataaga atctccaatt tcttgaaaac aatacaataa 240

aattgtcttt ggtgaataaa gagaaacatt aacaagaaaa gaaattagaa ttaaatagtt 300

attgatagtc atagtacctt ttgccaacta tgaactgcac aggcgtgcta agaatccatc 360

ttataaacaa cccaagagta agcgtattgt ggatc 395

<210> 752
<211> 451
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 752

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agatcagaaa tgtgccaacc aatagccgct ttacgtcgtt gtagaatttg caccagttat 120

tcttcttctt ctttcttcaa aaagttgcta attataacaa gtttggtctc atcttcttcc 180

aagaatacat actttaaatg tgccagaagg gtttttaatt ttgctttggg cttttctgtt 240

ggactcagtt tttccaattc ttcacaacaa ccttgtcaac ataattgtct tttgaatcat 300

caagctcttc atcacaagct aagcaatctc tcccatagcc aggttctttn tccaaaggag 360

actgtagcac catggntgag gctaataatg ttatttcctg ctccacctct tcttcttcga 420

aataggcatc acccatatct gagtggttca t 451

<210> 753
<211> 351
<212> DNA
<213> Glycine max

<400> 753

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ccgaatgaag ggctatgacc attcgagtct ctcgagagct acctttgatc aatctcagag 120

cgatcgatat attatgcacc tgaatcgcac ctccgcgaga caagattcac cgttctagct 180

tctcaagagc ttgcgctgga ctacttactc ccgcattaac agtgatgcgc ctacttaagc 240

catacgagtt tgacatcctg acctttagac tgagtcgcgc acctacgttg ctgaaatcct 300

atcgtcccaa gagtttttgc tctctggtga gccactacca gattattgta t 351

<210> 754
<211> 334
<212> DNA
<213> Glycine max

<400> 754

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tggctgcccg tggatataca agatcaagta taatgcagat ggtaacattg agctgtccaa 120

agcgagactt gttgcgaaag gatacacaca agtggaaggc ttagattacc ttgctacttt 180

ctcccaagtg ccaagctcac catagttcaa ctcattcttg ccctttgcag ccattttgat 240

tggcatctca agcaattaga cgtgaataat gcatttcttt atggagaatt gatgaagaag 300

ttacatgagt ctttctccag aatgcatcag ccta 334

<210> 755
<211> 463
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 755

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caagatcaat cactagcatt tgtgggtttg tacttgccta gaccgatgtt tagtcataaa 120

caattatatg tggcagtttc aagagttcaa agaaaacaaa gattaaagat cttaattcat 180

gacaaggaaa gaaaaccatt gaagtctgct actaatgttg ttttcaaaga ggtatttgaa 240

aacctttaat aagtatgtcc acaagtgcta ctaattctat ttgtatcaac tataatttga 300

tttacaatac tcgtatatct tatatgcaag tttcctcttg gagtggctgc attatttttg 360

gtccttggcc aaagttacat ttttctcctc tgaaatgtag atagatgcaa gtatcatggt 420

tcttaacata ttgcattggt gggaatatgt ggaaacaata tga 463

<210> 756
<211> 169
<212> DNA
<213> Glycine max

<400> 756

agaatcggaa gaagtaattg gctttttccc tggcgatcta actgcagatc tcttgacctc 60

tgccgtggaa gcagctgcat aagccattca tgatatttct acaccttaga tcaacatgat 120

gaaagcagct gggtgggacc ttgatgctga tgccaactga ctcgaacct 169

<210> 757
<211> 297
<212> DNA
<213> Glycine max

<400> 757

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taatatcggt tttgatcaaa attaatgtta acgagcattg tttattaagg tcgtcaaagg 120

aaacttattg atgcaatgct acccgccaag ggcattggat agaagactcc aagaagattg 180

ggtcagatag gcaagagaag gccctagggg tctcaagagc cttatggtag atttcgggac 240

catgggctaa gtatgagccc acttatcttt gtacatatca tattatgatt ccattat 297

<210> 758
<211> 359
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 758

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caaacacgtc caccacgaga atattgtcgc ggaacgaaac cgcagtgctg taatacagag 120

aattcttcca ccaaaacata aggaccctgg tagcgcaact actccttgat caatcgaaga 180

agtcactctc ggaaaggctc tcattgactg gggtgccaga atcaacctaa cggcgctctc 240

tatgtgtaca aggtcgggag agctggaaat cacgctcacg agaatgactt tacaacttgc 300

taaccgatcc atcacaagac cttacggtgc agatgaggaa gtactgacta gagtgaaac 359

<210> 759
<211> 389
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 759

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tgtctaagac gaggagcatt aagggttatc attgcctgac aataccgctc atcaacataa 120

catttgtgtg gtttgcagaa ttctttgagc ttaggatagt aagtattgtc ttcaactatc 180

ctaagagcta gttctcggct aatttcaaac cactgggagc cttttcacca ggcactcatg 240

ttgatttcaa attattttgt ttggtattag aagcatactt ccccaatgag tgagaaaagt 300

gtacataaca tatttaatag catgaacaaa caatttataa agactcagga taagatcatg 360

aacaagcatg agccagaaac ccatgatca 389

<210> 760
<211> 448
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 760

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ttttcaaaaa gaaaaagact taagttaaaa ggataatgca accagattaa tacttccaaa 180

gaaaaaaatg ttttgcaaag acattttcag acaatttaaa tatttttatt tgactatatt 240

agtataaatc atctctaatc catatatttt ttaatattat gttctttnta ttcattntct 300

tttgatatac tttgtgtttt aataatttga attcaatatg attntgttta tcaattattt 360

ctggatttga catntactta tacgaaattt ataagtttct ttttttggta gtatttacta 420

ggtttaaaat gttaattggt aaagacgt 448

<210> 761
<211> 427
<212> DNA
<213> Glycine max

<400> 761

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acgttgatgt ggatgatatc tccagagcta cctgcgtcaa ctatatcaga gaaaaatcac 120

acccctttga cgtattctag gagctgagtc taagacttca aagagaaaaa gactgtgtca 180

tcaagagaat cacgagtgac catggcagag agtgtgacaa cagcaggttt actgaattct 240

gcacatctga aggcatcact catgagttct ctgcagccat tacaccacaa cagaatggca 300

tagttgagag gaataacagg actctgcaag aggatgctag ggtcatgctt catgccacag 360

aacttcccta taatctctgg gctgaagcca tgaacacagc atgctacatc cacaacagag 420

tcacact 427

<210> 762
<211> 477
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 762

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attggataca tccacctgta ttgaacagga ccacctaatc taactttgtt tgccaagtga 120

acaggaaagt gaaccattat gtcaaaaaac ttggaggaaa aatcatctct gattgacaaa 180

gaatttcaat aatttgtgat tctatataat ccaaatcttc tacctggatc actntctaac 240

acaaagagcg aaagaaggat ccaaggtgaa ttaaaagatc aaccaccaca ctaggcattg 300

tgcttctaat tgctatttgt aataagtaat gtaacatgat atgtgtatca tgactctngt 360

agccagaata tttgtcagtg atatgcatgc attntgaaat atttgttgca ctcccatcta 420

ngcaattggc atctttcaag ataccacana aaatagactt ctttnttgta gtcatta 477

<210> 763
<211> 477
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 763

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tttagaagga gtgctctttt gatatcacct tttgttataa aatgattttc cttcttaaaa 120

atcttcttgg aggaatcctt ttcctctttt tccttcccct tggcctttga agagaaggcc 180

ttactatcct tctttttctt ttgtttttct agtttttctt cctcatccct attatctttc 240

atagttagtt gatctttggc cacctgtgaa ggtgtttgag gatgcaacac anatttagtg 300

ccaagatggg tgagggtaat ctcattagtt aggccatttt aaatgatctt cctatcanat 360

ttccatggcc ttcctaaaag aatatgcatt gcctccatgg gaactatatc acaattaact 420

tcacccttt atgtcccaat ggagaaaggt acctttactt gttggctaat tatcatt 477

<210> 764
<211> 449
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 764

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caagatcaat cactagcatt tgtgggtttg tacttgccta gaccgatgtt tagtcataaa 120

caattatatg tggcagtttc aagagttcaa agaaaacaaa gattaaagat cttaattcat 180

gacaaggaaa gaaaaccatt gaagtctgct actaatgttg ttttcaaaga ggtatttgaa 240

aacctttaat aagtatgtcc acaagtgcta ctaattctat ttgtatcaac tataatttga 300

tttacaatac tcgtatatct tatatgcaag tttcctcttg gagtggctgc attatttttg 360

gtccttggcc aaagttacat ttttctcctc tgaaatgtag atagatgcaa gtatcatggn 420

tcttaacata ttgcattggt ggaattatg 449

<210> 765
<211> 401
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 765

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gtcaatgtcg agcatctcga catattatgc gctcgaatca gacatccgtg tgaaaagtta 120

tgaccatttg aatttctcga gagcttccga tgtttaattt cgagcctctc gacatattat 180

gcgcccgaat cggacatccg tgtgaaaagt tatgaacatt tgaatttctc gagagcttcg 240

gatggttaat ttcgagcctc tcgacatatt atgcgcccga atcggacatt cgtgtgaaaa 300

gttatgatca tttgaatatc tcgagagcct tcgatgctta agttcgagcg gactcgatat 360

atataagcct gaattgccct cagtgtctaa agtatgacca t 401

<210> 766
<211> 356
<212> DNA
<213> Glycine max

<400> 766

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tcaaacttgc caaattattt tcattttcta agaaaactat tttaaattta gaaaagaaag 120

ttttgaaatt aaatgtagaa ttataaaatc ttaaagcaga agttaaaaca ttaaaaccaa 180

tagatacaaa ccaatcctct actaaatgtt taatacaaga tagcaatgaa gcatctcatt 240

catgtaaata ttgtaaaata tttaaagaag aaattaaaga tgtaaaagat tctctttcca 300

tacttactct tggcaaaaat aatttatata ttatactagg aaaacatata tgtgtt 356

<210> 767
<211> 444
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 767

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tgctctctca ataactcttg ggcaaacact tgcaaatcta ttgagagttc atccaagaac 180

ttcaaattgt attattcact ctaaaggaga ggaatctttc tgttcttctt agaaagtcaa 240

ttgtaatcaa aagactagtt gtctcttgaa ttatgagttt cctgaacaca acggaaaggg 300

attccttgng tgttcaaaag ttgcaaaagg gttgtttaca aagatagtgg aaaatctcaa 360

gtgggttgct tgaggactgg acgtangcac gggaagcggc cgaactatga taaatcgagt 420

ctgcatatct ctcttccctt atct 444

<210> 768
<211> 363
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 768

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attacaaggc aatgtaatcg attaccagaa gacaattttg aaaaacaact tttaaaaaag 120

gttttgaatt taaattttga atcatgtaat cgattatcag atgtttgtaa tcgattacca 180

acaacggcac ttcagtaaac actttgaaaa gtcatgaccc ttcaaaatat aattgtgtaa 240

tcaattacca aaaacctgta atcgattacc agtgaagagt tttaggaaaa atcttttgaa 300

aagacacatc tctccaaacc attttgaaaa ggcacgaagg gcctatatat gtgtgtgtct 360

gac 363

<210> 769
<211> 329
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 769

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ttggcaagta agtctcatta ctattttctt gatggttttt ctggttattt acaaattcat 180

attgctcttg aggatcaaga aaagaccaca ttcacctgtc cctttggcag ttttgcctat 240

aggaggatgc cctttggcct atgcaatgcc cttggtacct tccagcggtg tatgcttagc 300

attttcagtg attttttaca gacttgcat 329

<210> 770
<211> 385
<212> DNA
<213> Glycine max

<400> 770

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aggagagagc acgagatgaa gagccaatgg ttgatacatg gacggagatg aagatgatca 120

tgaggaagcg gattgtgccg gctagctact caagggactt gaaattcatg ctcctcaaac 180

taacccaagg caacgaaggg gttgaggagt atttcaggga tatggatgtg ctcatgattc 240

atgcaaatat tgaccaatat gaggagggag ctatggctcg atctcttaat gtgttgacta 300

atgacatacg cgatattgtt gagctgcacg agtttgttga aatggatgat ttgcttcaca 360

aagcaatcca agtggagcaa caatt 385

<210> 771
<211> 453
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 771

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ggtcataact tttcacccgg atgtccgatt atggcgaatc acatatcgag acgctcaaaa 120

ttgaacaacg gaagctcttg agaaattcta atggtcataa cttttaactc ggatgtccga 180

ttcacgcgca tcacatattg aggcgctcga naaggaacaa cggaagctct cgagaaattc 240

aaatggtcat aactnttcac actgaggtcc gattcaggat tataatatat caagacgctc 300

gaaattaaaa atcggaagct ctcgagaaat tcaattggtc atcacttttc acacggatgt 360

ccgatttggg tgcataatat gtcgacacgc tcgaaattga caacggaagc tctcgagaaa 420

ttaaatgggc ataactttat actgaggtcg atc 453

<210> 772
<211> 434
<212> DNA
<213> Glycine max

<400> 772

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atactctgat attgatggtc ttgatttatt ctcacaattg acagtactaa gagaagtgtt 120

aagagaagaa attagcacac caatagaact attgagttat attaaaactc tatattcttt 180

tccaaatgtt tacattgcat ataaaattct attgacaatc tttgtaacag ttgctactgc 240

tgaaagacgt tttgaaaaaa agttgttcat aacatacaca gaataaagat gatctatttt 300

gcatctaaat tatatttaaa taaacggcat attaaatgtg tacatgttaa ttgaagcatt 360

caaataattg gtgttacgag agaatgagaa gagaagtgat aacttggtac ttcaacgtgg 420

agcctaagaa tgta 434

<210> 773
<211> 301
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 773

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ctaggncaga tatatgctat tgtgtgcaca aattatatca acttgtcttc aacccctata 120

cgaaccacat gcatgctact aacatgtctc ttcggtacct taagcacact gttattcaag 180

gtatttttt tatggccaac ttatacacaa aattacatgc atatgtggat gcagattaac 240

gatcatgttc tgaaagttaa agatcaacca ctggcttctg tatcttctta gaaattcctt 300

g 301

<210> 774
<211> 467
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 774

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tccattaaga aagacagttt tcacatccat ctaatgtagc tccaagtcat aatgggctat 180

taatgccatg ataatcctga aagaatcctt tcatgagaac ggcgaaaatg tctcttaata 240

atcaatgtca tctttttgag taaaatccct tagtaacaag tctagcattg taatgttcaa 300

ggttgccatg agagtcatgt ttagtcttga agacccactt tcaactaact ctcttataac 360

cctttggtaa ttctacaagg tcccaaatat cattatgtgc catggaattt atctcttctt 420

tcatggtatt taaccacttc tcagaatcat cacagcttgc agcttgc 467

<210> 775
<211> 450
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 775

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aaagcactca ggttctccat catctgttag gatcacatac tcattagtag aatacctatt 120

agaaggttgt ctttccttgt tggacctcct gagttgaact tgaggtggct cgatagcacc 180

accaagattt tcatcttgtg acatgtcatg ctcctcttca tacatcattt tgaacatcag 240

tatttagatt ctgaatatgc ggctgaactg gttcaaaatc aaccacacca acattgtctt 300

ccttgggtgt agacttcttc accttatcaa tgtcttgaat ggtttggtct ttcatgaatt 360

tcacatcacg gcttctgaca agcttcttct caacaggatc atataacctg taaccaaatt 420

cattctcatc ataaccaatg aagatacatt 450

<210> 776
<211> 333
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 776

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ccgtaatata tccagacact cgaaattgaa taccgaagct ctgagcaaat ttaaacgaca 120

atacgttttt actcgtatgt tcgattgagt cccgtaatat attgaatcgc tcgaaattga 180

agaccgaagc tctgagcaaa ttcaaacagc aataaatttt tacttggatg tctgattgag 240

tcccgtagta tatcgagacg cttcgacttg aatgccgaag ctctgagtaa attcaaacga 300

caataacttt tttcctcgga tggctgattg agt 333

<210> 777
<211> 228
<212> DNA
<213> Glycine max

<400> 777

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taaaaagtta ttgtagtttg aagttgctca gagcttcaac attcaatatc gagcgtttcg 120

atatattacg ggactaaatc agacatcaga gtaaaaagtt attgtcgttt gaattatctc 180

agagcttcgg cattcaagtc cgagcgtctc gatttattac gggactca 228

<210> 778
<211> 425
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 778

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tgtagtttcg ttgttagatt ttttctttat aggaatttat ggtcctgtaa gttcattgag 120

agggcccagg cactaataca tggagatcta cacactggtt ctgtgatggt tactcgtgaa 180

tcaactcaag ttattgatcc agaatttgca ttttatggac caatgggttt tgatattgga 240

gcattcttgg gaaacttgat tttggctttc tttgctcaag atgggcatgc tgatcaagca 300

aatgatcgaa aagtaggtcc ccttttttcca tgtcttctgt ggtccttact tgtcctcttc 360

tttgcatact ataagttgta tttagtcaca tttcttgtta ttctccataa tctagctacc 420

actta 425

<210> 779
<211> 423
<212> DNA
<213> Glycine max

<400> 779

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tgtgttgttt gattctggtg ccacccattc ctttatatcc tgtttgtgtg taggaaaact 120

taagctttct gtgtcttctt taaataaaga tatagtagta gagaccccta ctagtggttc 180

tgtgttaact tctgatgtgt gtttgaattg ttctgtggag atttctggta ggatattctt 240

gattgatttg atttgtttgc ctttgagcca gattgatgtt attcttggta tggactggtt 300

atcttccaac catgtcttgt tgaactgttt tgagaaaagt gtggtgtttg atgattctgg 360

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tgc 423

<210> 780
<211> 372
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 780

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atcttaccag aagcagagct cattcaccct ttgaatcaag atgtatagta ggtccggttc 120

tgcaacagta atgcaggtga tcctcttcaa tttgatcatg ttttgtttgc tanaacatca 180

taccatctat tgccatttac tcgaatttat agtcgctaac attagctact acaattaaaa 240

taacttaaca ggttattgca attctatcta gtatatataa gaaataatat ggcatgcagt 300

ttatacatat attttcttta taaagaggaa tcataatttg tatatatttg atgcatttaa 360

agtttttact at 372

<210> 781
<211> 262
<212> DNA
<213> Glycine max

<400> 781

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gtgataactt atgaccatta taatttctcg agagcttccg ctgttcaatt tcgagcgtct 120

cgatatatta tgcgcccaaa tcggacatct cggggaaggg ttatgaccat atcaatatca 180

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gtgtcataac ctatgaccat tt 262

<210> 782
<211> 407
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 782

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ttgtggaccc tatttgcttc ttgatgcaat cctacccccc aaggacattg aataaaagac 120

tccaagaaga ttggaccaga gagatgcaag agaagacctt aggattctca tgagccttag 180

ggtagatttc gggcccatgg gttaagtata agtccactta tctttgtaca tatcatatca 240

aggttttatt atttttgggc cttgtattta gggctctata gtgtaggtag ggtacccttg 300

aaatgtagga tttttcagcc cttgtatttt agggcacctt gactagttta ttgtattagg 360

ggtagttctg taatttcaca tacattaagt gaatatttga tgtgtgt 407

<210> 783
<211> 386
<212> DNA
<213> Glycine max

<400> 783

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ggcattttta tttacacaac attaaatcat ataaaatatt gcctccccaa tggagatagt 120

gggataatta aaacattgga tgtcccaatt tatattacaa aggttgttgg aaacaccatc 180

ttctgcttgg gtcgcgatgg gaaaaacaaa gctataactg ttgatgcaac agaatatatc 240

tttaagcttt tcttgttgaa gaaaaaatat gatcatgtaa tgaacatgat aaagaattcg 300

cagctttgtg ggcaggctat gattgcttat ctacaacaga aagggtttcc tgaagttgcg 360

ctccattctg tgaaagatga gagaat 386

<210> 784
<211> 417
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 784

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ctccaatctt taatggagag ggttaccact actggaaaac ccgaatgcaa atttttatcg 120

aggcaataga tctaaatatc tgggaagcca ttgaaatagg gccttatata cccaccacag 180

tagaaagagt ttcaatagat ggtagttcat caagtgaaag cataaccata gaaaaaccta 240

gagatagatg gtctgaagag gatagaaaac gagtacaata caacctaaaa gccaaaaaca 300

taataacatc tgccctagga atggatgaat atttcagagt ttcaaattgc aagagtgcta 360

aggaaatgtg ggacactctt cgattaacac atgaaggaac tacagatgtt aaaagat 417

<210> 785
<211> 413
<212> DNA
<213> Glycine max

<400> 785

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caacagtcac atctttttat gtggttcttg aatggctatc aaaggcctat atatatatgt 120

gacttgagac acgaatttaa gaagagtttt tggagaacaa aaaggtctta tcctattaaa 180

aagcaaatcg tgttatcctc ttacaaattc cttggccaaa ttacttgtga ttcaataagg 240

aattatttga gtgctcaaat tgttcagtct atctctttca agagagattt cttcttttct 300

tcttcttcat tctgaaaagg gattaagaga ccgagggtct cctgttgtga aagaattcta 360

aacacaaagg aagggttgtc cttgtgtgtt tagaaccttg taaaggaatt tac 413

<210> 786
<211> 369
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 786

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taagagaatt cagatggact ttaatcctaa ttccacaagc gacctttca cgagatctct 120

acttaaccct ttgggtacat gatcagccac attatgctga gttctcacaa actccactga 180

tatcacacca tgcatgatta actcccgaac catgttgtgt ctaacaccca agtgtctaga 240

ctttccatta tacactggac tatatgcctt agccaaagnt aatatggggt aaccttattc 300

cttttggtag gaattcagtt taacatgtaa caggctgcca acatagcctc accccaaaat 360

ccttcactt 369

<210> 787
<211> 391
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 787

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tcccttcaaa ggtagaagtg atccagatgc ctacctggac tgggaaatga agactgagca 180

cgtatttgcc tgcaatgact acactgatgc gcagaaagtc aagctagcag cagctgaatt 240

ctccgactat gcccttgttt ggtggcataa ataccaaaga gaaatgttga gagaggaacg 300

gcgagaggta gatacatgga ctgagatgaa aagggtgatg agaaaaaggt atgtgcccac 360

tagctataac aaaaccatgc gacagaaact t 391

<210> 788
<211> 425
<212> DNA
<213> Glycine max

<400> 788

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agttcttgtt attcaattat ttgttttcta agaaatccga ctcaatacga attttctgag 120

acttcattca cttcaattta ctaccacaaa ttgcctcatg tacctacaac aattctttta 180

cctgtattga aaaatagggg tatggcaaaa aaattagagc aattgtcctc cactgagtgg 240

gcataagctt agcaagatga agtagctttt tatcctcttc tcttgtccac ccaatctata 300

cacaaaaagc atcagattga aaaatcactc attagaaaaa tatcacaaca attaataaca 360

tagttggtac atactcctta tcaataacat cttaaaaaaa gagaggctct taaacccaaa 420

gaaag 425

<210> 789
<211> 399
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 789

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gggaagagag aaatgcaaac ttgatttata ctggttcgac cactttccgt gcctacatcc 180

aatcctcaaa caacctactt gagattttcc actatctttg caaaaatcct ttttacaact 240

tctgaacacc caaggaatca ttttcccttg tgttcaagaa actcacaatt caagagacaa 300

ccagtctctt gattacaatt gattttatga gaagaacaaa aagatttctc tcttttagag 360

tggataatac aatttgaagt tcctggatga actctcaat 399

<210> 790
<211> 415
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 790

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tcctaagttt tcctttccat tgtttaatac aaagcatttg caaccaaaaa catgtagatg 120

tgagatgttt ggttttctac cattgaacaa ttcatatgga gttttcttta agataggtct 180

gattaaagcc ctattcatga tataacatgc agtattaaca gcttcagccc aaaaatattt 240

tggaagagga gtatcattca ataaggttct agcaatttct ttcacagacc tatttttcct 300

ttcaacaact tcattttgtt gaggggggtct aggtgcagaa aaaatatgtt caataccatg 360

cttttcacaa aataagtcaa attctttatt ttcaattccc cccatgatca cttct 415

<210> 791
<211> 410
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 791

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aggcaaaaga tcaagaggag ttagtgggtt aaaaccataa acaacttcaa aaggagaaca 120

attagtggca ttatgaacaa ctctattgta agcaaattca acatggggta aacaagcttc 180

ccaagttttt aagttcttcc tcaaaactgt tctaagcaaa gttcccaaag ttctattaac 240

aacttttgtt tgcccatcgg tttgtggctg acaagtggtt gaaaataaca atttagtgcc 300

caacttgctc cacaaagtcc tccaaaaatg gcttaagaac ttagagtccc tatcactaac 360

aatgctcctt ggcaaaccat ggagtctcac aatctcctgt tggatcaagt 410

<210> 792
<211> 410
<212> DNA
<213> Glycine max

<400> 792

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ggcatcaata ttgtatttgg aaagacccaa gagaaggaaa aaactaaaac ttccatatgg 180

aagaagaggt cgatattgtt tgatcttcca tactggtatg atctagatgt cagacattgt 240

attgatgtta tgcatgttga gaaaaatgtg tgtgatagtg tcattagcac acttggtaac 300

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cgagacccag tacattcaag gtctgatggt aacaaaatat acttgccttc 410

<210> 793
<211> 388
<212> DNA
<213> Glycine max

<400> 793

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catgtagaat ttgcctacaa taggggcgtt catagaacca ccaagcaatc ccctttgag 180

gttgtctatg ggttcaatcc cttaacaccc ttagacctca ttccccctccc acttgacact 240

tcttttatac ataaagaagg ggaatctagg tcagagtttg taaagaagtt gcatgagagg 300

gttaagaccc aaatagagaa ccaaacaaag gtgtattcaa ctaagggcaa tagaggaaga 360

aaggagctag ttcttaatga gggggact 388

<210> 794
<211> 380
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 794

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atcgagacgg tccaaattga aaatggaagc tcgtaggaaa ttcaaacgac aataactttt 120

tactcggatg tccgattgaa tcgggtaata tatcgacacg ctcaaaattg agactagaag 180

ctctgagcaa actgaaacga caataacttt atacatagat ttccggttga gtcccgtaat 240

atatcgagat gctccaaatt gaaaatggaa gctcttagaa aattctaacg acaataacat 300

tttactcgga tatccgacag agtctcgtaa tatatcaaga cactcgaaat tcagaacaga 360

agctctgaga atttcaaacg 380

<210> 795
<211> 411
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 795

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cgaacaatgc ctcgattgtc aacataccaa ttatatcact aggaaaccag ttggactact 180

tgcacccttc cctctaccaa ctcgaccatg ggaagacttt tcactcgatt tcattgttgg 240

tttaccatct tactgngggt atacaaccat attggtggtt gttgatagat tnttgaaggg 300

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<210> 796
<211> 404
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 796

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tcaggaagaa tggcgtgatc actagccgcc atgttttcta tgagttccat tgcctcctcc 180

ggtgtcttta gcttaatctt ccctcttgcg gatgcatcca atatttgctt tgattgtggt 240

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tttctaagta gtccatggaa acggtcgagt gcctcgctga gggattcatt anngaaatga 360

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<210> 797
<211> 394
<212> DNA
<213> Glycine max

<400> 797

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tgaggcaata gacttaagta tttgggaagc catagaaata gggccttata tacccaccac 180

agtggaaaga attacaatag atggtagcac atcaagtgaa agcataacaa tagaaaaacc 240

tagagataga tggtcagaag aggatagaag acgagtacaa tacaatttaa aagccaaaaa 300

cataataaca tcagccctag gtatggatga atatttcagg gtttcaaatt gtaagagtgc 360

taaggaaatg tgggacactc tacattaaca catg 394

<210> 798
<211> 416
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 798

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catcaaatat atagtactaa tttggattga aaatttacat tttctcgtag gttcttgatc 180

gtggagaaaa gattgagctg ctcgtggata agactgacaa ccttcggtca caggtttcat 240

tttcttcttt attcttttag atatattttt aatctaattt acacgacttt gtgttcattt 300

ttttttttatt tttttgttaa atatttctta cattatttaa atttttggtg ttagtatatg 360

ctgacatcat tagntacttg gttttaattt ctatctcaac ttgttatgcg atgact 416

<210> 799
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 799

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taaccctcaa tagcagtcaa ttcacacaac ataacccaca ggacagaaga ttaagacatg 120

gtgtgaagga acttaccgta ggtttgagca attctataat ttcttgagct tgccaaagcc 180

ttatgtcaac aatattagca agtaaatcaa cctcaatcaa aatgtgggat tgctcattgn 240

gatgctgcct ggtcttcctc ttaatttttt cttcctttac gattgaaagg ataataatct 300

tagacattac acaagaataa tatatagatc aataaaaata agcatcatat ttatttcaca 360

ctttntaata ttagacctag aaaggtcata tcaggccttc attacctt 408

<210> 800
<211> 427
<212> DNA
<213> Glycine max

<400> 800

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ctattacaat gcacccaaga gaccatatat ctaacgctgg ttcaatctga ccaacgaccg 120

attctggtga catgtaaaaa ggtgtccctc taaacttgac cttcccatac tcagcatttg 180

catcttctct agtcttggac aacccaaaat cagcaatctt cagttgatac cttgcatgat 240

catcagatga aggaaagaga aggatgttgt ccggtttgag atcacaatgg acgactcctt 300

ttcgatgaat gcaagaaagc cctttgagaa gcatacgagt gtagactctt acttcactat 360

ccgatattgg ccccttcttg ttactaaacc aagaagagaa ccataaggag cacactccat 420

gaaaaga 427

<210> 801
<211> 402
<212> DNA
<213> Glycine max

<400> 801

agcttttggt atctttgttt tccttggttc actccatata caactaacaa acttcagacc 60

aagtccgtac catgtgtttc ttatgttaca atcttactca aagtgcatat cttttgttat 120

gatctttcag agtctaagtt gttcacctcc cgtcatgttg aattcattga agatgttctt 180

tcgttttcct ccacttcaag tcaacaacac atgatccata accctcaaat tcaaaattca 240

caaccgaatc ttccaaatcc aacctccacc aattccaaca aacaattcag attccagctt 300

atattttaat atcaacattg tacccaccca agcacctcaa tatcaaccac ctttaaattc 360

aaattccacc ttctcacaat tccagcttat cttttaatat ca 402

<210> 802
<211> 360
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 802

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taaatatatt catcaggaaa acatcatagt ggaaggaaat tgcagtggtg tgatccaaaa 120

gatccttcca cctaagcata aagatcctgg gagtgtaact attccttgtt caactagaga 180

agtcaatgtg ggaaaagctc ttattgacct aggagctagt atcaatttga tgccactctc 240

catgtgcaga agattgggag agttggagat aatgcccact cgaatgacat tacaattagc 300

tgaccgctcc attaccangc catatggagt aattgaagat gtgttggtca tagtgaaaca 360

<210> 803
<211> 394
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 803

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gatatcttaa gaaggggggg ttgaattaag atattccaaa ctgtttcccc taattaaaaa 120

tctatttttc tttttactta agttatgaat tcccttaatg acaatcttct taaatattaa 180

ttcaaatgaa gcaacttgaa tatgaatata aagcaataat aaataaagga gattaaggga 240

agagaaaatg caaactcagt tttatactgg ttcggccaca cccttgtgcc tacgtccagt 300

ccccaagcaa cccgcttgag agttacacta acttgtaaat tccttttaca agttctaaac 360

acacaaggac aacccttcct ttgtgtttag agat 394

<210> 804
<211> 429
<212> DNA
<213> Glycine max

<400> 804

tgaggtccct cattgcaaag atgtttttca agatactata ctcatctggc acttcaatat 60

tcaaacttct tgcatgatcg agaagagagg ggaaagcaac ttcaaacccg ataggcatat 120

gttctgcatt ttcatcctga agcttgtaca aattctcctt aaaaaatgac attcctgtta 180

catatgaatg catatataca caatagaaac attaaattaa cataaacgtg ctgataaaaa 240

aataacattt atatcataat actttactat ttcccggtcc tcttctttta ctatggaata 300

gaggtgtgaa agtattgcag aaaagaaatg attaagagta tgtatctaac aaaagaaatg 360

attaagagta tgaaaatatc tgggttaaaa aaaaaagagt acgacaatat cacagtcagc 420

aaggaattc 429

<210> 805
<211> 353
<212> DNA
<213> Glycine max

<400> 805

tcctctcagt cacctgcggc atgcaagctt gtaaaaaggg aagcaagtta aaaactcttt 60

tcaaagtaaa aacgttgttt ctacttcaaa acccttgaa ctacttcaca tagacttatt 120

tggtgcctct aaaactatga gtttgggtgg gaattactat ggcttagtta tagtagatga 180

ttactcaaga ttcacatgga ctttgttttt gaaaaccaaa gatgaagctt ttgatggttg 240

ttgcacactt gccaaggtca ttcaaaatga aaaaaggtct taacattgtt tcacttagaa 300

gttatcatgg aggtgaattt caaatgagtc tcttgaaatg tttgtgagaa aat 353

<210> 806
<211> 412
<212> DNA
<213> Glycine max

<400> 806

tgttggtatg tgatcaaaga agatgtcatc ttatctatct ctgaatttca ttctcatggt 60

tccattccta cgagtgggaa cacgtcattt ctagctctaa ttccaaaaaa ggagaaccca 120

caagaattaa gtgaatacat actcttatta ggtgcattta taaaattatt gatgaacttc 180

tagcaaagag attgagatgt attatagggg tgttggtgga tgacaggcaa ttcacgtttc 240

tgggagatag gaacatgtta gatggagtgg tcattaccaa tgaagtgatt caagaggaaa 300

atcgttaagt taaatcatgt gtggtgttca agacaaatcc tggagtggtc attgtcaatg 360

aagtgattca tgaggcctac cagtttgggg ccgatgcttc tagactaact ac 412

<210> 807
<211> 383
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 807

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tttgtgccca tgcttgttcc acgtcggacc aaagaaaaag gaaacagaaa aggaaaaggc 120

cgaaacaccc aaaagccaaa ttccccacca aaattcaact tcctaaaagt cctattggcc 180

catgattatg catgttatcg ttgatttgat aggaaatgat ttgcaaagtc aaatcatgac 240

atatctatgg tttggaatta ggatgaaaca cttgcatgtg tgagatttta tacactntga 300

gtggttttcc tctatttcat tcgcacccag tgtttcttct aaatgccctt ttagaaatga 360

aatgctaata tcccacaatc tca 383

<210> 808
<211> 390
<212> DNA
<213> Glycine max

<400> 808

acaaagaata ggttcattca taagcttatc ttttaataaa ttataagttt tctcatgcac 60

atcagtccac ttgaacacca catccttttt tacaagttca tttaaaggtg cagcaagtga 120

actagctaaa ccacgaaaac ttcttacctc attagcattc ttaggtacag gctattccct 180

aagtgccttt actttttctt cctcaacact tattcctttt gagctagtga caaaacctaa 240

gaatacaaca aattcatggc aaaaagaaca cttttaaaga ttggcacaca atttattttc 300

tctcaaaaca ttaaaaataa catgtaaatg atcaacatgt tcctctaatg tttgctataa 360

atcaaaatat catcaaaata caccacaaca 390

<210> 809
<211> 394
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 809

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aatttgtacc tgttgcaagg gtctgtggtt tgtgctcctc tgctgaccac catacagacc 120

tttgcccttc catgcagcaa cctggagcaa ttgagcagcc cgaagcttat gctgctaata 180

tttacaatag acctcctcaa cctcagcagc aagatcaacc acagcaaaat aattatgacc 240

tctccagcaa cagatacaac cctggatgga ggaatcaccc taatctcana tggtctagcc 300

ctcagcaaca acaacagcag cctgctcctt ccttcaaaat gttgctggcc caagcagacc 360

atacattcct ccaccaatcc aacaacagca acag 394

<210> 810
<211> 411
<212> DNA
<213> Glycine max

<400> 810

tctgaaatat gaagtattaa cctatcaagg ctatcgttcc ctttaacatg accctgacca 60

ttctcagaac tccgcctaag tgaatgtacc tcttgttcgt agtctcttat tcctttggca 120

aactcatcac acaaattctc caaaaggatc cgtgcttttc tctctctttc aagatttctc 180

aaacaaccag agaaggaaga cttcacttca gaaagctccc tagccagctt ccgatgcagg 240

ctttctgaat gctgacgtaa cctcctctca tcttctagct cttccctgat tgattgaact 300

gcagctttaa ttctaccatg ttctttgttc ttcctaataa gtttgtcaat tgtaatttcc 360

tttatcaagt tctccacttc ctgcctattc atttgattct ctcgtagtaa c 411

<210> 811
<211> 397
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 811

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aagttattgt cgtttgaatt ggctcagagc ttcaacattc aatttcgagg gtctcgatat 120

attgcgggac tcaatcagac atccgagtaa aaagttattg tcgtttgaat tggctcggag 180

cttcaacatt caatttcgag cgtctcgata tatgatggga ctcaatcaga catccgagta 240

aaaagttatt gtcgtttgaa ttggctcgga gcttcaacat tcaatttcga gcgtctcgat 300

atatgacgag actcaatcag acatccgagt aaaacgttat tgacgtttga attggctcgg 360

agcttcaaca ttcaatttcg agcgtctcga tatatta 397

<210> 812
<211> 339
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 812

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atatatcgag acgctcgaaa ttgaatgttg aagctctgag ccaattcaaa cgacaataac 120

tttttactcg gatgtctgat tgagtcccgt aatatatcga gacgctctaa attgaatgtt 180

gaacctctga gctaattcaa acgacactaa ctttatactc ggatgtctga ttgagtgccg 240

taacatatcg agacgctcga aattgaatgt tgaacctcta agccaattaa aacgacaata 300

aacgtttact cggatgtctg attgagtccc gtcatatat 339

<210> 813
<211> 413
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 813

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taaaccttct tttgcccacc atcttttgcc tccaaagtga tggtgtacaa ggtaccagaa 120

accacttgct gtttcgcagt taccaccttt tcaaactcca aaagggcatt ctgcatagcc 180

atttacaatt caataaaaat aaaatataat tcatatttac cacaaaataa aaagaaaata 240

gaagcccgtt cgtggttatt gaaattgacc ctaccaatct atttattcct tgacataatg 300

gaaatgcaaa tttatcctaa caatcaatta atttttggtg aacaaaattt tggnggaggg 360

gtaatgcccc agtacaagac agaanaagcc tccaagctca aagaacattc aca 413

<210> 814
<211> 426
<212> DNA
<213> Glycine max

<400> 814

tcttacatag tccgcctttg cttgaccttc tttatgctta aaaacagaaa cattaggcat 60

aggcaaaaga tcaagaggag ttagtgggtt aaaaccataa acaacttcaa aaggagaaca 120

attagtggca ttatgaacaa ctctattgta agcaaattca acatggggta aacaagcttc 180

ccaagttttt aagttcttcc tcaaaactgt tctaagcaaa gttcccaaag ttctattaac 240

aacttttgtt tgcccatcgg tttgtggctg acaagtggtt gaaaataaca atttagtgcc 300

caacttgctc cacaaagtcc tccaaaaatg gcttaggaac ttagagtccc tatcactaac 360

aatgctcctt ggcaaaccat ggagtctcac aatctcctgt tggatcaagt ggcctcagaa 420

taatta 426

<210> 815
<211> 387
<212> DNA

<213> Glycine max

<400> 815

agcttatcac ctttatcggc aattgaaaaa agattttaat gtaagtcaag agcatgatag 60

tgtgtcgata ccattaactg gtcacaggtt cttaagcagg ccgagggcat caatattgta 120

tttggaaaga cccaagagaa ggaaaaaact aaaacttcca tatggaagaa gaggtcgata 180

ttgtttgatc ttccatactg gtatgatcta gatgtcagac attgtattga tgttatgcat 240

gttgagaaaa atgtgtgtga tagtgtcatt agcacactgg ttaacattca aagaaagaca 300

aaggatggtt tgaatactca ccaggatcta gtttagatag gtatacgaga ccagttacat 360

ccaaggtctg atggtaacaa aatatac 387

<210> 816
<211> 375
<212> DNA
<213> Glycine max

<400> 816

gggatcctct tagtcacctg ctgcatgcaa gctataagaa attttgcaac atcgttttgg 60

atatttaaca agaacattct atttcttgac attggtacct tggtaattat attatttctc 120

ccatctctga tggaaagact ggaatctttc atgtgaatat catagccttt tttgaggaat 180

tgtcccaaac tcaaaatatt gttcttcata tttgggacgt agtagacatt tgatatgaat 240

tcatgtcttg catccttcaa atggattatg atcttacctt tttcctttta taggaatatt 300

ggaattatta ccaaattaag cattgccact tactgactca tcaagatcca cgaaacatgc 360

ttcttttcca cacat 375

<210> 817
<211> 414
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 817

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cctcttgatg tcatttctca tcatttcacc cttaatcttg tcaatcattt accaccccat 120

atttctggtt gtcatatatg tacattcgca tcctcaccaa caaacaaaat tagaatctag 180

agcaatgaaa tgtgtttttg tgggatacaa caccactcaa aagggatata aggcctatca 240

tccatctaca aaaagatttt ttgtatcatt ggatgttaca tttcatgagc atgaaatgtt 300

ttttcccttg aaaacacttc attcttcacc ttatagggga ggtgatttgg aggtgcagaa 360

tcatgataga cttgaccaag atatcaggtt atttgatatt atgccaacaa caac 414

<210> 818
<211> 390
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 818

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ctatacgaga catcttgcca aacaaagtca agttagccat aactcgcctg tgctttttct 120

tccatgccat atgtagcaaa gtcgttgatc ctgtcaagtt tgatgagttg gaaaatgaga 180

ccgcaattat actatgccag ttggagatgt attttccccc tgctttcttt gacatcatga 240

ttcacttgat tgtgcatctg gtcagagaaa tcaaatgttg tggtcctggt tatttgcggt 300

ggatgtaccc ggttgagcga tacatgaaga tcttaanagg gtatacaaag aatctatatc 360

atccagaagc atctattgtt gagaggtaca 390

<210> 819
<211> 416
<212> DNA
<213> Glycine max

<400> 819

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acacacactt tttcctagtc gatcactcac ataaatttcc attctccccc tttgtttttg 120

aatttatgct tcacttaaaa ttaagttaat tactcatgtg agttcttgat ttaatcccta 180

tttctctccc cctttggcat caacaaaaag ccaaagtgcg taacaagtat gaaacataca 240

aatacaacta gtcattcaca caacaatcat ggaaaaaata taaactaatc ataccagaga 300

acagaaaaca attaagcaag atattttaac cattcatcaa acttagaaac gttaagaaat 360

ataaaaacca tacataattg acatacccca gaatagaaaa acaatcaaac agatat 416

<210> 820
<211> 388
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 820

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ttcaaaaccc tttgaactac ttcacataga cttatttggt gcctctagaa ctatgagttt 120

gggtggtaat tactatggct tagttatagt agatgattac tcaagattca catggacttt 180

gtttttgaaa accaaagatg aagcttttga tggtttttgc aaacttgcca aggtcattca 240

aaatgaaaaa aggtcttaac attgtttcac ttagaagtta tcatggaggt gaatttcana 300

atgagtctct tgaaatgttt tgtgaagaaa atggaattca ccacaacttt tctaccctaa 360

gaacacctca acagaatggt gtcatgga 388

<210> 821
<211> 312
<212> DNA
<213> Glycine max

<400> 821

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gcagagcaat tatgaccttt ccaacaacag atacaaccct ggatggagga atcaccctaa 120

cctcagatgg tccagccctc agcaaacaca acagcaacgc tgctccttcc ttccaaaaag 180

ctgctggccc aagcagacca tacattcctt caccaatcca acaacagcaa caaccccaga 240

aacaaccaac agtttaggcc cctccacaac cttccctcga agaacttgtg aggcaaatga 300

ctatgcagaa ca 312

<210> 822
<211> 707
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 822

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acaaaaggct caaaagtcaa gaacacttca tgataacaaa gatgatgatc tcaagaatca 120

aagaatgagt tcaagattga atcaagtaca cttcaaggat caagaggaaa gttgaattca 180

ataatcaaga atcaagtttc aagattcaag ctccaagaat caagatcaag attcaagact 240

caagattcaa gaatcaagag aagactcaat caagataagt attaaaaagt tttttcaaaa 300

actaagtagc acatgaattt ttctcaaaaa ccttttatca aagagttttt actctctagt 360

aatcgataac caaattattg taatcaatta ccagtagcaa aatttttttc aaaaagcttt 420

caattgaatt tacaatgttc caattgattt caaaatgttg taatcgatta caatgatttg 480

gtaatcgatt accagtatgt ttgaacgtta gaattcnatt taattgtgaa gagtcacatc 540

ctttcacaaa atagctttgt gtaatcgatt acactgattt gggaatcgat taccagtgat 600

agtttctgaa caaaatcaaa agatgtactc tttccatagt tttcaaggtt ttctaaaagt 660

cataactttt ccaaatggtt tttaagtttt tctaaaggtt ataactc 707

<210> 823
<211> 629
<212> DNA
<213> Glycine max

<400> 823

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aatctgcacc tgtcgccaga ctctgtggtt tatgctcctc taccgatcac cacacagacc 120

ttttcccttc tatgcaacaa tctaaagcca ttgaacaacc tgaagcttat gctgcaaaca 180

tctacaacag acctcctcaa cctcagcagc aaaatcagcc acaacagaat aattatgacc 240

tctccagcaa catgtacaat cccggatgga ggaatcatcc caaccttaga tggtcgaatc 300

cttcacaaca gcagcaacaa caacaacaac cttattttca aaatgctgct ggcccaagca 360

gaccatacgt tcctccacca atccaacagc aacagcccca gaaacaacaa acaattgagg 420

cccctccgca accttccctt gaagaacttg tgaggcaaat gactatgcaa aacatgcagt 480

ttcaacaaga gaccagagcc tccattcaga gcttaactaa tcagatgaga cagttggcta 540

cacaggtaaa tcaacaacag tcccagaatt ctgatagatt accttcttaa tctgtccaga 600

atcccaaaaa tgggagtgcc attacattg 629

<210> 824

<211> 640
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 824

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cttgtcataa aaagtttgtg ttctatttaa tgtaactatg ctaaattttc cttatcataa 120

ttgtcatgat gtagaattgt agttgattca gaggaatttt ttatttacat tttatgcata 180

caatgcaatt tgtcatccat actcctatct attcactgat aataataaaa aaatactcct 240

aagtcctatc tattcattta acataaaatt tctaaaacga gaattattag gttgccgttt 300

cggcggtttg gttggcttta ttgtgtcgtg caacactttt gtatgtcccc tccttcaatc 360

taagacgcca cgacatagat attcaattca gttttcactt taactttgta ttatactctc 420

aagtctcaat cttttaaatt atttttattt ggtgtataat gccagcaacg gaatttgaac 480

ttaagacctg aaaactactt gaatcctcca ccactagttt gccttttcaa ttatttgatc 540

tttatctttc gctttcctct tatttctaat attnttttttc tttatatttc tttaaaaata 600

ttccaaatcc atttatgtat gatcaatgga acttaataat 640

<210> 825
<211> 632
<212> DNA
<213> Glycine max

<400> 825

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taaaccaaaa accctaaaaa tgtgaaaaca cgtcttagaa ttctgcatag attttagatt 120

aatatgcaat tttgaatatg tgatatatgt gaaaggaact tttaatcaca ccgtaagtta 180

taaaacaata ttatttagtt gaaagttata gaatggtata ataattgtca atgttacact 240

ggtgtaattt gatccttcct tatatattaa agttttagaa ctccccttga gtccaacatc 300

ttttatgtat gctcagtaag atatataaga tcaaagtgga catgcataca tatgtaaaaa 360

gcatagttaa gaggcgaaat tgaataatcc aaccaactca tttataaaag caacataaca 420

tatgttacaa catatatatt acaacaaagc atataaagat gaaagataag tctaagctca 480

tgatacatca aaattccaat ttctccctct tatgtaatca acaaatacag gtttgaaaga 540

tggaaaatga taaactatca ttatcattta tggctgctga ggtggatctt catttcgtgg 600

tgaatttgga tgtggatgtt aaagttgatc at 632

<210> 826
<211> 548
<212> DNA
<213> Glycine max

<400> 826

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caacagtctc atctttttat ctgattctta aatggccatc aaaggcttat atatatgtga 120

cttgagacac aaatttgaaa agagttttca agaacaaaaa ggtcttatcc tcttaaaaag 180

caaaatagtt ttatcctctt acaaattcct tggccaatac acttgtgatt caataaggaa 240

ttatttgagt gctcaaaatg ttcaatctat ctctttcaag agagattact tcttctcttc 300

ttctttattc tgaaaaggga ttaagagacc gagggtctct tgttgtgaaa agaattctaa 360

acacaaagga aggattgtcc ttgtgtgttt agaacttgtt aaaggaattt acaagatagt 420

ggaactccca agcggattgc ttggggactg gacgtatgca caaaggtgtg gccgaaccag 480

tataaatctg agtatgcact ttctcttccc ttaaactcct ttatttatta ttgatttata 540

ttcatatt 548

<210> 827
<211> 544
<212> DNA
<213> Glycine max

<400> 827

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tccagcatgt atattgatgg aatttgtgca aaaaacagcc aagagcccca tatatagttt 120

atacatccat cctgccccat aaaacaaagt caaaatagtg aatctttaca gtaattagta 180

ataactcctc aagtatcatt tacataaagg tacaccatca atatggaagc tcagaaatga 240

cattatcttc aacaatcatc cttttgtcat atcgaggctg ttggacaata caattttcct 300

ctcttggtct tggatgaggg ggtgggaaaa ggattttaat gttccttttc accaatggtc 360

ttcatctatg gctttggttt ttaagtagtg atagtgttgt tgggttgggt tgaattgttt 420

ctgctgggat gttgcataat tttatttact tttctgtccc aggagaacct acctcctgtg 480

gcttcttgta atacctctgg tactatgtat cttctattct ataaaaaact tcgtacccca 540

ttgc 544

<210> 828
<211> 536
<212> DNA
<213> Glycine max

<400> 828

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tttccttatt ttccaaaata agcaatttta gtcctatcag ttgaccatcc aaagtctaat 180

gttgacttct atgtgacata ttggtgctga tatggaactt atgtatgcaa atgacatgac 240

acttatgtga aaaaaaatta aatgacgtga ataataaaaa aacatcttaa tatgaattaa 300

acttgtgacc ctttattcat agacaatgga ataaactact aatatactca atttgtctac 360

ctaaatatat tactattatt ctctatgtat tcaatagtca agagttatat ttttttgca 420

gattatcaaa atctataaat taaaaatatt taatatataa atctttttaa tcctataata 480

tataaattta tatgtttcta ttttgaataa tttaccatct aatttttatt tttacc 536

<210> 829
<211> 362
<212> DNA
<213> Glycine max

<400> 829

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acaaacttct attgcctgaa agatcccgca tttctcctgc tttccattgt tccttcctta 120

aacccttcca ccaatcatct gaagaagatt gtgtcccact agcattgcct tccaatgatg 180

ttgaaaatca accagttatc tctcttttaa ccattctggg cactcattag gcctctgaat 240

ctactgatcc aaagctaagg tattaattca atgggcaggg ttgtctcttg atgacattac 300

atgggaagat tgtgaaaaac tcaagactgt ctatcacctt gaggacaaag tgtttttttg 360

at 362

<210> 830
<211> 496
<212> DNA
<213> Glycine max

<400> 830

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atcgagaggc tcgaaattga aaaatggaag ttctcgagaa attcaaatgg tcataacttt 120

taacttggat gtccgattca cgcacataat atatccagac acacaaaatt gaaaaatgga 180

attctcgata aattcaaatg ttcataactt ttgcctccaa tgtcagattt aggcgcataa 240

tatatcgaga cgctcgaaat taaacaagaa agctctggtc caattcacac ggccataact 300

tttgacatga gtgtatgatt gatgcccatg atatatagag acgctcgaaa ttgaataatg 360

gaagttctcg agaaattaaa attgtcataa cttttcactc ggatgtccga ttcagacaca 420

taatatatcg agacgcttga aacctaacaa ggaagctctg gtcccattca gagggccata 480

acttttgaca tgggtg 496

<210> 831
<211> 576
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 831

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tccttctttt gcagcaatct ggagtcaatg agcaacatga agcttatgct gcaaacattt 180

ataatagacc tcctcagcag caaaaccaac aatagcagaa taattatgac ctttcaagca 240

atagatacaa tccaggttgg aggaatcatc caaatttgag atggacaagt cctccacaac 300

aacaacagtc tgttcctcct ttccaagatg ctgctggtcc aagcaagcca tatgttcctc 360

ctccaataca gcagcagtca caataaagac aacaagagac tgaggctcct cctcaacctt 420

acttagaaga gttaatgagg caaatgacca tccagaatat gcaaattcag caagagacaa 480

gagcctccat ttagagtctg acatatcata tggggcagat ggctactcag atgaaccaag 540

ctcagtccca aaattctgac aaattgtctt cacaaa 576

<210> 832
<211> 389
<212> DNA
<213> Glycine max

<400> 832

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gatggtacag cgggtgaacc ataatcggaa gattcttttg gtgaagtagc catggaaaag 120

cagagcgttt ggaatgattt cgtaaatctc agaaggctat tgggaaatgc tggtataaac 180

acgaatgcca agcagatata aatttgaatg aggaatgtac agggtcgtgt gaagcaacgg 240

tcaaattttc ctgggttcat tagagaacgc gctataaatg ttaagagatc cgttggggca 300

ctttcacatt gctggaggtg ctataatccc tctagcacac aaatgcccat cttgcccctc 360

agtttttcaa actgatgcgc ctccaaagc 389

<210> 833
<211> 194
<212> DNA
<213> Glycine max

<400> 833

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tgaaaagttg tgaccattct aagctctcga gcgcttccga tgaacaatgg ccagcgtcat 120

gatcataaat gatgctgaaa cagacatccg agagatatgt gctgaccatt ctaccctgtg 180

cagagctttc gctg 194

<210> 834
<211> 610
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 834

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cctcaatttc attgtctccg tgttgaatgc attgctctct ctacagacat tatttcccaa 120

atctcaacgg tgagaatgtg aggaaatgag ttctaaaggt ggtatccaaa tttcatgatg 180

atccaatggt taaaaggttt gggatcatat ttttactgag atagatttga gtgtatgcgg 240

gaaagaaaag aaggttttgg gagaggaaaa aaggaaaacg aatttgagag gaaaaaagag 300

catagagacg tatcgtaaat attaaaattg acctaatatg tctctattta tagctggact 360

actctcagcc tattatttac tttatttttc tttattttat tattttataa aaagaaactc 420

tattttactc tctcattgaa taaataacca attaanatat ctttatattt tctaaaacat 480

cattttactc tatttgcttt ctaatgctat gaaaccatta ttttaattaa aaaaaaccct 540

tttccctcaa ttatngtaat tctaaaaact ctataaattt tagataaatc tctatttatt 600

ttacgaaaaa 610

<210> 835
<211> 423
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 835

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cattaagatt ccttgggtga ggtgggacat agtctgccta cctaagagta aaggtgggtt 120

agggatcaaa gatttgatta aattcaacga ggctttgctt gctaaatggg ggtgggagtt 180

ggcaaataat cagaatcagt tgtgggccac aattctattg tgtaaatatg gtggttggag 240

ggatttgatt tctcatagga actgcagttt agactctcct tggtggaaag acctcaaggt 300

tatcttcaag cagcagcaaa gcaacacaat ttgtaaaaat agctttattt aggccatang 360

taaggacggt ccatggaata caaaccaagt acttattggc ttgacaacaa aaaaaacact 420

cat 423

<210> 836
<211> 470
<212> DNA
<213> Glycine max

<400> 836

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gtgggcttaa tatggaagtg agggacaagg ttgaactcct tccatatatg gacctagatg 180

agctagtcca actttgtata gagtggagc tacaacttaa aagaaagtct tctttaaaat 240

cttaaggctt tcactcttat ccaaggaagg accaagccca aggaattttg gaggctgcac 300

cttgaaaacc caaggaagat aagggtaaga ccatagagaa atccacccct aagactagtt 360

cccaagaaag gactagcaac ataaaatgtt tcaaatgtct tggcagaggt cacattgcct 420

cttaatgccc cacaaagaaa accttgatta tgaggggtga agacatttat 470

<210> 837
<211> 581
<212> DNA
<213> Glycine max

<400> 837

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acacacatga cctttattta tagcctaagt gtcacacaaa attggaggga aatttgaatt 180

tatattcaaa tttcacttga atttgtggag ccaaaatttc actaattatg attaatgaat 240

ttttgctatg ggtcagccca ctaatccaag atcaagtcca agattaagtg tgcttaggtg 300

tcatcagaca tgtaaagcaa gaaggacatg cacaaagtgt gactatatga tgtggcaatg 360

gagtgtagca agcaaatgct cacctccctt tctaaaattt aattggattg ggcttctccc 420

aattctatta aatttatttc tcaacacaca catcaaatat tcacttaatg catgtgaaat 480

tacaaaagta cccctaatac aaaaactagt ctaggtgtcc taaaatacaa cggttgaaaa 540

atcctacttt tctagggtac ccttccttca ttatggatcc c 581

<210> 838
<211> 506
<212> DNA
<213> Glycine max

<400> 838

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gttccccctt taatataagg aaaatgcact tttcatgatc attacatgtg ctgatttttc 180

aggttgatct tgatccttat ggctcacctt cagggtttct ggatacatca gatcactcta 240

ctgctgatgg aggtatgctg atgtgtactg caacaaacat ggctgtgctc tgtgggggaa 300

atggggaggt ctgctattca aagtaatgtg catactctta ttcacaatca actttcattt 360

tgtttgattg gtggactgaa cttttaacaa ctgctattca tactacatat ggatcatacc 420

cattgagagg gaaatcttgc ccttcaaatg gctttgagga acaagccggc ctgcattgac 480

gtatggtata taacgcagaa actctt 506

<210> 839
<211> 512
<212> DNA
<213> Glycine max

<400> 839

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cgtcttgtaa taacaaagtc attgacattt ggcatttcca tttgggtcat ccttcatatg 120

ataggatgca attgttctaa caaacttatc ctatgttgac ttgtgataaa acctttgttt 180

gcgatacttg ccctagagcg taacagagaa aactttcatt tcccaatagt gactcataag 240

cttctagtcc tttcaatttt atacatgtag atatttgggg tccttgtgcc acaactgctt 300

tgaatggaca taagtatttt cttacaatta tggatgatca tactaaaatg gattggattt 360

ttataatgac ttcaaaagtt gagactcaaa ctcatttaca agcctttgtt gcctatgttg 420

agaggcaatt taatacaaaa atgaaagcta ttcgatcaga taatggtgct aagtttatca 480

tgaaacacgt ttatcataat actggtatca ta 512

<210> 840
<211> 572
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 840

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atttccaaga gtcacatctg ttcaaatgat tttttaatgg ccatcaaatg tctatttata 120

tgtgacttgg aacacgaatt tgcttagagt tttttagaac aaaaaggtct tatcctctca 180

aaagaaaaat catcttatcc acttaaaaat tccttggcca atacacttgc aattcaataa 240

ggaattattt tagtgctcaa ttgttcaatc tatctctttc aagagagatt tctttttctc 300

ttcatcttat ttctgaaaag ggattaagag accgagggtc tcttgttgta tagcaatcta 360

aacacaaaag agggtttgtc cttgtgtggt ttaaaacttg taaagggctt ttgcaagata 420

gtggaactct caagcgggtt gcttggggac tggacctang cacaagggtg tggccaaact 480

tgtataaatc tgaatttgca atttttttcc cttgaaccct tttattggtt aatgcttatt 540

gcttctattc agaaagttta aattcgcata at 572

<210> 841
<211> 603
<212> DNA
<213> Glycine max

<400> 841

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attatcatat aatgtaaatt gattgatagt aataataaaa atataaaatt catattaatt 180

atgatttaag ttctaaacat tatagatgat atgataaaaa aaatgtgtat aaaaatgaga 240

aattaagcaa taatgagaga aaataaaatt gaataatgaa agagagaaag agtgtgaccg 300

tcacagcttc caatagattg gtgttgtcgt gcaagtactt gaggacccat gttagaacac 360

ttgctgtggt gtcatgtgca gcaaagatga caccaatgag attatcaaca acttgagaat 420

ctgtgtgctg ctgatagtac atcttgttct tctcacctcg agcttgcaat agaactccca 480

atagcccccc accataattt aacagattat agactcttat aattacattt caacagaaaa 540

acccaagtca gtgtgaccat caacaaatgt tacatattat atataaccag tgctggataa 600

aaa 603

<210> 842
<211> 606
<212> DNA
<213> Glycine max

<400> 842

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ttctattttc agattgggaa tgcctctaac agcacttttg tcaaggattt tcttcatgcc 120

tcttaagtgc agatgtccca acctttgatg ccatattctg acttcatctt ctttggagga 180

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gaaagttaca ttgaatcctt catcaaacag ctgactgatg ctgatcaagt ttgcagtcag 360

tcccttcacc agcaatactt tgttcagact aggaagtcca tcatgaacta cctttcccat 420

tccaatgaac tttcctttag agccatctcc aaatgtcaca taactagtgg agcccggctc 480

aatgttcacc aggaattctt tgactcctgt atgtggtggg aacaaccgct atctaagtac 540

ccatcttcct taactgatgc tctaatggag gatgaacaac aagaatgaag tcttgtgttt 600

aggaac 606

<210> 843
<211> 605
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 843

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taaagtaata gcttccacta gtgctttttc tttcaacttt atcaccaaca tagtcaacat 180

cataatagct tgtaagtctg aaactttctc ttcttttgaa cataagacca agattagaag 240

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tttgaaatct tgcacataga taaacattga acataatatc agaaatggat gcagtgagat 360

agaccagtga gttgcatcca ctttttttga tccttgtcca atccaaggta tgtcatggtg 420

tgcattggag tcttcatttc ttttcatcgc ccatgttgaa tttcttcagc aattctttca 480

catacttagt ttgatgaatg tagatgcatt tggctttttg gtttatttgt aatccaagaa 540

agaatntcat ctctcccatc atgctcattt caattttgtc tgcataagca tagaaaaatc 600

ttcat 605

<210> 844
<211> 529
<212> DNA

<213> Glycine max

<400> 844

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ccgtcgtgga ttcagtcaca aaacaaactt caatatgttg gactgtctaa cacggggatt 180

ttagatttta ttcccacttg gttctgggaa gcacattctc aggttttgta tttaaacctc 240

tctcataatc atatccgtgg tgagcttgtg actacaataa aaaatccaat atctatccaa 300

actgttgatc taagcacaaa tcatttatgt ggtaaattac cctatctttc aaatgctgtg 360

tataggttag acctttcaac caattcattc tctggatcca tgcaagattt tttatgtaac 420

aatcaggaca aaccaatgca attagaaatt ctcaatcttg catcaaataa tctatcacga 480

gaaatacctg attgttggat gaattggcca tttctagtgg aagtgaatt 529

<210> 845
<211> 548
<212> DNA
<213> Glycine max

<400> 845

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cacatcagga aggtataaat tatactgaga cctttgcttt tgttgctcgt ttagaggcaa 180

tacggattct actatccttt gtttcccatt atggtatgat gttgtatcaa atggacgtat 240

aaagcgcatt cctcaatgct attattaagg aagaattcta tgtggaacaa ccccctgggt 300

tttagagttc tatttaccct catcatgttt tcaaacttaa taaagctttg tatggtttaa 360

agcaagctca ttgagcttgg tatgaaaagt taagttcctt cttaactgaa aatggtttta 420

taaaacggaa cgttaacact attttttttt gcaaagatta tataaatcca ttcctaattg 480

tccagatata tgacgatgat atattattta ctgcttctaa tgacttttg tgtgaggact 540

ctttcaaa 548

<210> 846
<211> 589
<212> DNA

<213> Glycine max

<400> 846

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accgtgtcta caacttgcaa actaagaaac tcgtcatcag tcgagatgtt gaagttgatg 120

aatatgcttc atggaattgg gatgaaaaaa aagtggagaa gaacgttctt atacccgctt 180

aactacctca agaagaatat gaggaagaag atctaggtga accaccttca cctacatcac 240

aacaacaaga tcaagaacta tcatcaccag agtctactcc aaaacgagta agatctttgg 300

tggacatata tgaaacttgt aacttggcca tacttgaacc tggaagcttt gaagaagcgt 360

caaagcacga agtatgggtc aaggcaatgg aagaagagat acagatgatc gagaaaagca 420

acacatggga gttagtaaat cgtccccatg gaaaagatat cattggggtt aagtgggtct 480

ataagacaaa agctaaaccc tgatggcacc atacagaaac accaagcgag gcttgtagct 540

aaaggtttct catagcaacc cggaattgac tacaatgaga catttgccc 589

<210> 847
<211> 525
<212> DNA
<213> Glycine max

<400> 847

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tatgttatat atctaacaat aatgaatcta ttaatatagc ttacaagttc attatgcata 180

caattttagg tccaagtcat tgcatatatt ttcatgaacg aaatcaggac ctgcatattc 240

attattagat tcatatataa atttttgtcc gtacttccat agtgtccatt gacacatttt 300

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aggtcatttt tatttgtctt agaataggca ttatgtgcac tttct 525

<210> 848
<211> 468
<212> DNA

<213> Glycine max

<400> 848

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atgataatta tatttacttg cttttggttg tttatggtta tgaattttaa acttaattat 180

tttgataata tatgatcagt ggtatgtttg atcaaatatt aattatgtta tttgataatg 240

tggtttttt tatatatttg atctatttat ggttcttgct atgatttggt ttatattttt 300

ccatgaatga ttgtatggat gcttaagtta tatttgtatg tttttaattt gttacgcact 360

ttggcatttt gttgatgccc aaggggggaga aaaatatgga ttaaatcaac aactcacacg 420

agtaatcaac ttacttttta gagaagcatt aattcaaaaa caaagggg 468

<210> 849
<211> 572
<212> DNA
<213> Glycine max

<400> 849

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gtcaatttgg taaacaaaat agaaaatcat tccccaaatt agcttggaga acctctcaaa 240

agttgcagct aattcacact gatgtggcag gacctcaaag aacaccatca ctacaaggta 300

gtctctactt tattcttttc atagatgact ttacaagaat gtgctggatt ttttttcttg 360

aaattcaagc atgaagtggc tgaagttttt tgtaaattca agaaaatggt ggaaacttca 420

agggacctga agattcaatg aaaatgggaa agaatatcca tccccataat tatttacttt 480

ggggaacacc ttggtttgaa tattaactca cagcccccta ccctctgaac attggggatt 540

ttgaaggatt aacaattcat tgttgggaag gc 572

<210> 850
<211> 528
<212> DNA
<213> Glycine max

<400> 850

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tttacaatag acctcctcaa cctcagcagc aaaatcaacc acagcagagc aattatgacc 240

tttccagcaa cagatacaac cctggatgga ggaatcaccc taacctcaga tggcccagcc 300

ctcagcaaca acaacagcag cctgctcctt ccttccaaaa tgctgctggc ccaagcagac 360

catacattcc tccaccaatc caacaacagc aacaacccca gaaacagcca acagttgagg 420

cccctccata acctttcctc gaagaacttg tgaggcaaat gactatgcag aacatgcaat 480

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<210> 851
<211> 589
<212> DNA
<213> Glycine max

<400> 851

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tttctggctt cagcaagagt catgtctcca agggctccac cactggcagc atctatcata 180

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tctccactga gttgtctaat acctgagata tccttcctga tggctgtggt cctggaagca 360

gggaaatttt ttttctaaga atactctctt aaggtcatct cagcttgtga tggaccttgg 420

agcaaggtaa tacagccagt cctttgccac tccctctaat gaatgaggaa aagccttcag 480

aaatatgtga tcctcttgga catctggggg tttcatggtg gagcagacaa tgtgaaattc 540

tttcaaatgt ttgtgcgggt cttcacctgc aaggccatga aactttgga 589

<210> 852
<211> 603
<212> DNA
<213> Glycine max

<400> 852

aacatgatca cgcttattaa ttactcagtt ttatttcatt ttgactagaa tatttttttt 60

aagaatgaat tttgactaga aaattaatca catatttatg tttatcttta catttatata 120

catacaggac atatcatatg agagaaatat atattatatg agagtgagaa aattaaatct 180

aatccatata actaaaatat tgatcatcat catttaatgt catttgaccc cttaagaaat 240

catgtgactt tttgacatta aatcttaatt ttttatatat gattatataa ttcaaattta 300

atcatttcac tctcatataa tatgttttct cttaaaagat atgtcatata tatataaaag 360

gagaagggtg ggatattttt acatataaaa ggagatggtg aaggtagttt tgaaagaaaa 420

tcaaattcat gaggatcact ttaatttatg agaaacacat ttcattatgt taattgtcac 480

ctaatgtaaa ttcaagattt gggttaaaac accagggaat aaaaataaaa attttaatat 540

attatgtact taaaacaaca aaaaaattat tttggactca gaaacaaaat ccctttctta 600

tta 603

<210> 853
<211> 539
<212> DNA
<213> Glycine max

<400> 853

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tatcttttgg tgtcaccctg attcactgaa gttagtcaac gcatgtaatt tggtgttttt 120

gatagacagc acctacaaaa caaaccggta tagactccca ttgctcgatt ttgttggggt 180

gacaccgact gggatgacat tctctgccgg ttttgcatat gtggagggtg aacgcgttaa 240

taattttgta tgggctttac aacgcttctg aagccttttt ttaaagcgtg atgccctccc 300

tggagttatt gtcactgata gagaccaagc attgatgaat gtagtgaaag atgtattccc 360

tgaatgcaca aatttgttgt gcatctttca cataaacaag aatgtgaagg ccaaatgtaa 420

atcactaatt gcgcaaaaaa atgcttggga ttatgtcatg gattgctggg gatctctgac 480

tgattgtcct tcaaaacaac agtttgatga atgccttgaa taagttcgaa atagcttgc 539

<210> 854
<211> 558
<212> DNA

<213> Glycine max

<400> 854

tgtgcatggg aaaatagttg tttgtgaaag aggtaaaaag ggaataacta agatgggaga 60

ggtagtgaaa gtggcttatg gggcgggaat gatagtactt aatactaaaa atcaagctga 120

agaaatttat gttgatcttc atattttgct agccacttcc ttaggagcct ccagtggtaa 180

gactattaag acctatattc tatctgataa gaaaccaaca acttcaattt cctttatggg 240

aataaagtat attgaccctg caccagtaat gagagcattt tcttctaaaa gaccaagtat 300

agtgggacta gatgtgactg acccaactgc gaatatcttg gctgctcggc cactaaaaac 360

taacccaagt tttatcatga atgacataag agaagtacta tttaacattc tcttaggtgc 420

ttcaatgtct atgcctaatg ttagtggcat agcaacactt tttaaatatt tgcacactga 480

ttggtcccct gcagctatca aatctgcttt gatgactact gcttacacat tgaacaacag 540

aggagctgca atttcata 558

<210> 855
<211> 619
<212> DNA
<213> Glycine max

<400> 855

tctagaatct agtgttttgc gaaatcaaat tggaatttgg aacagtgcga cgttgctcat 60

gactttgagg tccctcaatt aaaggtttag tgtaacattt gagtgagtaa tttcagtgta 120

aactggaaaa ttaaatgtat agtatacttg tatacattta gttgtaattg tatagaattt 180

ttagtaaaag agaaccaaaa ctaatataag attaccagaa atgttaaaac taaaatattt 240

aaaatgcaaa acacaagata caacatttca cttgttatta aataattatg aacaaagtca 300

ctgagttgaa aaccaactct aattatacat aacacaactc aacattcaaa gttgtaaaac 360

cccccaaaag taaaacataa gtcatccttg aaaagaataa atgaaaatca aatctaataa 420

aattgaaata cgtaatatat tatatataat aaaattgtct agttcaaaaa tgatagtaga 480

atcattccca acatcatttc tcacaaaata caccaaagag ttataaacat aagtttatag 540

agattgatag agtataatgt acttaaatta caaacaaatg cagaatagaa cagagttaga 600

ttttggattt gggaactca 619

<210> 856
<211> 503
<212> DNA
<213> Glycine max

<400> 856

agctttatca aatggatgta aaaagtgaat tctcaaatgg ctttattcaa gagaaagtat 60

atgtagatca acccccctgga tttgaaaact cagacaagcc caatcatgtt tttagattaa 120

aaaaggcttt atatggctta aagcaagccc ctagggcttg gtatgagcgt ctaaataagt 180

tccttttaga aaaggatttc tctagaggcc aagtagatac tactcttttc ataaagagaa 240

aattacatga tattttattg gttcaaattt atgttgatga tattattttt ggatctacta 300

atgaattatt gtgcaaggaa ttctctcatg acatgcaaaa tgagtttgaa atgtcaatga 360

tgggagaact taatttcttt cttggattac aaattaaaaa aaccaagact ggaatttttg 420

tcaatcaatc caagtactgc aaagagttaa ttcacagatt caggatggaa aatgctaagc 480

acatggctac accaatgagc act 503

<210> 857
<211> 401
<212> DNA
<213> Glycine max

<400> 857

agctttgagc caattcaaac gacaataaat ttttactcgg atgtctgatt gagttcaata 60

atatatcgag acactcgaaa ttgaataccg aagctctgag caaattcaaa agacaataac 120

tttttactcg gatgtctgat tgagtctcgt aatatatcga gacgctcgaa attgaatacc 180

gaagctatga gcaaattcaa aagacaataa ctttttactc ggctgtctga ttgagtctcg 240

aaatatatcg gaacgctcga aattgaatat agaagctctg agcaaattca aacgacaata 300

actttttttt cggatgtctg attgagtccc ataatatatc ggaacgctcg aaattgaatg 360

tagaagcttt gaaccaattc aaacgaccag aacttttttac t 401

<210> 858
<211> 455
<212> DNA
<213> Glycine max

<400> 858

agcttgtaat cgattacaca catactgtaa tctattacca gaggagattt tcagaaaata 60

ttctcaacag tcacatcttt tcatttggtt cttgaatggg catcaaaggc ctatatatat 120

gtgacttgag acacaaattt gctaagagtt tatctgaaca acaagtgttt attctctcaa 180

aaagcaaaat cgttatatcc tcttaaaaat tccactggcc aatgcaattg caattcatta 240

aggaatcatt tgagtgctca aattgtaaaa tctatctctt caagagagat tcattcttct 300

tctctttcta attcactaac ggattaagag accgcgggtc tcttgttgta aaagaattct 360

aaacacaaag gaaggaattt ccttgtgtgt ttagaacttg gaaaaggaat ttacaagata 420

tggtaactct caagcgggtt gctatgggac tggac 455

<210> 859
<211> 620
<212> DNA
<213> Glycine max

<400> 859

agcttgtagg taaactagat gccttggtta acctggtaac ccaactggcc atgaataaaa 60

aattttcacc tgtcgccaga ctctatggtt tatgctcctc tattgaccac cacacagacc 120

tttgcccttc tgtgcaacaa tctgaagcaa ttgaacaacc tgaagcttat gctgcaaaca 180

tctacaatag acctcctcaa cctcagcagc aaaatcagcc acaacaaaac aattatgacc 240

tctccagcaa caggtacaat cccgggtgga ggaatcatcc caaccttaga tggtcgaatc 300

cttcacaaca acagcaacaa caacaatagc cttattttca aaatgctgct ggcccaagca 360

gacatacgtt cctccaccaa tccagcagca acaacaacaa caacaacccc agaaacaaca 420

aacagttgag gctcctccgc aaccttccct tgaagaactt gtgagacaaa tgactatgca 480

aaacatgcag tttcaacaag aaaccagagc ctttattcag agcttaacta attaatggga 540

caattggcta catagttaaa tcaacaacag tcctaaaatt ctgacagatt accttcttaa 600

tctgtccaga aatcccaaaa 620

<210> 860
<211> 532
<212> DNA
<213> Glycine max

<400> 860

agcttctggt gggacatctt gacttgcttt ccaatctgac attcaccaca gattctgcct 60

tcttctattt tcagattggg aatgcctcta acagcacttt tgtcaaggat tttcttcatg 120

cctcttaagt gcagatgtcc aaacctttga tgccatattc tgacttcatc ttctttggag 180

gatagacatg tagaggagta gctggtttct tggggtgtcc ataggtaaca attgtccttt 240

gatctgctgc ccttcattag aacttcactc ttctcatttg tcaccaagca ttctgacttt 300

gtgaagttta cattgaatcc ttcatcacac agctgactga tgctaatcaa gtttgcagtc 360

agtcccttca ccagcagtac tttgttcaga ctaggaagtc catcatgaac tagctttccc 420

attccaatga tctttccttt agagccatct ccaaatgtca cataactagt ggagcagggc 480

tcaatgttca gcaagaattc tttgactcct gtcatgtggc tggaacaacc gc 532

<210> 861
<211> 591
<212> DNA
<213> Glycine max

<400> 861

tgactcattt atttaaacaa acctaattat aagcttgagt ttggcttttt tgaaaaaact 60

aaagcatgag cttgagcttg aatggtttag ctcatttaaa atttgattat tttttaactt 120

gcaaaaaaat tattaaatca ttttttaact gtcaatttat tatttaataa aatattttaa 180

tactatgtaa taatctacaa ataaaatatg tgttaaacat atgatatgat attgtagaat 240

ctatgtaatt ttaattttta tattctattt ataaacgagc tatttatgag ttattaatgt 300

caagcttgta aaacttaggc ttagcttgag tttgtttatt tcattaaaca aacgagtttg 360

atggagcatt tagcaagttg aactcgagaa gttcacgaat aacttgactc atttacatct 420

ctatctagaa atacttttga atttttaatt aagtgtcgca ttatatatag attgttaaca 480

tagtggtaat aaatgacatt tgtttatagt gataactatt atttatggtg atgaaaattg 540

aatgaaaaat aattttcatt tatagaaata agaaatatta tattttatat t 591

<210> 862
<211> 501
<212> DNA
<213> Glycine max

<400> 862

agcttctgac gagtgattat cgatcctctc atcaccttca ataatatctt tgactatata 60

tataattgat atttttttcac aataaaccac taaaaataat ataacttata gcacataatc 120

aaaacactac gatttgaaac atttttttcag caatttattt tatcccgtga ttttaaactg 180

ctaccaattt taaatatttt tgttcacctg ttactatagt ctttatttaa agaaccttgc 240

tatttggtac gaaatataca cgctagaaag tagctaagac atacctgaac caatcacggt 300

tgtatggggt cacttaaaat ctgatgatta atatttttttt cttcaaaaat acaatttgta 360

actagtatgt aatttttttcg tacaatattc atctttttcg ttattataaa tactcaagga 420

caaatatggt acatcataaa tgaagcccac ctctgtcagt ataataaaaa attctaacac 480

aagtgaataa gatcgaggac a 501

<210> 863
<211> 617
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 863

tcacagcaaa tgatagaatg tctatagttt tatcatttga caatttattg ttattatatg 60

tcttatcctt catatatata gactcttttt tttcatcttt ttcaactgtg aatttttaca 120

taattcataa attttatttg ataccttgca tagcattgca tttagcaaat acaatttaac 180

atgcttggtt tataagtatt gacacaaaaa aggcttatga aaataccttg tattgcatgt 240

tgctagggct tattaaaaat atcaaataat tttacatgtg tctgtgaaat cagacttatt 300

aatgatgcga taaattatgt aactatcatg tctctcgttg atgttgctaa aaaaattgtt 360

tatgaagtat agggattaaa agtgcatttt gcaaaaagtt taaagatcga gaacataatt 420

aacccattaa attattatca ataaaataac cttaaatnta aaatacaaac ataggtacat 480

gtaatntata ttatcaatta ttgataaaaa aaaatataat aatgtttatg tgaacaaaat 540

atttttttga ccaaaaaata aacgcatgtt ttttatattc aaaatcattt tacagttaaa 600

tatttaatgg ttataaa 617

<210> 864
<211> 377

<212> DNA
<213> Glycine max

<400> 864

ttgacagaaa tccgacatcg taacattgta aagttacatg ggttttgttc acattcacaa 60

tactcatttt tggtgtgtga gtttctggag aatggcgacg tcaaaaaaat ttttaaagat 120

gatgaacaaa caattgcgtt tgattggaat aaaagggtgg atgttgttaa aggtgtagca 180

aatgctttat gctatatgca tcatgattgc tcacctccaa tcgttcatcg tgatatatca 240

agcaagaatg ttcttttgga ttccgattat gtagctcatg tcttagactt cggaacagcc 300

aaatttttta atccagattc atccaattgg acctcctttg cagaaccttt gatatgctgc 360

tcccggttaa tttcctt 377

<210> 865
<211> 612
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 865

tcatgggaga gtcaaagatc aaattgagag gaaaaataat ttctatgcta aacaagccaa 60

caaaggaaga aagaaggttg tcttcgaacc cggagattgg gtttgggtgc acatgagaaa 120

agaaaggttt ccggaacaga ggaaatcaaa gcttcaacaa tggggagatg gaccatttca 180

agtgcttgaa agaatcaatg acaatgctta caaagttgag ctgcccggtg agtataatgt 240

tagttccacc ttcaatgtct ttgatttacc tctttttgat gcagatgtag aatccgattt 300

gaggacaaat ccttctcaag agggagagaa tgatgaggac atgaccaaga gcaagggcaa 360

ggatccactt gaaggacttg gaggacctat gacaagggct agagcaagga aagccaagga 420

agctcttcaa caagtgctgt ccatactatt tgaatacaag cccaagtttc aaggagaaaa 480

gtccaaggtt gtgagttgta tcatggccca natggangan gactaaatga caccactttg 540

tctcaatttt tagagtgttt agtttgtcta ataatggcc caatccttgt aaagttgctg 600

accaaaaata tg 612

<210> 866
<211> 555
<212> DNA

<213> Glycine max

<400> 866

agcttatgac cattcgaatt tctcgagagt ttccgttgtt caatttcgag cgtgtagatg 60

agttatgtcc ccgaatcgga catctgtgtg aaaagttatg accattcgat tttctcgaga 120

gcttccgttg ttcaatttcg agcgtctcga tatattatga ccccgaatcg gacatctgtg 180

tgaaaacgta tgaccattcg attttctcga gagcttccgt tgatcaattt cgagcgtcta 240

gatgagttat gtccccgaat cgaacattcg agtgaaaact tatgaccatt cgaatttctc 300

gagagcttcc gttgttcaat ttcgagcgtc tcgatatatt atgttcccga atcgggcatc 360

cgagtgaaaa gttatgacca ttcgaatttc tcgagagctt ccgctgttca atttcgagcg 420

tctcgatata ttatggcccc gaatcggaca tccgtgtgaa aacttatgac cattcgaatt 480

tctcgagagc ttccgttgtt caatttcgag cgtgtagatg agttatgtcc tccaatggac 540

attgggtgaa aagtt 555

<210> 867
<211> 554
<212> DNA
<213> Glycine max

<400> 867

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ggatcaactt gaaacttatg tgcttcaagt gagaagaaat gcttcttttt ccacttgtga 120

agatgttcaa agtttggcta tgaagatggt tcaaactgag aaacatttgg tatttccatt 180

ggtttataaa cttattgagc tagctttgat attgccggtg tcgacagcat ccgttgaaag 240

agctttttca gcaatgaaga ttatcaagtc taaattgcgc aataagatca acgatgtgtg 300

gttcaatgac ttgatggtat gttacaccga gcgggagata ttcaagtcac ttgatgatat 360

tgatattatt cgaacattta ccgcaaagaa gtctcggaaa ggacacttgc ctcgtaattt 420

tatttaaccc gctattgtaa gaatatgctt atctctttta ttttaaacta tatttttggt 480

gacaaaatga cgagtctctt ttattttgat tgattactat ttacatatta tatacaaggt 540

gaatttgcta tctt 554

<210> 868

<211> 615
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 868

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acctcattaa ctatcattac acccgggagg atatgtctgc ctttgaaaaa aacaatttgt 120

ctttaatcaa ttaaatgaag cagcacaaga gccagcctat tagccagact ttggacatta 180

ttttgtagac acaccctatg agagagatgg gtctatagtc attaagagat tgggggctat 240

tggttttggg gatgagggct atgaaggatg cattacttcc tttggggaat ctgccattaa 300

tgaataattc atcaaagaat ctgataaaat taggttttag agtttcccaa aactgtttga 360

tgaaattgaa attcaaacca tccgagccaa gacttttatc tcccccgcaa gcccaaactg 420

cagacttgat ttccagctcg gtgaatctat caacaaggct ttccttctgc ctttgatcaa 480

gggaagagaa ctagatccct tcaaggttgg tctgcaagga ttctactttg agaatctttc 540

tttanagtgc tgaagaactg caatcttgac actgttaggg tcantggatc catcctccat 600

caatacacag acctt 615

<210> 869
<211> 558
<212> DNA
<213> Glycine max

<400> 869

ttcatcctaa gcctaaactg tattatttga tttgatcata ggaaaagggg gaaaaagata 60

caagatataa acatgaatac aaataagaaa ttgtaaacta cattacttga attcctatta 120

tatacaacca gcataccgag ttgaatttgg ataatttcct cccaccacca acttcaacct 180

caaggggaga attacaagaa caaatggttt agtgtcaaaa aagatagcac acagacaaat 240

taaaaaagat agcctgaaca gctactggag ttctatgaat atgtcttggc acttaagatg 300

acctgccata cttgttaact gaattcatat gattcatcta catctgcaag ttgtttggtc 360

ttgaaaattg attatgcatg gctgagttaa caacaaggtt attatcacaa ccaacaaatt 420

gctgactaaa tgccggagaa acagtatcag gcagaatagg tagctcagag ttaccaattg 480

tttgggtatc agacctatta cggataaaac aaactcttgg ctaaaagtat ctatttgagt 540

gttaacattt tgattaac 558

<210> 870
<211> 636
<212> DNA
<213> Glycine max

<400> 870

tgttccggcg ccaccagcga ccgctcgcaa cgacgacact tgttgggtac catgctgaat 60

tttactaatt tacgggatca aaccacgcgg tgatgatatg gtttgccttt aagaaagtca 120

aaaagtatat taccagtttg ttggaaatcc ccattgggcc ttctgttgtt aaaacgtgac 180

tccaagttct ttcaaagata aatgataaag tgatattctc atggaacatg agaaattatt 240

gactattatt ttgaatgata aaaattattt ccgtaaaata ttaaaattta atcaaacata 300

ttaaaagata aatagaatgt gatgggatta aaacaagaaa aaggttttac agcctaaaaa 360

aagttacata gtatgtgttt agtcctttca aaatgagtga aatttaactt tggtttctct 420

aaatttcttt ttgaatttta ttcttaagaa atataatttg gcctattctt atgaatttaa 480

tggttataca ttattcatgt aaaacctaac tctatatcat tattgaatca ttagtcatca 540

tttaaattac tttaggacaa ttattttgaa aataataaat ttatcatact taatttaaaa 600

ttattttaaa agtaaccaaa tttatcattg tgaatt 636

<210> 871
<211> 463
<212> DNA
<213> Glycine max

<400> 871

agcttatcct gccattttat tcattcacgc tattctgcat cattcttcct ttgaccatgt 60

tccttcctga agccgagctc ccagcctggg ttgtttgtta cattcctgga atcatgtccc 120

tcctaagtgt tctcccagct ccacggtcat ttccatttat agttccttac cttctatttg 180

agaacactat gtcggtaact aaatttaatg ccatgatatc tggattatta cgctttggaa 240

gttcttacga gtgggtggtt acaaaaaagt tgggaaggtc atcagagaca gatttggttg 300

cctttgagaa agaagctgaa cctctaatgc gatctactag tcttcataga tcatcctcag 360

attcaggcat tgaggaacta agcaaactag aattgtcaaa gaaaactggg aagaccaata 420

aaaatcgtct tttcaagaaa gaactttatc tcgcattaat ttt 463

<210> 872
<211> 501
<212> DNA
<213> Glycine max

<400> 872

acactatcta gatctcaagc ttacaacata aactaccctc attctttgat tcatttaata 60

taggggaact tattccaagg attaccaaat gaggacccct atgaacattt ggcaacattc 120

attgaaatct gtaacactgt aaagattgca ggtgtgccat atgaagccat tatactcaat 180

ctatattcaa tttccttagt aggagaagcc aaaaggtggc tacactcatt taagggtgac 240

aatctgaaaa cctgtgaaga agttgttgaa aagtttctga agaaatattt cctatagtca 300

aagactgtga aagggaaagc tacaatctct tcatttcatc agttgcctga cgagtccttg 360

agttaagcgt tggaaaggtt tacaggtcta ttgagaaaga ctcccaccca tgggttcttt 420

gagccaatta agttgaatat gtttatggac tggctgagac cacagaccaa gcaactacta 480

tatgcttcat aaggggggaaa a 501

<210> 873
<211> 630
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 873

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atgcagggaa gaatttctcc aagaacaccc tcttaaggtc atcctagctg gtaatggacc 120

tgggagcaag gtagtacaac caatcttttg tcactccctc cagagaatga ggaaaagcct 180

ttagaaagat atgatcttcc tggacatcag ggggcttcat ggtggaacag acaatatgga 240

actctttaag attcttatga ggatcttcac ttgcaagacc atgaaacttg ggcagcaaat 300

gtattagtcc agtcttgaga acatatggaa catcgtcatc aggatattga atgcacaagc 360

tttcataagt gaagtcagct gcaaccatct ccctaagagt cctctcacga ggtggagatt 420

gagccatgtt cttagtatga aaattagcag ccgaatgctc aaaatcagaa tgttcagacc 480

aacaacagaa tgctcaaaat gcacagaatg attaggatgc acagaatgat aaggatgccc 540

agaatgatca ngatgcacac tatgccttac taatatatga aaggttctat cttattcagg 600

gatcaagggg tgtaaatcac ctggattggc 630

<210> 874
<211> 634
<212> DNA
<213> Glycine max

<400> 874

tgaaggtaaa ctagatgcct tggttaacct ggtaacccaa ctggccatga ataaaaaatc 60

tgcacttgtt gccagactct gtggtttatg ctcctatgct gaccaccaca cagacctttg 120

cccttctatg caacaatcta aagtaattga acagcctgaa gcttatgctg caaacatcta 180

caatagacct cctcaacctc agtagcaaaa tcagccacaa cagaacaatt atgacctctc 240

cagcaacaag tgcaatcctg ggtggaggaa tcatcccaac cttagatggt cgagtccttc 300

acaacaacat caacaataag attagcctta ttttcaaaat gctgctggcc caagcagacc 360

atacgttcct ccaccaatcc ggcagcaaca acaacaacag ccccagaaac aacaaacaat 420

tgaggctcct ccgcaacctt cccttgaaga acttgtgagg caaatgacta tgcaaaacat 480

ccagtttcaa caagagacca gagcctccat tcagagctta actaatcaga tgggacaatt 540

ggctacacag ttaaatcaac aacaatccca gaattctgac agattacctt cttaatctgt 600

ccagactccc aaaaatgtga gtgccattac attg 634

<210> 875
<211> 458
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 875

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agggtaggac cacttaactt ttcactaaaa taagcaattg gatggtcttc ttgcatcaac 180

acagccccaa tcccaacatt tgaagcatca cactcgattt caaaagattt ttgaaagttt 240

ggcaacgcaa gtatggnggc attaattagc tnttgcttaa taacattgaa agcttcttct 300

tgtttctctc cccatttgaa accaacattt ttcttgagca cttcattgag aggtgctgcc 360

aatgtgctaa aatccttcac aaatcgtcta taanaactnt ctaagccatg agaactcctc 420

acctcggtca cggacttatg tgtaggctat tcttgaat 458

<210> 876
<211> 454
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 876

agcttcttat ccaaggctca tcttggtggt gaagctcctt ctttcatggc ttattcccta 60

gtggatggcg ccgcctctta cctcttctcc tttgtcttcc gctgcatctc catggtggaa 120

aatcaccatt aaaggacctc attgaagctc aaagatccag cttccataga agctccacaa 180

gcaagtttcc atcaggaatg atgcaatcct accccgcaag ggcattggat agaagactcc 240

aagtagattg ggctagagat gcaagagaag gccctagggt tctcatgagc cttaggatag 300

atttcgggcc catgggctaa gtatgagccc acttatcttt gtacatatta gattaaggtt 360

tcattaattn tgggtctttt atttaaggct ccataatgta ggaagggtac cctagaaata 420

taggaatttt cagcccttgt attttagggc acct 454

<210> 877
<211> 396
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 877

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tacttgtgaa agagagccat gtgggtgggt tcatgggcca ctttggaata gacaagaccc 120

ttgtcttact caaagaaaag ttttattggc cccatatgaa gaaagatgtc cataagcatt 180

gcactacgtg tgtggcttgt ttacaagcca agtctagggt gatatctcat gggctataca 240

caccettacc catcccatct gcaccttgng tagacattaa tatggacttt gtncttgggc 300

tttctagaac ccaaagaggt gtagactcta tctttgtggt ggtggatagg tgtagcaaga 360

tggcacactn tataccatgc tacaacgtgg atgatg 396

<210> 878
<211> 428
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 878

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atccgattta ggctcatcac atatagagac gctcaaaatt gaacaacgga agctctcgag 120

aaattcaaat ggtcataact tttaactcgg aggtccgatt caggcgcata atatatcgag 180

acgctcgaaa ttgaacaacg gaagctctcg agaaattcaa atggacataa cttttaactc 240

ggatgtccga ttcaggcgca tcatatatag agacgctcga aattgaacaa cggaagctct 300

cgagaaattc aaatggacat aacttttaac tcggaggtcc gattcaggcg cataatatat 360

cgagacgctc gaaattgaac aacggaagct ctcgagaaat tcaaatggac ataacttnta 420

actcggat 428

<210> 879
<211> 397
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 879

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atgcatcaaa atgctcgaaa ttgaaaacag aagctcggtg caaattcaaa cgacaattag 120

tttttactcg gatgtccgat tgagtccctt catatatcga gacgctcgaa attgaaaacg 180

gaagcttgta ctatattcaa acgacaatca tnttttactc ggatgtccga tggagtcccg 240

taatatatcg agacgctcga aattgcaaac agaagctctg agcaaattca aacgacaata 300

actttttttt cgaatgtccg atggagtccc gtaatatatc gagacgctcg taatggaaaa 360

cagaggctct gacataattc tacaacaata catttta 397

<210> 880
<211> 434
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 880

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aagtttccaa aatcttgttc tcaaactcgt gactcttccc tcacgtcgat gatcatcttc 120

ttcaagaaac gccgtctgaa cttgcgagcg tctatcgggt gcgggcgtag ggggacacat 180

aaaattgcac ctgccagtca tgggagcagt tgtcgctatc catcacgtga cggaggtgct 240

tgccggcgcg gaggatctcg atcattcctt ggatcgctga cggaatgctg tggtcgggtg 300

aggtgatgta tgtcgccgta tcccgattcc cctacgactt cccatgccgt atcagtattc 360

ttaattttag aagcacacca accatatatt ctcttctctt tgcattccat tttctttcat 420

gctgacaaat ttaa 434

<210> 881
<211> 415
<212> DNA
<213> Glycine max

<400> 881

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atgtcttgaa ctaagaagat gttgtccatc atctttctgt tcttgatgaa ggcagtttga 120

gtttccccaa caatagtctc acgcactgtg gctatgcggt tggccaaaat tctagacaca 180

atcttgtatt acaaattaca gcaagatatg ggtctaaaat ggttaacctg agaggtctga 240

tcatgcttag gaataagcgc aataataaca tggttgagtt gctttaaaaa tttgtcagtg 300

gtaaagaatt catttaccgg ctcatagata tcatcaccaa tgatattcca agccttcttc 360

gaaaataaat cattgagacc atctggccct acagctttat tgttatccat cacag 415

<210> 882
<211> 462
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 882

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tttgctttta tcgattaaca tggaccgttc aaaagcataa aatcaatatg taactttact 120

gcttttgcaa gaactacgta ggtctgattt cctcatcgca attgaggata tgtaggagca 180

aaagccccgc ttttgtcgac caccccaaga gatcgttaat ggttcaacgc cttaacattt 240

ctctcctttc aaaaacaaga gatcgttaat ggtccaacgc cttaacgttt ctctcctttc 300

aaaagaatca aagatcgttt aatggtccaa tgccttaaac gacttttgtg cggttaaaat 360

cgatcttgcg aaaaaagatc aaaacaactt aactggaaat actgatcata cattagtatg 420

attaaacatt gtanacacaa tcaaacaatt ttcaacaatt at 462

<210> 883
<211> 353
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 883

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accaagatat caagttggga ccaacataca ctgctgcacc agagttagag tgcctatcaa 120

tagggtctga agcccagtaa gaatcacaaa aaccttacat gggaagagtt ttatgaggtg 180

aggcaagata caaaataagt cctgaatgta aagcaccctt aagatacctt aaaattcttt 240

ctactgttgt ccagtgggat tcaagaggtg cagacatgaa ctggcaactt tatttcaaca 300

naactaactc tagatgagtg atagtacata ctgacagctc cacaacagat ctg 353

<210> 884
<211> 370
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 884

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cctcttttgt attaggaatc aagatactaa gagatcactc tcaagcatnc taaggttgtc 120

acaagagagt atatcgataa ggcctagata gattcggcat gaaagatagt aaaccagtag 180

atacccagat agctaaagga aacaaattta gtctcaaaca acaccccaat aatgaccttg 240

aaagaataga gatgcaaaat atttcttatg cattagcatt agaaagtcta atgtacgctt 300

aagtttgcac tcgtctcgat atagcatttg tagtaggagt tctgggtaga tattttgagt 360

atcctggaat 370

<210> 885
<211> 495
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 885

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cattcttgga tggccttgat tntctcaggg tccacttgga ccccatttct accaactaca 120

aaccctaaga aaactatatt ttctacacaa aaagtacact tctctatatt tgcatagagg 180

gtgtttttcc taaggactga aagaacttgt ctgagatttc ataagtgatc atctaggctt 240

ctactgtaca ctaaaatatc atcaaaataa acaactacaa atctacctat gaaatccctt 300

aagacatgat gcataagcct cataaaggtg cttggtgcat tagtgagccc aaaaggcatc 360

actagccatt catacaaacc aaacttggta ttgaaagcgg ttntccactc atcacccttt 420

ntcatcctga tttggtgata cctaacttta agatcaatnt ttgaaaagat attggcacca 480

tgcaactcat caagc 495

<210> 886
<211> 356
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 886

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cagtgccccg atcctcctag tgtcggcatt tgtggaggag acgtgatgca attctacctc 120

gcaagggcat tggatagaaa actcctagta cattgggcca gagatgcacg agaaggccct 180

agggttctta tgagccttac ggtagatttc gggcccatgg gctaagtacg agcccactta 240

tctttgaaat attagattaa ggtttcatta tttttgggcc ttggatttag ggctccataa 300

cgtacatagg gtaccctaan atataggatt tttcagccct tagattgtag gacatc 356

<210> 887
<211> 392

<212> DNA
<213> Glycine max

<400> 887

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gctccattgg agcttgtagg cctaggatct tcttcatcaa tggattcctt tgcttcttgg 120

aagatgaatg gcagtggaat gaagaaggaa gagagagagg agacgccact tcaaggagaa 180

gatgagtcta gaagaagctc accaccatat gaggccatgg ataaaagctt ggaggaagaa 240

agagatgaat gaagggagag ggagagaaga gcacgaaatt ttgtgctcca aatgagctct 300

gaaatctgaa gtttaatatt caaatgatca aagttgaaaa aaatgcacac acatgacctc 360

tatttatagc ctaagtgtca cacaaaattg ga 392

<210> 888
<211> 472
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 888

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tatgcaggtt gaaagccttg gaggaaagag gtatgcctat gttgttgtgg atgatttctc 120

cagatttacc tgggtcaact ttatcagaga gaaatcagaa acctttgaag cattcaaaga 180

attgagtcta agacttcaaa gagaaaagga ctgtgtcatc aagagaatca ggagtgacca 240

tggcagagaa tttgaaaaca gcaggttcac tgaattctgc acatctgaag gcatcaccca 300

tgagttctct gcagccatta caccacaaca gaatggcata gttgaaagga aaaacaggac 360

tntgcaagag gctgctaggg tcatgcttca tgccaaagaa cttccctata atctctgggc 420

tgaagccatg aacacagcat gctacatcca caacagagtc acacttagaa ga 472

<210> 889
<211> 411
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 889

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ctcctttcta gttnttttat ttttttttt atttttttat gcagctgaat agtgtgcttc 120

atgttatgtt tttgcagagt tgctgtggat aacatttcaa gcggaacaga cactgtcata 180

aaggttccaa attcaccttt cgttggcttt gtcttttctg cattgccaaa gggtcctttt 240

tctctttgtg tgaccaattt tccgtgtgtg ttgttgcagg ttgatagcgc gaacaagcgt 300

gggagcttgt tggaggtggt tcangttctc actgatatga atctcagtgt tagaagagct 360

tatatttcct ctgatggaga atggttcatg gatggtacgg atcccttcac g 411

<210> 890
<211> 471
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 890

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ttaattcaat cttgaacatc ttgaacatct tgattcaatc ttgaacatct tgaacatatt 120

gaactcattc tttgattatc atgaattgac ctttgagctt tttgtcatca cctttgttat 180

catcaaaaca tctttgaatc aatcttgatt catcatgaag ctttgcttct acacatactt 240

agtaggatca aaagttattg tttatactga ccatgaaccc attaagtacc tgttgaataa 300

agctgattcc aagcccagat taatcagatg aatcttgttg ctttaagaat ttgatctggt 360

tatccaagac aagaaaggat ctgaaaatct tgtagctgat cacttatcaa ggttagtcaa 420

tgaggaggtg actttgaaag agctatagat aanggatgaa tntcctgatg a 471

<210> 891
<211> 452
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 891

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caacagtcac atcttttatg tggttcttga atggctatca aaggcctata tatatgtgac 120

ttaagacacg aatttgctaa gagtttttca gaacaaaaag gtcttatcct cttaaaaagc 180

aaatcgtttt atcctcttac aaattccttg gccaaattac ttgtgattca ataaggaatt 240

atttgagtac tcaaattgtt caatctatct ctttcaagag agatttcttc ttctcttctt 300

cttcattctg aaaagggatt aagagaccga gggtctcttg ttgtgaaaga attctaaaca 360

caaaggaagg gttgtccttg tgtgtttaga acttgtaaaa ggaatttaca agatagtgga 420

actctcaagc gggttgcttg gggactggac gt 452

<210> 892
<211> 456
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 892

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caattcatca gtgggctttc cttctgtgtc cagcatcttg ngatgttccc agcctatgat 120

gacagctttc caggttctgc tatccactga tttgaggaag gccaccattc ttgctttcca 180

gtattcatag ttgcttccat caagaattgg tggtctgttc actggtcctc cttctttctc 240

catgttcatc agaatttatc tccccagatc tcactctgtg atttcgagtg tttgctctga 300

taccaattga aattctgata ccacgggaca gatgtcgtac aggatgtcac gacatcacgc 360

ttcataacat gcagattgta tgtgtccgta tgaacagact acacaagtna ataacacaag 420

agaattgtaa cccagtcggt gcacctcacc tacatt 456

<210> 893
<211> 348
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 893

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ttntgaaacg gaccctctct cgtaaattgg ttctaaaagg aaccccatac agtaaatttg 120

ccaagaaatt aatgctgtac ccataaaata atttttaaa atgaatacta atgttatacg 180

agataataaa aactgatatt aattctatga ttttatttt taatattata gtatcgacca 240

tgaataaatt atataatatt tttgaaaata tatatacgcg taaagaataa ttataatttg 300

ctacaatata agcattctga atccttttat catgagatta tatatttt 348

<210> 894
<211> 467
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 894

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actatgtaag agccttgtcc attgggtcac ctctttttta ttttgtaaca tttatattaa 120

taaagcaaag tatgatacat agtaggaaca caataatata caaaagttaa ataatatatt 180

ttatcgctca atatataatt cgctgataaa tgaatccttg aacgatgaat atataaaatt 240

tagtccctaa aagtataaat agtgtgaaaa gtaagtaatc gacaacgtga ccatgctgat 300

tagatttgat gaaaatgtca acaagataca acgtaaatgt taatcattnt ttggtggaca 360

aaaaatgtca atatttctta ttgaagataa tatcagtaat ttgttattta cctaaatgtc 420

aatacatttc attggatcaa aatatcaata cgttatcatt attggac 467

<210> 895
<211> 452
<212> DNA
<213> Glycine max

<400> 895

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tgagggcatg tgtcttagaa caaaagagga gttgggagag ttaaagacta ctcaaagtag 120

gcagaaaaac tatcaggctg ctcaagaaaa actgagaagg tcaagttaat ccaagaaagg 180

ctaaagactg ctcaaagtac gcagaagagc tatcatgaca agaggaggaa agacctgaaa 240

tttgagattg gtgatcatgt attcttgaga gtcattccat tgattgcgtt ggtcaagcat 300

tgaaatccca aaaactcata cctcgtttta tcaacccttg ttaaattctc aacagagtca 360

gtcctacggc ataccatatt gcattacctc tgtctctgta caatcttgac aatatctttc 420

atgtgtctca actcagtaat tatatctgtg at 452

<210> 896
<211> 446
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 896

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ttaattcaat cttgaacatc ttgaacatcc tgattcaatc ttgaacatct tgaacatatt 120

gaactcattc tttgattatc atgaattgac ctttgagctt tntgtcatca cctttgttat 180

catcaaaaca tctttgaatc aatcttgatt catcatgaag ctttgcttct acacatactt 240

agtaggatca aaagttattg tttatactga ccatgaaccc attaagtacc tgttgaataa 300

agctgattcc aagcccagat taatcagatg aattttgtcg ctttaagaat ttgatctggg 360

tatccaagac aagaaaggat ctgaaaatct tgtagctgat cacttatcaa ggttagtcaa 420

tgaggaggtg actttganag agctag 446

<210> 897
<211> 459
<212> DNA
<213> Glycine max

<400> 897

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gtcgctgtgt gagcattctg gacatacacg cacactttct gattcatgct cttatgcaca 120

cacacacaga gagattcgtt ctctcgtcag aaacactacg catacgaaca ggcagacgct 180

cacgctgaga acctgtaaca cagacacttg tcagactcac gcacttacac agacaccaca 240

gactgactat gacctattca gagacaagcg cactcccaga tacacgcact ctgatagact 300

tagatggcag aacttttcac agaagcacac acacccacag attcactgtc acacagttgc 360

tgacacacag agaccatgcg ctcatccaca cttgtagaca cacacataca cacacgcaca 420

ctcacactga gaactagccc cagacacaca cacacgctg 459

<210> 898
<211> 451
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 898

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ctagtggagt tggcattggg gctgttttga tacaaaacaa aaggcctata gcttatttct 120

cggagaaatt gggaggagcc agattgaact attgcaccta tgacaaagag ttctatgcca 180

ttgtgagagc tcttgatcat tggaatcatt atttgcgttc taatcacttt atattgcatt 240

cagatcatga gtcattgaag tatatcaatg ggcagcagaa gttgagtcca aggcatgcta 300

aatgggttga atttcttcaa tcttttaatt tctcttcaaa atacaaggat ggtaagagta 360

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tacttggttc tgagactctg aaagattata t 451

<210> 899
<211> 376
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 899

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tatatattca gacgctcgaa attgaatgtt gaagctctga gcaaattcaa acgacaataa 120

ccttcttact cagatgtcgg atagagaccc gtaatatatt gagacgctcg aaatggaata 180

ccgaagctct gagcaaagtc aaacgacaat aacttttac tcggatgttc gattgagccc 240

cgtaatatat cgaaacgctc gaaattgaat gctgaagctc tgagcaaact caaacgacaa 300

taaatcttta ctcggatggc cgattgagtc tcgtaatata tcgagaagct cgaaatggaa 360

taccaaagct ctgagc 376

<210> 900
<211> 453
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 900

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ccctgggatg ataagagcaa agaaataata aatttggaaa tctcttttgt tagctcacta 120

aaaggtgata cttaaaagca aacacttttc aagtttcaaa actgtatata aagaatgtat 180

acttacagta ttctttgtca atacattaag tgaatcctca tgaaaccaca atcgactgcg 240

cttcccaggt ttctttgttg aactttcacg aattatctct cttcccatgt ctcgtagtaa 300

tggatgcatt ccaagttcgt tgttctttgc aacttttacg aggctacgct ccatgagaac 360

tgttattcct atatcagcat gtagtccaca gccatntagt atctctgtaa cataagctct 420

atctttacca ataaagagac aacatacatc aag 453

<210> 901
<211> 396
<212> DNA
<213> Glycine max

<400> 901

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aggcttcatc tttccccacc ttgataagag aatcaaactc attctcaaag aatgatttaa 120

aatcaggttc tcggcaactt ggcctaaaac cacataatcg atacaaaaca gcatcctgta 180

tgccaaatgc tcaatatcaa tggacaggct tacctttagg cttaaaagta gcttcttctc 240

tcttgcagaa agccatgacc aaaatctttg aacccattct ggaaaacact cttgtctaca 300

tagatgacat tctcctttgt tcaaaagata ttgcctctca ctaaaaattg ttgaaccaat 360

tctttgaaat agcacaccaa catgggatca tgcttt 396

<210> 902
<211> 364
<212> DNA
<213> Glycine max

<400> 902

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gggccatggt tgggtccact cttctttgta aatattagaa tatgtttttc cttcttttgg 180

gccttgtatt taggccattc tagtagtata ggattttagc cttgtctttc atggcaattt 240

gagtagactt tgtagtaggg acttttattt ttcatgtatt ttggcatggg ggcgagctta 300

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tctt 364

<210> 903
<211> 461
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 903

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gaagaataca cattcgttta tttattattt attattttaa aatgataaca aaattgaata 120

aaagtgagtt tattctttat tcgttgcaag tgtaattttt ttatattgtc aagtaactag 180

aaatcatgtt agatattatt tttaagatca ttttataaaa ttcaagaaac ttatttaatc 240

tataattgaa taattctgta aatttaaatt aaactttaaa agtaattata aacattcaat 300

agataattta acttcaaacc ataattatga atgcctcctt ttcataacta taagatgttt 360

tagctntatt tcttatctta naataattga tattntagaa attcanaatt taattaatat 420

tttttccaat tatatcctta tttattatct cattattaat g 461

<210> 904
<211> 372
<212> DNA
<213> Glycine max

<400> 904

aagtccaacg cagcacgcgt gtcgttaaag ttgttatatg ttatgctttg aaggagatga 60

acgtggagtg tagttaccac tgtactctac tctagcagtg gttgtggtgt tatcaaaggc 120

aacaccaaca ccacttgaat atgctcttgc agcaagacac ccatgattag gttcttggtt 180

ggcatgcaat aacacataca ttggtcgtcc cggtgatatg caaatgtatt cccttgccaa 240

tggcttggtt aacataccat cagcaccaac aacagcgagg ttgtgttctg tatcatagaa 300

caagagaatg agattcattg ccgcattgtc tacacggaga taataagtcc tgccttgctc 360

tacatgaaac tc 372

<210> 905
<211> 469
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 905

ggatggagaa tatgggtcca tacttgtcag ccaagtcacc caatgttnta tgaggtgtct 60

ttgaaccaag caacaatggg aggtgaccaa ttattggcca cgcacctgca actgtgggag 120

gaccctcttc gccactcttc gaggaacgac gacacaaaaa caagtataag aggatcagag 180

aaacaacacc aactccaatt gttgtggtgt ttagaactaa gtccattntg acttgttttt 240

gtgttgttgc atgcagatcc tcatcagttt aaataggaac tgcaccgtgc atctgtgtgc 300

cgttgtacga cctgactaga tcgagtagag atatttagat attntaatat tntagaatat 360

attcattact tgaattaact aanaaataaa ataatgttgc tgaaatgatg aaataatata 420

gccaaataaa atcttgatat tntaagatat nntttaattt tatattaca 469

<210> 906
<211> 465
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 906

taacgtctnt cacagtanaa ggaccactcc atctctcaat tntaattntc caggaaacaa 60

ctttagttnt aagttgtaga gcaatacttg ttgtctggga ctaaattctt tgtggaggat 120

ctttttgtca tggtccctct tataatccct gaacacttta aacttggagc caaacaggta 180

atgcctccac atcttaaggg caaaaactac agtagccaac tccagatcaa gggtgggata 240

attcctctca tgagtcttga gttgtctaga agaataggcc actccttggc cattttgcat 300

caacactcct cctaaacgca tctttgatgc atcacaatac acctcaaggn gttctcttgg 360

gttaggcaaa actagcatgg gagcggccgt caacttttcc ttaagggttt ggaaactatg 420

ctcacattag gtatcccaca caaaagcttg acccttacga gttag 465

<210> 907
<211> 456
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 907

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gagtataatg tttgttctac cttcaatgtc tctgacttat ctctttttga tgtagatgaa 120

gaatccgatt tgaggaaaaa tccttctcaa gagggagaga atgatgagga catgactagg 180

agcatgggca aggatccact tgaaggactt ggaggaccta tgacaagggc tagagtaagg 240

aaagccaagg aagctcttca acaagtgttg tccatactat ttgaatacaa gcccaagttt 300

caaggagaaa agtccaaggt tgtgagttgt atcatggccc acatggagga ggactaaatg 360

gcaccacttt gtctcaattn tagagtggtt agtttgtcta aataatggcc caatccttgt 420

aatgttggct gaccaaaaat atgttttggg ttaatc 456

<210> 908
<211> 449
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 908

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gaatagagaa ggaagaaaga tgattggaga ccccacttca aggagatgat gagtcaagaa 120

gaagctcacc accacaggaa gccatggata agagcttgaa ggaaggcgaa gatgagtgga 180

gggagaggga gagaaggggc acgaaattnt atgcctcaaa tgaggtctga actttgaagt 240

gtaattctca aatgatcaaa gttcaaaaaa tgcacacaca tggcctctat ttatagccta 300

agtgtcacac aaaattggag agaaatttga atttctattc aaatttcact tgaatttgaa 360

attgaatttg tggagccaaa atttcaataa ttatgattaa tgaattttag atatggttca 420

gcccactaat ccaagatcaa gtccaagat 449

<210> 909
<211> 434
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 909

nttataanaa gcatttctaa gcataaaact aaaatatgtt gtattgagct cttggtattt 60

tttttatgat aacatttta attatgagta taattttata attattaaaa gccatcagtt 120

ttttttaaa taataatttg ttcacatttt gttcaaataa acttaatgta agttctctga 180

atttattgca ttctggcgac tgaaattcac aatcaaaact taaagtgtgc tgaataaaag 240

tttttcatag atgtaatcta gtaaaataat gcttcataaa taattaggtg tctaatagaa 300

gaataaagtt aatacaactg ttctcgaaat taaagtagaa tcgatacatt cacagatgtg 360

tatacataat aatggtgtag tattcaatac atattgtttt gctttactgt cgaactatgg 420

aattccatat acat 434

<210> 910
<211> 330
<212> DNA
<213> Glycine max

<400> 910

agcttgagct ttgaattgag tgtcattgtc agtggcaatg gcgtaaagaa gaccatattt 60

tcatatgaag ggtttgcatg agaacttctc tacctcatct ggtgaaattt ctcgcaatgg 120

tcttgcctta atccacttag tgaaataatc aatagcgact aataagaatt tgacctatcc 180

tgcggctttt gccaatggtc ctagtatatc catcccccac atggaaaaag ggccaggtcc 240

tagtatgacc aataagaatg tacccttttgg ctcgctcacg tagctcgtcc atgctgctag 300

ggggtttctt gcatatacta tcagggaact 330

<210> 911
<211> 444
<212> DNA
<213> Glycine max

<400> 911

ctcagcttga atgaagtcca acgcagcacg cgtgtcgtta aagttgggaa ggttaggcaa 60

tgaaggagat gaacgtggag tgtagtttcc actgtacttt actctagcag aggttgtgga 120

gttatcaaag gcaacaccaa caccacttga atatgctctt gcagcacgat agtaatgatt 180

aagttcttgg ttggcatgca ataacacatc cattgtttgt cccggtgata tgcaaatgta 240

ttcccttgcc aatggcttgg ttaacatacc atcagcacca acaacagtga ggttgtgttt 300

tgaaacagag aagaagagaa tgagattcat tgccgcattg acaacacgga gaagataagt 360

cctgccttgc tctacatgaa actcgaacgt ttctgaaaat taaaagaaag ttttgtgttt 420

agatgagctt aacctcatag atac 444

<210> 912
<211> 347
<212> DNA
<213> Glycine max

<400> 912

ttagaccttt gatggcatgc tggcatcacc ctcattcttg ctcttgtcag cttcaaactt 60

atcaattgct acctgcagtt catcagtgcc tccaacagcc ctcatggtgt agaagtatgc 120

accaaagaca aaagctgtca aacccccagc aactaccaga ttctttgcct taggtggaag 180

gctcctatat cctaaaagtc cagccatctt gatcaatgtg ggaaaaaagg gttagcacaa 240

tttcacacaa ttacaattac ccttcaattg cagaaagcac aaaagatcac aaaacagata 300

attcagatct gtaaagaata atgagtagac attttcacaa acagatt 347

<210> 913
<211> 464
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 913

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gaatgtatgt atacatgatt ttgatgatgt caaaagaaga atcaaacaag gctcattttg 120

cttcaagatt aatacaagat tggttcatca aacaaagcct tgattcaaga tttcttcaag 180

atcaagcctt gcctcacaat gaaaggtttc aagtcattca aggcacatgt aatcgattac 240

caatacatgt aatcgattac caatggtttg aaagtgtgta atcgattaca catcatatgt 300

aatcgattac cagagactct gaacgttggg aattcaaatt ttacatgaag ggtcacaact 360

gttcaagaca aacaactgtg taatcgntac actaattatg taatcgatta ccagagagga 420

ttttcaggaa tatcgccaac agcacatctt atcatttgaa tttg 464

<210> 914
<211> 416
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 914

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tcaaccaact ggagggtcat gcatgtgggc attatctcta tctctccaag tcgccgacac 120

atggagagag gcattaaatt gatactagct cccaagtcta tgagagctnt acccacaaca 180

acctcaccaa tagaacacga tatactgaca cttccaggat ctttgtgctt cgggggaagg 240

atgcgttgaa tgaccacact atagttacct tccacaacta ttgtgtcact gtggatatac 300

cggttattct ttgtcagcat gtcttttaaa aatatggcat aaagtggcat ctgttggaga 360

gcttctccaa aaggcaaagt gatcttcatc ttcttgaaga tgtcaagaaa tctggc 416

<210> 915
<211> 402
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 915

taagctcttt caactgcaca aagctattaa tattngaaga gtatccatat ggaaccttca 60

cccgacgaag acactgacaa aaacttatct tctccttttt ggacaaagca tggcaagcta 120

ggggcaagta aattttcttc ccatcagacc ttggatgcaa ctgtgatcgt atccccatat 180

aagctagatc ttgatgggta ttcaagccat ccttcgtctt tccttgaatg ttaaggagca 240

tcccaatcac actgtcacaa acatttttct ccacatgcat aacatcaata caatgtctaa 300

cgtctagatc agaccagtac ggaagatcaa agaaaatgga cctcttcttc catatgcaac 360

tcttactttt atccttcttt tgggtttttc caaatataat at 402

<210> 916
<211> 350
<212> DNA
<213> Glycine max

<400> 916

agaatcggac ctcagtgtga aaagttatga ccatttgaat atctcgggag cttccgttgt 60

acattttcga gcgtctgtat atgagatgcg cctgaatcgg acatccgagt gaaaagatat 120

gaccatttga atatgtcgag agctttcgat gtttaatttt gagcgtttag atataagata 180

agcctgaatc ggacatcctg gtgaaaactt atgaccattt gaacttctgg agagcttccg 240

ttggggattt tttaacgtct ctttatgtga tgcgcatgaa ttggacatcc gaattaaaag 300

ttatgaccat tagaatatct caagagcttc cggtgtacaa ttctgagcgc 350

<210> 917
<211> 399
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 917

agcttctata gaaggttcgt tcctaatttc tctacaattg catcacctct caatgagcta 60

gtgaagaaga atgtggcatt taactggggt gaaaaacaag agcaagcctt tgctttgctt 120

aaagaaaagc ttactaaggc acctgttcta gctcttccta acttttctaa aacntttgag 180

ctagaatgtg atgcctctgg agtgggagtt ggagctgttt tgttgcaagg tgggcaccct 240

attgcttatt ttagtgaaaa acttcatggt gcgacccttа actaccccac ctatgataaa 300

gagctttatg ccttaataag agcactccga acttgggaac attaccttgt ttccaaggaa 360

tttgtcattc atagtgatca acaatcactt aagttcatt 399

<210> 918
<211> 399
<212> DNA
<213> Glycine max

<400> 918

tagtatatgg acttgggtgt tgcccagttt catcatatct tccgtaatac ttatcacctc 60

tatcatatct aataattttc acatttatgt ctaattgcca ttttacttca ttgtagtaaa 120

tttctaaagc atccattgcc taagaaatct cgggcagtaa gtagacataa ccgtaacgtg 180

aataatcatc aataatggtg ataaagtatt attcctttcc gaaagaacta acatcaaaag 240

gtccacaaat attagtatgc acaatttcaa gaagctgagt gcttcttgta gctcttttct 300

ttgtatgttt tgcttgtttt ccattaatac aacccacaca aatatttaga tccataaaat 360

ctagataagg aagaatttca ttctttatta atttttcca 399

<210> 919
<211> 381
<212> DNA
<213> Glycine max

<400> 919

taaagcacaa cattgaccat gagctcttca tatcgccctc agtccaatgg ccagactgag 60

aatcttaata agaccattga gatgtatcta aggtgctttg tatttgaaca tcctaagagt 120

tgggttacta tgctaccttg ggcttaattc tagtataata cttcctttca ccaaagcttg 180

ggcatgacac catttcaagc agtttttggt agacctccac caacggtgat gcactacgag 240

gttgatccta aagatcccga tccactcaag gctttattac aactacgtga tcaacttttg 300

agcaagctta aaggtaattt actaaaggct caacaatata tgaagatgca agctgataag 360

aaaagaagag aaagagaatt g 381

<210> 920
<211> 402
<212> DNA
<213> Glycine max

<400> 920

tgtaagattt gcaagatcat cttccttgac aactccttga aaattattgc catcaatacg 60

cagagatgac aatttagaga gtgatccaat actttcaaat ggatttccac tgaatttatt 120

aatagacaga ttgagatatc ttaatgatga aagttttcca aatgatattg gaagagcacc 180

accaattaag ttgttggaaa aatctagcat gtcaatattt ttaaaagccc caatttgatc 240

tatcagattg cctgaaagtt gtgaactccg aactgcaagt gttgtgattc cctaggaaat 300

acaaagagca agaatttcta aaagttcatt aacctgttgg ttgagtttga gatatgataa 360

acctatctcc cttaagttgc agagattatc caaagaagtt ga 402

<210> 921
<211> 397
<212> DNA
<213> Glycine max

<400> 921

ggacactatg aatactcagc tcgattggag cggatgggcc agtctgcctc gtttttcacg 60

aatcaataaa tgattcgccc tgcctcgtga ccccacgggt caaacgtgcc gatccgcgac 120

ctaatttaaa agaattcgat tttataaaaa tacaatacaa tgaaattaag ttgaatacaa 180

atgtaaataa aatctcaata attagtcaat tacatcaata aaataaatat tgtcttaata 240

aaagaaaatc caagcaatac atctaaaata tgaaatttaa acatctccaa caacaaatga 300

ttccatattt gataatgttt aatgaattct gactttaata aaaatataat acaatgaaat 360

taagttgaat acaaatgtaa ataaaatatc aataatt 397

<210> 922
<211> 361
<212> DNA
<213> Glycine max

<400> 922

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cagagaaggt ctaaacattg aagagtaatc ctcaaataat acaaggtgaa aaatgcacac 120

acatggcctc tatttataga ctcagtgtcg caaacaattg gaaggaattt ataatttctt 180

ttcaagattc acttgaatct gaatttgaat tggtggagcc caattttgga gccgaaattg 240

cagtaattat tattagagaa tttcagttat ggttcagccc actaatacaa gacctggtgc 300

aagagtttgg actaatagtg ctgatgtggc atgacgaatg tatagcatga aagacatgca 360

c 361

<210> 923
<211> 380
<212> DNA
<213> Glycine max

<400> 923

ttggagaatg atttctatac aaaagttagt cgtataaagc gactaacagt gtgttacatt 60

atggcatttg cctatgttcc tgatgcagga ggcttgagga agaagatttt ggaggaagct 120

catcattcct tttacaccac tcatccgagt tctactaaaa tgtatcaaga cttaaaggag 180

ttttattgga agggagggat gaaaaggatg tagctgaatt tgtatctaaa tgcctagtat 240

gtcagcaagt taagacagag catcagaagc ccgtaggttt gttttagagg attgatatac 300

ttgaatggaa atgggagaga attgtaacac cccagattct agttcaaaac attgctttga 360

aaactctcgt taattatttt 380

<210> 924
<211> 397
<212> DNA

<213> Glycine max

<400> 924

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gctccattgg agcttgtaag cctaggatct tcttcatcaa tggattcctt tgcttcttgg 120

aagatgaatg gcagtggaat gaagaaggaa gagagagagg agacgccact tcaaggagaa 180

gatgagtcta gaagaagctc accaccatat gaggccatgg ataaaagctt ggaggaagaa 240

agagatgaat gaagggagag ggagagaaga gcacgaaatt ttgtgctcca aatgagcttt 300

gaaatctgaa gtttaatatt caaatgatca aagttgaaaa aaatgcacac acatgacctc 360

tatttatagc ctaagtgtca cacaaaattg gagggaa 397

<210> 925
<211> 391
<212> DNA
<213> Glycine max

<400> 925

taataagtgc atatgatgta gctccatgta gagcttgtaa gccttggatc ttcttcatca 60

atggagtcct ttgcttcttg aatatcaatg gtagcggaat ggagaagggg gaaaggtgat 120

tggagacgcc acgtctagga gaagatgagt caagaacaag ctcaccacca tatgaagcca 180

tggataagag cttgaacgta tgagaagata aatagaggga gagggagaga aggggcacga 240

aatttatgcc tcaaatgagg tatgaccttt gaagtgtaat ttctcaaata atcaaagttg 300

aaaattgcac acacatggcc tctatttata gcctaagcgt tacacacaat cggagggaaa 360

tttgaatttc tattcaaatt tcacttgaat t 391

<210> 926
<211> 304
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 926

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atttaaagac gatgttttgg tggcccaaca taaagagaga ggttattgag tttgtgtatg 120

catgcctagt ctgtcagaag gctaagatag aacattagag accttcaggg aagttacaac 180

ccttatagat accctagtgg aagtgggaca gtatttccat ggatttnnnn ggtggactac 240

ctangacccc tatagggtta gattctatct gggttattct cnatagattg actaagnctg 300

ctca 304

<210> 927
<211> 376
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 927

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aacgagacgc tcgaaattga atgttgaacc tcagagcgaa ttcaaaccac aataactttt 120

tactcggatg tgtgattgag tcccgtaata tatcgagacg ctcgaaattg aatgctttag 180

ctttgagcca attcacccga caataacttt ttactcggat gtctgattga gtcccgcaat 240

atatcgagac gctcgaaatt gaatgttgaa gctctgaacc aattcaaacg acaataactt 300

tttactcgga tggctgaatg aggcccgcaa tatattgaga ccctcgaaat tgaatgttga 360

atctttgagc caattc 376

<210> 928
<211> 325
<212> DNA
<213> Glycine max

<400> 928

agcttcaaca ttcaatttcg agcatctcta tatgttacgg gactcaatca gacatccgag 60

aaaaaagtta ttgtcgtttg aattagctca gaagttcaac attcaatttc tagcgtctcg 120

atatgttacg ggactcaatc aaacatccga gaaaaaagtt attgtcgctt gaattagctc 180

agaggttcaa cattcaattt cgagcgtctc gatatgttac gggactcaat cagacattcg 240

agaaaaaagt tattgccgtt tgaattggct cagagcttca acattcaatt cccagcgtct 300

cgatatatta cgggactcaa tcaca 325

<210> 929
<211> 439
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 929

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cactccttaa attatgacaa atgatgtagt tccatgtaga gcttgtaggc cttggacctt 120

cttcattaat ggagtccttt tcttctagaa gatcaatggc agtggaatgg agaaggagga 180

aaggtcattg aagatgccac ttcaaggaga agatgagtca agaacaagtt caccaccata 240

ggaaaccatg gataagagct tgaaggtagg agaagatgag tagagggaga gggagagagg 300

gggccacaaa atttatgcct caaatgaggt ctgaaatttg aagtataatt tctcanatga 360

tcaaatttcc aaaaaatgca cacacaaggc ctctatttat atcctaagtg tcacacacaa 420

ttagagggaa atttgaatt 439

<210> 930
<211> 429
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 930

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gatatcttaa gaaggggggg ttgaattaag atatcacaaa ctatttccct tattaaaatt 120

ttatttcact ttctattcaa gttataaatt cccttaaaaa tgaacttctt aaatattgat 180

tcaaatagag caatttgaat atgaatataa aacaataata aataaaggag tttaagggaa 240

gagagattgc aaactcatat ttatactggt tcggtcacac ccttgtgcct acgtccagtc 300

cccaagcaac ccgcttgaga gttccactat cttgtaaaag cttattacaa gatctgaacc 360

acacaaggac aacccttcct ttgtgttcag atttctgtac aacaagagac cctcggtctc 420

ttaatcctt 429

<210> 931
<211> 406
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 931

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ccggtaattt atctagacgc tcataaatga atacggaagc acgtaacaaa tgcaaactgc 120

aataaatttt aactcagatg tccgaatgaa tcccgtaata tatcgagaca ctcgtaattg 180

aaaacagaag ctctaaacaa attctaacga caataacttt ttactcagat gtccgattgt 240

gtccagtaat atatcgagac gcttgaaatt gaaaactgaa gctctgagca aattcaaacg 300

acaataactt tttactcgga tgtatgattg agtcccggag tatatcgaga cacttgaaat 360

tcagaacaga agctctgagc aaatttaaac gacaataaca tttaac 406

<210> 932
<211> 431
<212> DNA
<213> Glycine max

<400> 932

agcttctttc aaaatgctac tcacaatatt gcggattctc ttgtccatct ccgtgtctac 60

ttccctagga attgttgcag ggctagggtt ttcagcaatc ttcactccct gttgtcttct 120

gggaaccagt gtctcaggga ctgaagcttg accaggaatt acttgtatgg gttggatgtt 180

gaaatctggt tgttcctggt gcggagatga tggtacagcg ggtgaaccag aagcggaagt 240

ttcttttggt gaggaagcca tggaaaaaca cagcgtttgg aatgatttcg taaatctcaa 300

aatactattg ggaaatgctg gtgaaaacac taatgctcag cagatattaa tttgaatgaa 360

taatgtatag gggcgcgtga agcaacggtc aaatacgttt cgcttaatag tgaacgtgct 420

attaatgtta a 431

<210> 933
<211> 351
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 933

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aattaatata tgccaaactt ttctctctaa ttaagaatct atcttacttt ttactaaaga 120

tatgaattcc cttggtaaca atcttcttag atattgattc agctgaatca acttgaatat 180

gaatataaag caatattcca tcaaggagat taatggaata gagaatgcaa actcagtttt 240

atactgtttc ggccacaccc ttgtgcctac gtccagtccc caagcaaccc gcttgagagt 300

ttcactaact tgttaattcc ttgtacaagt tctaaacaca caaggacaac c 351

<210> 934
<211> 350
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 934

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tcatcagtgg gctttccttc tgtgtccagc atcttgggat gttcccagcc tttgatgaca 120

gctttccagg ttctgctatc cagtgatttg aggaaggcca ccatccttgc tttccagtat 180

tcatagttgg gtccatctag gattggtggt ctgttcactg gtcctccttc tttctccatg 240

ttcatcagaa tttatctccc cagatctcac tctgtgattt cgagtgtgag ctctgatacc 300

aattgaaatt ctgataccag gggacagatg tcgtaccgga tgtcacgact 350

<210> 935
<211> 398
<212> DNA
<213> Glycine max

<400> 935

tgtagcatat tcaaaccaca ataactgtta actcggatgt ctgattgagt ccggcaattt 60

atctagacgc tcataaatga atacggaagc acgtagcaaa tgcaaactgc aataaatttt 120

aactcagatg tccgaatgaa tcccgtaata tatcgagacg ctcgtaattg aaaacagaag 180

ctctaagcaa attctaacga caataacttt ttactcagat gtccgattgt gtccagtaat 240

atatcgagac gctcgaaatt gaaaactgaa gctctgagca aattcaaacg acaataactt 300

tttactcgga tgtatgattg agtcccggag tatatcgaga cacgtgaaat tcagaacaga 360

agctctgagc aaatttaaac gacaataaca tttaactc 398

<210> 936
<211> 426
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 936

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tccctaggaa ttgttgcagg gctagggttt tcagcaatct tcactccctg ttgtcttctg 120

ggaaccagtt tctcagggac tgaagcttga ccaggaatta cttgtatggg ttggatgttg 180

aaatctggtt gttcctggtg cggagatgat ggtacagcgg gtgaaccaga agcggaagtt 240

tcttttggtg aggaagccat ggaaaaacag agcgtttgga atgatttcgt aaatctcaga 300

aaactattgg gaaatgctgg tgaaaacacg aatgccaagc agatataaat ttgaatgaag 360

aatgtagagg ggcgtgtgaa gcaacggtcg aattcgtttt ggcttaatag tgaacgtgct 420

attaat 426

<210> 937
<211> 387
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 937

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caattgtctc atcttttcat ttggttcttg aatggctatc aaaggcctat atatatgtga 120

cttgagacac gaatttgcta agagtttttc agaacaaaaa ggtcttatcc tcttaaaaag 180

caaaatcgtt ttatcctctt acaaattcct tggccaaatc acttgtgatt caataaggaa 240

ttgtttgagt gctcaaattg ttcaatctat ctctttcaag agagatttct tcttcttttc 300

ttctttattc tgaaaaggga ttaagagacc gagggtctct tgttgtgaaa gaattctcaa 360

cacaaaggaa ggattgtcct tgtgtgt 387

<210> 938
<211> 298
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 938

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taagctccat tggagcttgt aagcctaaga tcttcttcat caatggattc ctttgcttct 120

tggaagatga atggcagccg aatggagaaa ggaacagaga gatgagactc cactcgatga 180

gaagatgagt ctagagaaag ctcaccacca tatgaggcca tggataagag cttgtangaa 240

gaaggagatg aatgaacgga gagggagaga agagcacgan atattgtgct ctaaatga 298

<210> 939
<211> 402
<212> DNA
<213> Glycine max

<400> 939

tatcctttga aagatcaata ctctcagttc ttttgaattc gttcactaga aaatccaata 60

aagcattatc aaaatcctct cctcccaaga aagtgtcacc atttgttgct ttcacctgga 120

cacaaaaaag ttattagtga caatttccaa cattatttcc aattactggc tatgaaatat 180

aagcatagaa taaacaagtg ttaatacctc aaaaacacca ttagaaatct ctaagatgga 240

cacatcaaat gttccacctc caagatcaaa aactgcaatg agaccctcct tgttgttcat 300

cccataggaa agtgcagcgg cagtgggctc attgatgatt ctctgaacat caagaccagc 360

aattctaccg gcatcttttg ttgcctgcct ctgagcatca tt 402

<210> 940
<211> 375
<212> DNA
<213> Glycine max

<400> 940

acaagtctcc tttgatgagt ctgatctcat tcttccaagg aaggattttt tagatgatat 60

ttcagatacc ttagaagata cacatattca tggaaatgac tctgaagaac aagatgaatg 120

aagctatgac gattctcaag ataatggagt tagaggaaat aatgatcttc cgcgagaatg 180

gatagcctca agagatcatc ccctcgacaa cattattggt gatatatcag aaggggtaac 240

aactagacat tctcttaaag agttatgcaa taatatggct tttgtatcta tgattgcacc 300

taagaatata aaagaagcga tagtatatga taactggata atttccatgc aagaagaact 360

gattcaattt gaaag 375

<210> 941

<211> 391
<212> DNA
<213> Glycine max

<400> 941

tgaaagtgca taccccacca tttttcatag taaaacactg gtaatgtgtc tactattatt 60

gagatcatat ctttctttgt cattggaggt gccacttgag ctgccaggtc tctccacctt 120

tgggcgtatt ctttgaaaga ttcgtgcccc tttttgcaca tgttctgtag ttgcatccta 180

tccggagcca tattagaatt gtattgatac tgcccaatga aggcaaccat taagtctttc 240

caagaatgga ctcgagaaag ttccaagtta gtgtactagg taacagctac cccgataaga 300

ctttcttgga agaaatgtat caacagtttc tcatcttttg cgtatgcccc catcttccga 360

caatacatct ttagatggtt cttggggcaa g 391

<210> 942
<211> 421
<212> DNA
<213> Glycine max

<400> 942

agcttgtaat ctattactag aagatttaaa cgttttatta caacctttag aaatttgaat 60

ttaaatttta aagcctgtaa ttgattacaa cttgtgtgta attgattacc aacatgagaa 120

ttcaaatttc aagtctgaag agtcacaact cttcagaaat taactgtgta atcgattaca 180

acagttatgt aatcgattac caataaggaa ttttcgaaaa taactcccaa gagtcacaac 240

tgttcaaatt ttttttgaat ggtcatcaat ggcctataaa tcaattacca gacatgaaaa 300

ttcaaatttc aagtctgaag agtcacaact ctttagaaac taattgtgta atcgattaca 360

acaattatgt aatcgattac cagtaacgaa ttttcgaaat aacttccaag agtcacgact 420

a 421

<210> 943
<211> 432
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 943

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acaataccat catttcttgc actgaattgt tgngagttgg aagccatctt ctcaatcaaa 120

ttcctagcct caacaggggt catatcacca agagctccac cactgggagc atcaatcata 180

ctcctctcca tgttgctaag tcccttgtag aaatattgaa gaaggagttg ctcaaaaatc 240

tggtggtgag gacagcttgc acacaatttc ttgaatcttt cccagtactc ctacaagctc 300

tctccactaa gttgcctgat gcctgaaatg tcttttctga tggcagtggt cctagatgca 360

aggaagaatt tctccaagaa caccctctta aggtcatccc agatgaaaat ggacctggga 420

gcaaggtagt at 432

<210> 944
<211> 417
<212> DNA
<213> Glycine max

<400> 944

gcttgttcag aaatgtgcat ttgtgtgtaa tacacaatta atggttcacc acaacaaaat 60

ggtgtatcag aaaggcggaa tagaacttta atggatatga ttaggagtat gttaatcaat 120

tagactttat ccgtatcctt gtggatgtat accttgaaaa ctgccatgta gttgttgaac 180

aggattccta gtaaggtagt tccaaagaca ccttttgagc tgtagacaaa taggatacct 240

agtataaggc acctgcatgt ttggggttgc caggcagaaa taaggattta taatccgcaa 300

gaaagaaaat tggatgcaag aacaatcagt ggatatttca ttggttatcc agaaaagtca 360

aaggggtata tgttctattg tcctaatcat agtatgagaa ttatcgaaac tggaaat 417

<210> 945
<211> 371
<212> DNA
<213> Glycine max

<400> 945

ctcaagctta acaaaatata aatctaggag cttctaccta tgtattataa acaaatttaa 60

attaaaactc atggagagtt tagtaaggga actcagaaaa atagccccgt aaaataaaac 120

tcatggggtg cctcctcaca aaggggggtcg cagtgaccag gcttgggcga ctggttatca 180

aaaacacagg tgttcacaaa ggcataagat catttatggg ggcttagatg taatctggaa 240

tatgagagat gtttaatgaa aggaaaatgg actccatttg gataaaaata actactttct 300

ttagacgcct ttttttgcc tagattcttc acaacctatc taagtggtta agctactttc 360

cgcgttttat a 371

<210> 946
<211> 404
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 946

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tcattgtcat cgtttttttc gtcattgagg tgccacttaa gttgccaggt tctctccacc 120

tttgggcgta ttcttttgaa agaatcgtgc ccccttttg cacatgttct gtagttgcac 180

cctatccgaa gacattatac tgacactgcc taacgaaggc aaccactagg tccttccaag 240

aatggactcg agaaggttcc aagttagtgt accaggtaac agctacccca gtaagactnt 300

cttggaagga atgtatcagc aattccttat cttttgcgta tgcccccatc ttgcgataat 360

gcatctttag atggctcttg gggcaagtag tcctctcgga cttg 404

<210> 947
<211> 294
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 947

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tctcaacgcg tttgtttcca ctgtgaatgg aaggctgaac tcatgcaagg ccagcacagg 120

cgccgtcgac aatgcatgtt tgagattgtc aaaggccaaa tgagctngcg gggtccagtg 180

gaagggatca acantgatga actagactaa cggagttgca atcgttgcat atccactaat 240

gaagcgacga taaaatccta ccacactaan gaagctttgc acagctttta tgga 294

<210> 948
<211> 393
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 948

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ttcttcatca atggagtcct ttgcttcttg aatatcaatg gtagcggaat ggagaagggg 120

gaaaggtgat tggagacgcc acgtcaagga gaagatgagt caagaacaag ctcaccacca 180

tatgaagcca tggataagag cttgaacgta agagaagata aatagaggga gagggagaga 240

aggggcacga aatttatgcc tcaaatgagg tatgaccttt gaagtgtaat ttctcanata 300

atcaaagttg aaaattgcac acacatggcc tctatttata gcctaagcgt tacacaaaat 360

tggagggaaa tttgaatttc tattcaaatt tca 393

<210> 949
<211> 421
<212> DNA
<213> Glycine max

<400> 949

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taagtgtgat tccttttctt ttcttatcat tctcctcatg ttgattcagt ctcattagat 120

ccatttcgtg ttcctataac tttccaaata aagttgcaag agacatgtta gaaagatccc 180

ttgattctgt aatagttgtt acctttggtt gtcattccct acttaaacat cttagaactt 240

tattaataag atcctcattg ggaaatatct ttcctaatga tgcaagatga tttactatgt 300

gtgtgaatct cttttgcata tcatgtatag tttcatttgg attcattcta aacaattcat 360

attcatgggt taaggtattt attctagacc cttttacatc tatggttcct tcatgggtta 420

c 421

<210> 950
<211> 398
<212> DNA
<213> Glycine max

<400> 950

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caagtgaggt ctaaaatttg aagtgtaatt ctcaaatgat caaagttgaa aaaaatgcac 120

acacatgacc tctatttata gcctaagtgt cacacaaaat aggaggggaa tttgaatttc 180

tattcaaatt tcacttgaat ttgaatttaa attggtggag ccaaatttgg agccaaaatt 240

tcactaatta tgattagtga attgtagcta tgattcaacc cactaatcca agatcaagtc 300

caagattctc cactaagtgt gcttatgtgt catgaggcat gtaaaacatg aaggatatgc 360

acaaagtgtg actatatgat gctgtaatgg ggagtagc 398

<210> 951
<211> 383
<212> DNA
<213> Glycine max

<400> 951

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cggctcacaa atggcggtga gctgtgatat gaatctggca atataattca agcgtcccag 120

gaagcctcgg acttgcctct cagtacgtgg ttctggcatc tcaaggatgg ccttcacctt 180

ttcggggtct acctctatcc ctttctggct tacaatgaaa ccaagcaatt tccctgattt 240

gaccccaaag gtacacttgg cggggttcaa ccttaactga tatttcttaa gcctttcgaa 300

caacttccgc aggttgacaa ggtgttcttc ctcagattta gatttagcaa ttatgtcgtc 360

cacgtagacc tcgatctctt gat 383

<210> 952
<211> 421
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 952

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agcttggtca acaggtattg ttatttaatt cttgattaag attgtttcca agtaagctga 120

aatccaagtg gtctagacca ttcatcatca aagaagttat gccatatgga gcagtgatat 180

tggaggaccc aaccaccaaa aggacatgga ccgtgaatgg tagaagaatc aaacactacc 240

taggtggaga tttcgagagg ataatcactg ttgtccagat gcaaaaggct tgaaccataa 300

cgaagacgtc caattataaa gacgttaaag aagtgctctt gggaggcaac ccagtgtttt 360

ttaaactttg tcttaacttg tgttacttta atcttatgcc ttatatatct aanacttact 420

t 421

<210> 953
<211> 409
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 953

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agcttggtca acaggtattg ttatttaatt cttgattaag attgtttcca agtaagctga 120

aatccaagtg gtctagacca ttcatcatca aagaagttat gccatatgga gcagtgatat 180

tggaggaccc aaccaccaaa aggacatgga ccgtgaatgg tagaagaatc aaacactacc 240

taggtggaga tttcgagagg ataatcactg ttgtccagat gcaaaaggct tgaaccataa 300

cgaagacgtn caattataaa gacgttaaag aagtgctctt gggaggcaac ccagtgtttt 360

ttaaactttg tcttaacttg tgtactntaa tcttatgcct tatatatct 409

<210> 954
<211> 374
<212> DNA
<213> Glycine max

<400> 954

agcttcttat accaatgtca cgaggagtgt ggtagtcaga ttcatcaaga aggagctaat 60

ttgtcgatgc ggactcccta ggaagatcat cactgacaat ggcaccaatc tgaacaacaa 120

gatgatgtag gaaatgtgcg aggatttcaa gatccagcat cataactcca ccccttatcg 180

tccaaagatg aatggggctg tagaggctgc aaataaaaat attaagaaga ttgtccagaa 240

gatgaccgtg tcatacaaag attggcatga gatgttgcct ttcgccctac atggatatag 300

aacttcagta cgaacttcta ctggggcaac gccgtattcc ttggtttata ggatggaagc 360

aatactccta tttg 374

<210> 955
<211> 338
<212> DNA
<213> Glycine max

<400> 955

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gcatgtccga gaaaagaacg tacttcctgc atagaagcga cgtaaggaag agaagtaata 120

acatcgatct tggccttatc aacctcaata cctttactaa agaccaaatg ccctaagact 180

ataccttttat ggaccataaa atgacatttt tcaaagttaa aaacaaggcc aatctcaatg 240

cattggtcaa aaaatctaga gaggctactc aagcaaccca cttgagattt ttcactccct 300

ttgtaaaaat cgtttacaac ttctgaacca cacaggga 338

<210> 956
<211> 423
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 956

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taatcataag ctacaaatgt tcaatttcat aaaaaataac ttttttctta gaaagaaaag 120

cattttgtaa atttaattta ggattccaaa tatccaactt aattgtttcg gaaaaaactt 180

aaaaaaaaac agttaaaatt ttagattatg agttctccca aacattttaa tcacataacc 240

ttatatttcc tagattaata cttaaccttt ctactatttt tgtccctttt ttttctctct 300

tcttcaatca atttaattct ctcacaatct tatctaatat tatcaagtgt cttaatttag 360

tcatatttac tatatttttt taaataaaat gtttaataaa aaaattaatg aaacatataa 420

agc 423

<210> 957
<211> 417
<212> DNA
<213> Glycine max

<400> 957

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acaatagcat catcacttct atcactaaat tgatgggagt ttgaagccat cttctcaatt 120

aaacttctgg cttaagtagg ggtcatgtct ccaagggctc caccactggc agcatctatc 180

atacttctct ccatgttact gagtccttca taaaaatatt ggaggagaag ctgctcaaaa 240

atctggtggt gagggcaact ggcacatagt ttcttaaatc tctcccagta ttcatataag 300

ctatctccac tgagttgcct aatgcctgaa atatcctttc taaaggttgt ggtcctggaa 360

acacgataat attttctaaa aagaatactc tcttgaggcc gcccatctcg tgatgga 417

<210> 958
<211> 418
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 958

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atggctattg tcaagttgag ttatttgacc cttttgctgc tactacttgc aaggaaggga 120

tgaatggatt ttttttaatt ttaatttaat ttttcattct aaattaattt taatttaatt 180

aaaatatgat gttatatcag atgacaagtg gtcagcatac atgtcacact taatctaacg 240

tgatatcaca agtagtttgt cgacgtatca aataaataac cacatcagca attaatggat 300

cctttntaac gacagagacc tcatacaaaa cttttaaatt atagtgaccc atctcannaa 360

tgaaaaatta tgaggaatca aatgtaaaat tcaagtatat atcangggat caaaatat 418

<210> 959
<211> 440
<212> DNA
<213> Glycine max

<400> 959

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acactttaaa ctgaattaga gacatggagt tacaagattt gctaccactt tcttaacttt 120

gcaaagattg cataagcaaa aggccaatct tagaaggatg tttaattcag atgaatggtt 180

gaagtctaag gcagctaaag agcccaaggg gaagcaagca acagatgttg ttcttatgcc 240

atcattttgg aatgatgttg tttatgcttt aaaggctatg gggcctcttg taagtgtgtt 300

gaggttggtg gataatgaaa aaaaacctac aatgggtttc atttatgaag caatggatag 360

ggccaaagaa gcaattcaaa gagctttcaa taacaatgaa gggaagtata aggatatcct 420

ttgcatcatt gataaaagat 440

<210> 960

<211> 366
<212> DNA
<213> Glycine max

<400> 960

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tatatattta ttatttctaa catttaaatt ttatgtctaa taaatttcat cttaaaaagt 180

aggtaaaatt ttaatctctt tttgttgggg tttcaatgct atacaatgga ttatgcataa 240

ttttgatatt tttatcatca actctgattt agaaaccaaa tattttaacc ataaatccaa 300

ataaacaatg caataattca ttaaaataaa tagtttgaca ttaaataaat taataaaaaa 360

gtagaa 366

<210> 961
<211> 278
<212> DNA
<213> Glycine max

<400> 961

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ccgattcacg cgcataatat attgagacgc tctcgtgaaa ttcaaatggt cataactttt 120

cactcagagg tccgattcat gcgcataata tatcgagatg cacataattg aacaacggaa 180

gctctcgaga aattcatatg gtcatacctt ttaactcgga gctctgattt aggcgcataa 240

tacattgaga cgctcgaaat tgaacaatgg aagctctc 278

<210> 962
<211> 383
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 962

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attctcatga acctcanggt aaaattttga gcccatgggc caaggctggg tccactcttc 120

tttgtaaata ttagaatagg ttttctttct tttaggggtt gtattttgat gcaatnctac 180

cccttaagct tattggatag aagactccaa gaggatcggg ctagagcagc taaagaaggc 240

tctaggcttc tcatgtacct cagggtagat ttctgagccc atgggccaag gctgggtcca 300

ctcttctttg taaatattag aatagtgttt ccttctttta ggccttgtat tttgaccatt 360

ctagtagtat aggaatttac cct 383

<210> 963
<211> 374
<212> DNA
<213> Glycine max

<400> 963

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tatcccgaca ctcaaaatgg aacaacagaa gctcttgaga aattcaaatg gccaaaactt 120

ttctctcgga tgtctgattc acgtgcattt tatatcgaga ccctcgaaat tgaacaggga 180

agttttggca aatatcaatg gccatatttt ttagtcgaat atatgatcga cgcccatgaa 240

atatcgagac gctcaaaaat gaaataagac agctcgcgag aaattgaaat ggttataact 300

gtttacctgg atgtgagatt tacgcgcata atatattgaa gttttgaaat tgaaaacgaa 360

aagtgttggc taat 374

<210> 964
<211> 381
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 964

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tacactctga gtgcctttga agtttgaaag tatccaagaa atatctcatt atcacttttc 120

gagtcaaatt ttcccaagtt gtcctttgtg ttgagaataa aatatttgca tccaaatgga 180

tgaaaatatg ttatgttggg tttcatccct tccataattc ataaggagta tttttaaggt 240

taggtcttat gtaaattctt ttttgaagat aacaagtagt attcactgct tcaacccaga 300

agtgtttaag ggttgaatta tcattaagca tgggcctagt catctcttgt agatatctat 360

taattntttc aattacccct g 381

<210> 965

<211> 421
<212> DNA
<213> Glycine max

<400> 965

tatcataggt ggggtagttg agggaggcac tatgaatttt ttcactaaaa taatttatag 60

ggtgcccacc ttgtaacaat acagctccaa ctcccactcc agtggcatca cattctagct 120

caaaaggttt agaaaagtca ggaagagcta gaacatgttc cttattaagc ttttctttga 180

gaaaagcaaa ggcttgctct tgtttttcac ccaagtaaat gccacattct ttttcactag 240

ctcattgaga ggtgatgcaa ttgtagagaa attaggaacg aaccttctat agaagcttgc 300

taacccatgg aagctcctaa tatctcccac acttttgggg gtgggccatt cttggatggc 360

cttgatattc tcagggtcca cttggacccc atttctacca actaccaacc ctaagaaact 420

a 421

<210> 966
<211> 412
<212> DNA
<213> Glycine max

<400> 966

agcttgaaga gaatggaaga gggaggatat taaaacttga gatagcaaca tggaaagaaa 60

tgaaggtgtt tatgaggaag acattcttac caccttcttg tgagaaagat gcttatgaaa 120

ggcttcaaaa cctcacacaa ggtagcaaga gtcttgaaga gtaccatcaa gaaatgataa 180

tgactatgag gagagctaat tacaagagcc taaaacttcc atggcaaggt tcctatgtgg 240

gcttaataga gacattcaat gcattgtgaa gttgaagcac tatgaaagtt tggaggatat 300

ggtgcagaaa gccaagaaag tggagagaca acctgagagg aagcattcct acaagaagac 360

ctatcactat gacttttcta gtggtaaaga caagtccaag aaggagggat ct 412

<210> 967
<211> 361
<212> DNA
<213> Glycine max

<400> 967

tgccgcgaca cctaaattcg atgtacggca aatcctcatg cgggatcagt tggaacatgg 60

atgccagagt ggcaagggca tcggccatct aattctccac tctggggatg tggtgaaagg 120

atacatcatc aaagtactct atcagttttc taatgtaggc ctggtagggt atcaacttat 180

gatccctggt ctcctattct actttcaatt ggtggattac caaggctaag tccccatata 240

ccttgagcaa cttgaccttg aagtcaattt ccgcttggat cccaagggca tacgcctcat 300

attcagccat gttgttcgtg cagtcaaagc ccaacctagt cgtgaagggt atacattgat 360

c 361

<210> 968
<211> 403
<212> DNA
<213> Glycine max

<400> 968

agcttgacac aatttatctt tctcaaactt gagtttctga agaccaatta ctaagtcttt 60

cgtaactaga tgagttagat tatgcatatt agtatgtgca gtcctacaat gccacaacca 120

tgaatcatct attttactca ccaagcaact aagctcatga aaagatgcat gctcaatatt 180

cagcatatag atgttaccta ttctcttacc aaggtggaca actttaccgg atatggcttc 240

acttatcaga caacaatttt tgttgaattc aatcttgaca cctttatcac aaagttgact 300

aatgcttata agactatgct gtagtccatc cacatataac acattcttta tctgattttt 360

gaggtgatcc cctatatttc cttctcccat tatattacct ttg 403

<210> 969
<211> 377
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 969

tcaatttgct tggatagcaa cttgttatgt gccaacaatg catcatatga tgaaagttcc 60

agcacgcttc ttttggttgg gatgtccttc agcagtcttg gactctgtga agtatttctt 120

caagaatctt tcaaccactt catcccaagt cttaagacta ttacctttaa atgaatggag 180

ccatctttgt gcctctccag acatggaaaa tgaaaacaag ctcaatctaa cagcatcttc 240

atgcacgcca gccagtctga cagtgttgca aatttcaata taagtggcta gatgtgcata 300

caggtcttct tttggcagac catgaaacan attgttctta atcaactaaa ttaatgaatg 360

tggataggtt atatttt 377

<210> 970
<211> 412
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 970

tatgctgcaa acatttataa tagaccctct cagtagctta accaacaaca atataataat 60

tatgatcttt caagcaacag atataatcca ggttggaaga atcatccaaa tctgagatgg 120

gcaagtcttc cacaacaaca acagcctgtc cctcctttcc agaatgctgc tggttcaagc 180

aggccatatg ttcctcctcc aatgcagcag caacaacaac aacaaagaca acaagcagct 240

gaggcccctt ctcaaccttc cttagaggag ttagtgaggc aaatgatcat ccagaatatg 300

caattntagt aagagacaag agcctccatt cagactctga canattagat agggcagatg 360

gctacttagt tgaaccaagc tcagtcccaa aattctaaca aattgtcttc ac 412

<210> 971
<211> 404
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 971

agcttgttga tctcttcatg atgatcaaca caatattgca tttgctgctt caattttggg 60

ctgcagattt cataagcaat gcatttagta tgtttacttg gtaggtttaa attttcaata 120

aaagtaatta atttttttag aatttaattt tttatgcaag gtcaatgtga gttcttgtta 180

cacaaatgta attcatttta ttaccatatt acccaattca ttaatatgat gcagtgaatt 240

tgtattaaaa aaatatactt ttaattatat ataatataga agttttagca tttagcaact 300

cactctttaa cacattttta tataagaaat tntattatac gttaaaattt attanaaaat 360

ataaaagaaa aaagactcac aaaaattatg aattttaatt aatt 404

<210> 972
<211> 404
<212> DNA
<213> Glycine max

<400> 972

tataatatat tgatatgctc gaaactaaac atcggaagct ctcgagaaat tcaaatggtc 60

ataacttttc acacggatgt ccgattcggg tgcataatat gtcgagatgc gtcaaagttg 120

aacaacggaa gctctcgtga aattcaaatg gtcataactt ttcacactga tgtttgattc 180

aggcttataa tataacgata cgctcgtaat taaacatcgg aagctctcga gaaattcaat 240

tggtcatcac ttttcacacg gatgtccgat tcgggtgcaa aatatgtcga cacgctcgaa 300

attgaacaac ggaagctctc gagaaattca tatggtcata acttttcact cggatgtccg 360

attcaggcgt atcacatata cagacgctca caatttgaca acgg 404

<210> 973
<211> 398
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 973

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tcactggctt agctccatcc tctaaaagta tcctatgcat gcaggtagat gggctaatgc 120

caagaatgtt ttctaaagtc catccaatgg atttcttgtg cttcttgagc actagcagca 180

acttctcctc ttgctcagta gcaagggagg canagatgat cactgtanat tnttccttgt 240

cctcacagta agcatacttg aggtttactg ggaaggactt caactctggt gtgggtggtg 300

gctgaacagt gngaggaacc acngtaggag aagaagaaaa acgttctcgg cttgtacctc 360

ataaagcaag taagaagata tgtaccttct gcaacatg 398

<210> 974
<211> 365
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 974

tattgggcat taaagttttt gaacttcgat tcanatgcat ctagtgaaca caggaagctc 60

ccactccatg anatggaaga attgtggttt ccagcttatg agaattccca gctttataag 120

caaagaagta aaatttatca tgacaaaaaa gttgtcaaaa aagaaaattt tcagctttgg 180

tcaacaagta ttggtattta attatagatt aagattgttt ccaggtaatc tgaaatccaa 240

gtggttcgga ccattcatca tcaaagaagt tatgccacat ggagcagtga tattggagga 300

cccaactacc anaaggacat ggaccgtgaa tggaacataa taaacactag ttagatgata 360

tttca 365

<210> 975
<211> 380
<212> DNA
<213> Glycine max

<400> 975

tgtaagaatt gcaagatcat cttccttgac aactccttga taattattgc catcaatacg 60

cagagatgac aatttagaga gtgatccaat actttcaaat ggatttccac tgaatttatt 120

aatagacaga ttgagatatc ttaatgatga aagttttcca aatgatattg gaagagcacc 180

accaattaag ttgttggaaa aatctagcat gtcaatattt ttaaaagccc caatttgatc 240

tatcagattg cctgaaagtt gtgaactccg aactgcaagt gttgtgattc cctatgaaat 300

acaaggagca agaatttcta aaagttcatt aacctgttgg ttgagtttga gatatgataa 360

acctatcttc cttaagttgc 380

<210> 976
<211> 389
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 976

agctngctcc actatatttg gattggatca taaagtttgc acccctgaat caataacatt 60

ntgttcactc attgatggct tggccagaca tggcaaggtg aatgatgcct atatgcttta 120

tgaaaaaatg ttagattatg gtcagactcc aaatgcagtg ttgtatacat cccttattag 180

gtacttttttc tcgtgtggta ggaaggaaga tgctcacaaa atttataaag agatgatgta 240

taagggctgg tctcctattc cttgctcctt aataattaca tggattgtct tttcaaagct 300

ggtgaaattg agaaaggtat ggctctattt caagagataa agcctcaagg tctaacttct 360

gatgtaagac gtattcaatt tttattcat 389

<210> 977
<211> 409
<212> DNA
<213> Glycine max

<400> 977

agcttaaaga taaattaaga ataatgattg aatatcttat cttatattct gataatatat 60

tctatcaaat acaaactgat tagttaggct aaaaatactg atataatatc ttatcatata 120

ttctataact cgtaaattac cccacaaaaa ttatttactt cgaaatcttc tagctgaaat 180

ttcttggaca aatttccaaa ttcaattgta agcattatta tcacagtttc agataaaaca 240

aaaataacat tacctctcta ctcttataat ccatacaaaa attatcatat taaggctatg 300

caacttcttc tgaattcttt ttaaccactt gatcaagcat aattaaaata tccaatatcc 360

aatgtcaatg gataaaaaca tgtagaatgg gagtataatt ctacatgtt 409

<210> 978
<211> 333
<212> DNA
<213> Glycine max

<400> 978

tgtccaaaat gcagacaata ataattttta actcggatat tcaattgagt attgtaatat 60

atcgagacgc tcgtaatgga aaacagaagc tcgtataaaa tgcaaatcgc aataactttt 120

aactcggatg atcgagtggg tcccgtaata tatcgagaca cttgaaattg aaagcagaag 180

ctctgagcaa attcgaacga caataacttt tgactcggat atccgattga gtcatttaat 240

aattcgagac gctcacaact gaatacacaa gctctaagct tattcaaatg acaataactt 300

ttgactctga tgtccgattg aggcattata taa 333

<210> 979
<211> 305
<212> DNA
<213> Glycine max

<400> 979

agctattgta ttcaattttg atgcgtcttt aactattaaa tgactcaatc ggatatccga 60

gtcaaaagct attgtcgttt gaatttgctc agagcttctg cttgaaattc gagtgtcttg 120

atttattacg ggactctatc gatcatccga gttaaaagtt attgtctttt gaatttgctt 180

agagttactg ttttcaattt cgggcatctc gatatactac aggactcact tccacttttc 240

agtaaaaagt tattgccatt tgaattttgt gagagcttct atattcaatt tcgagcgtcc 300

tgaat 305

<210> 980
<211> 396
<212> DNA
<213> Glycine max

<400> 980

agcttgtgca tccaatacct tgatgaggat gtcccatatg ttcttaagac tggactgatt 60

catttgcttc caaagtttca tggccttgca ggtgacgacc cgcacaaaca tttgaaagaa 120

tgtcacattg tctgctccac catgaaaccc ccagatgtcc aagaggatca catatttctg 180

aaggcttttc ctcattcatt agagggagtg gcaaatgact ggctgtatta ccttgctcca 240

aggttcatca cgagctggga tgaccttaag aaagtattct tagaaaaatt tttccctgct 300

tccaggacca catccattag gaaggatatc taaggtataa gacaactcaa tggagagagc 360

cttgttgagt actgggagag attaagaaac tatgtg 396

<210> 981
<211> 240
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 981

agcttntcgg tatattatgc acctgaatca gacctccggg tgacaagtta tgaccatttg 60

aatttctcga gagcttccgt tgttcaattt cgagcgtctc gatatcttat gcgcttgaat 120

cggacctccg agcgaaaagt taagaccatt tgaattgctc aatagcttcc actattcaat 180

ttctagcgtc tcgatatatt atacgcctga atcggacctc cgagtgaaaa gttgtgacca 240

<210> 982
<211> 257
<212> DNA
<213> Glycine max

<400> 982

tctcgatata ttatgcgcct gattcagagt ttcgtgtgaa aagttatgac tcttggaatt 60

tctcgagagc ttccgatgtt ctatttcgag cgtctcgata tattatgcac ctgaatcgga 120

cttccttgtg acatgttatg accattttag gtactcccga gattctggtg ttcaatttca 180

cacttctcga tatattatgc ggctgaatca gacttccgtc tgaagagtta tgaccatttg 240

aatttatcgg gagcttt 257

<210> 983
<211> 302
<212> DNA
<213> Glycine max

<400> 983

agcttctcga tatattatgc gcctgaatct gactttctgt ttcagaagtt atgaccatat 60

gaatttctcc actgtattcc gtgtgacaag atatgaccat ttgaatttct cgatagcatt 120

cgttgttcaa tttcgagcgt ctcgatatat tatgcgcctg aatcggactt ccgtgtgaca 180

agctatgacc atttgaattt ggcgagagca tgcggtgata gatttcgagc ggctcgatat 240

attatgcgcc tgaatcagac attcgtgtga caagttatgc gcatttgaat ttctcgagag 300

ca 302

<210> 984
<211> 414
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 984

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cctactttta atggagaggg ttaccattac tggaaaaccc aaatgcaaat cttcattgag 120

gcaatagact taaacatttg ggaagccgta gaagtacggt cttatgtacc cactatggtg 180

gctggaaatg caacaataga aaaacctaca gaagagtgga ctgaagatga aagaagatta 240

gtgcagtaca atttaaaggc taaaaacatc attacttttg ccctaagaat ggatgaatat 300

tttagggttt caaattgtan gagtgctaag gatatgtggc acactttaca agttacacat 360

gagggcacaa ctgatgttaa acaatctang atacatactn taactcatga gtat 414

<210> 985
<211> 404
<212> DNA
<213> Glycine max

<400> 985

agcttcatgc ttaagtatgt atggcaaaat cttattactg ttgttcaaga catacaagtg 60

agcttgtaac aaatcttcta gacttggagt gatcacatgt agtcctcttg aacccttacc 120

acccactcag gaaggccaac aggtttagcc ttctcaatgt attttgaaca aaattcaatg 180

gcttcttctg caatgtacct ttcaacaata gatgcttctg gatgatatag attctttgta 240

taccctttta agatcttcat gtatcgctca accgggtaca tccaccgcaa ataaacagga 300

ccacaacatt tgatttctct taccagatgc acaatcaagt gaattgtgat gtcaaaaaaa 360

gcaggggga aaatacatct ccaactggca cagtataatt ggga 404

<210> 986
<211> 369
<212> DNA
<213> Glycine max

<400> 986

gttttagttt cagatgatgc ttatgggttt gtagctacct catgcactcc tctaatgact 60

atggcatgat ttctggcgct aaactgctag gagttggagg ccatcttctc aattaaattt 120

ctagcttcag caggagtcat gtctccaagg gctccaccac tggcagcatc tatcatactt 180

ctctccatat tactgagtcc ttcataaaaa tattggagaa gaagctgttc tgatatctga 240

tggtgggagc aactggcaca tagtttctta tatctctcct agtactcata caggctctct 300

ccactgagtt gtctaatacc tgagatatcc tttctgatgg ctgtggtcct cgaagcaggg 360

aaaaaattt 369

<210> 987
<211> 332
<212> DNA
<213> Glycine max

<400> 987

agcttggggg agccttgatg ctctcatagg gaggcttagg gctgcttatg aggaaaatgg 60

tgggtcccca gagactaacc cttttgcaag tggctccatc aaggtgtatc tcaaaaaggt 120

tagggagtgc caagccaagg caagaggtat cccttacaag aagaaaaaga aggcctcaaa 180

tcaaagcaag ggaaatgatg aatcatcctc caccatgcac ttctcttgaa caacatcttc 240

agtatcgatc cctttggacc tttcaagtca tggtaattaa ttaattaact aatcttgctt 300

gccatcacac tcatgatcat aaactatgct ta 332

<210> 988
<211> 412
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 988

gtaacccccc ttntaaatga taggcttaga atgcagatta agacgaagaa gaagaagaag 60

aagaagaaga agacgaagaa gcaatcaatt taacaatgtt cttttaaatg cgtaagatca 120

aattgattgc gataaaataa atgagataag ggaagagaga aatgcaaact caatttatac 180

tgggtcggcc acttctcgtg cctacgtcca gtcctcaatc aactcacttg atattttcac 240

taacttcgta aaaaaacctt tttacaactt ctgaacaccc aaggaatccc tttcccttgt 300

gttcangaaa ctcacaattc aagagacaac cagtctcttg attacaactt actttctgag 360

atgaatataa agatttctct cctttagagt ggataataca acttgatgtt ct 412

<210> 989
<211> 400
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 989

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ctcaagccag gagtaccttc acttctatac ctctcagtgg ctgacaaagt tgtaagctta 120

aaccttgtac aggaggacgg gaaacaccag cttcccatct attttaccag tcgtatcctt 180

catgatgctg aaaagtggta ccagatgata gagaaggtag tgctggcact cataacctca 240

gatcgacgcc tcaggttgta cttccaaagt caccaagtgg tagtcaagac aaactaccct 300

gtcaaacagg tgttgtgaaa gcctgaactg gaggaaatga tggtattatg gtcctaagtc 360

gacccaagct aggagtacct ttacttttat acctctcaat 400

<210> 990
<211> 335
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 990

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cgatctatgt gccgaanagg gtttaaaact acagggtggg ttaggctatt ttaattatat 120

gctatcttgc tattttgaat tttcttcgaa ttggtatttt tgttttgata tttgaaatag 180

ctcatctttg aagagtgata tgtacaaacc ccaatttgct gggtttgtag atgtggattt 240

ggccgcagat aagaacattt ttcttaagag tttggtatgt gaaaattcaa ttcatttggt 300

gcttatatat agccattatg agctcgaana tacta 335

<210> 991
<211> 316
<212> DNA
<213> Glycine max

<400> 991

gctacctgaa tgcccgcatc gagaattaat atgccaagag agatttttct gtctttgaag 60

aaggatgtgc ggctctcatc aatgaggacc tgtataacat gcctcagcct atttgctaat 120

aacttagcga tcaccttggg catacaccca atcaaagaaa tggggttgtg atcatcaaaa 180

gactgatggt gattaactgt gggaagtaaa gccaaaagag aaacattact gcctataggg 240

aatcttccat gcacaagaga atcatgtaca aatcttctgg agtcaattat taccactccc 300

cacaattact taatga 316

<210> 992
<211> 318
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 992

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aactcttgta aatgggagag aaatgttcat ctaaagcata caagtcccta atgttatcaa 120

atcctaaaat ttgagctcct atggagcaaa acaatgtgtg tctcctaaag agggcatcaa 180

ctacaacatt ttgttttccc tttttgtatt tgataacata tnggaaatgc tctangtact 240

ctacccattt tgcatgcctt ttgtttaact tgctttgcca tctaatgaac taaatgattg 300

atgatcacta tgaatgac 318

<210> 993
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 993

gaaaaatcta gtctttgtgg gtgtcgtgga tctaatttgt tttncttcct gtgttgaaaa 60

tggagctntg caaattagag gaaaaatgaa ctttatggta atgcaaagga ctaaagcaag 120

gaaagttgta catccttcta nggtccacta taacaggctc tatcttaact atttcacaag 180

ctgggagcca tgcgtccaat gataatttgt tgtgacatct gtgtctagcc cacatgagtg 240

aaaaaggact ggaaattatg agcaagcgag gcttacttgg aaatcacaat gtggaacctc 300

tttagttttg tgagcactat gtctatatga agcaacatcg aaagaaattc ccaaagggtt 360

tgtagactac caaagtcaca ttggactatt gccattctta ttgttggg 408

<210> 994
<211> 333
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 994

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caagttatga tcatttgaat ttctcgatag cttccgttgg ttaatttcga gcgtcttgat 120

atnatacgcg ctggaatccg acctacaagt gaaaagttaa gaccatttga atttctcaag 180

agcttccatt ggtcaattta acccgctcga tatttatgtg cctgaatcgg acctccgcgg 240

taaatgttat gacccttga atatctcgag agcttccatt gtcaattgcg accgtttcta 300

ttgtgatgcg cctgaaatgg accaccgagt aaa 333

<210> 995
<211> 326
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 995

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gtaaaaatta attgtcatta gaatttgctc agaagattta ttttcaatgt cgagcatctc 120

gatatattac gagactcaat cagacattcg agtaaaaagc tattgtcata agaattgcac 180

agagcttctc tttttaattn tgagtgtctc gatatattac gggactcaat cagatatccg 240

agttaatagt tattgccgtt tgcgtttgct acgagcttcc ggttcaatta ctagcggctc 300

gatatattat ggcactcaat tggaca 326

<210> 996
<211> 312
<212> DNA
<213> Glycine max

<400> 996

agcttatgct gcaaacatct acaacagacc tcctcaacct tatcagcaaa atcagccaca 60

acaaaataac tatgaccttt cctgcaacag gtacaatcct ggatggagga atcatcccaa 120

ccttagatgg tcgaatcctt cacaacatca acaacaacct tattttcaaa atgttgctgg 180

cccaagcaga ccatacgttc ctccaccaat ccaacaacaa caacaacaac agccccagaa 240

agaacaaaca gttgaggccc ctccacaacc ttcccttgaa gaacatgtga ggcaaatgac 300

tatgcaaaac at 312

<210> 997
<211> 167
<212> DNA
<213> Glycine max

<400> 997

tgcacccgaa tcagacataa gtgtgaaaag tcatgactat ttgaatttct cgagaggttc 60

gcgtgttgaa agcttagcgt ctatacatag aattaccctg atctggacct gagagagaat 120

agttgtgaac atgagaaatg gacgagagct tccgaggttc ttttata 167

<210> 998
<211> 361
<212> DNA
<213> Glycine max

<400> 998

aagctggaat catttatttt atctccgata gtctatgggt tatgtccgtc caggtagtgc 60

cgaagaatac tggcctcaca gtgatcataa atgagaagga ggagtttatt cctactcagg 120

tgcagaacag ttggagagtc tgcattgact attggaggct gaaccaggct accaaatagg 180

accatttctc cctgccattc attgaccaga tgcttgaacg cctggcaggt taatcccact 240

actgtgtcct gatgagtttc tggtatatgc aattactatt gctctgagat cacgaaagac 300

cacttacctg cccataggac tttgctataa gagatgcctt ctgctggcat gcccctgtcc 360

t 361

<210> 999
<211> 356
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 999

tcgaatgggc atcgtttcat cttatttgcc aatgatatct ttaccaaagg gtggaaaccg 60

gcctcatatg ctaacctgac taagaatgtg gtggttagaa ttcatcagaa ggagataatt 120

tgcagatatg ggttacccaa aaagataatc accaataatg ccaccaattt gaacaacaaa 180

atgatgaacg agatgtgtga gggattcaag aaccaacacc ataattcgac gccttatcgg 240

cccaagatga atggggcagt tgaggcttgc caataaaata tcaagaagat tattcagaag 300

atgacaatgt catacanaga atggcatgaa atgctacccg tcgcattaca tggtta 356

<210> 1000
<211> 387
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1000

agctntntgt tgtttttgaa aaatttattc cagacttcgg ataaacttta atttatggct 60

aattcaagac caacttttg atatatttct tgctaggact atccctaatc ctagggataa 120

ttagtaggac caaataaatg gaggttgtcg aattatacca catgatttca gcaacaacaa 180

aagttgcaat aaagacaaca atgatatttt ttttattgca ataaagacaa caatgatatt 240

tatggacatt atcaatgttt cccatgtgta atcctttata taaaccttga gctggtcaca 300

cagtaagatg aaagagaccc cgntaatata ttatctaaca ttctgcaatg atgataaact 360

atttctcttc ttcttcaaaa aaaaaaa 387

<210> 1001
<211> 338
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1001

ntgatgttat ttttttatgc atcgctntga ttttntgttt taatgttngt gctagtccaa 60

attttttttt aataattttc ttttaataaa actcatttca tgatattttg caaagtgatg 120

catatcaagc tattggctac taaaatttct tacctcaatg attattcaag tcaatagtga 180

aatagcaatg ggtgcaacca tttccccaat tctgcatacc gaaactccca gttcaatatt 240

agtgtactta tctggaagga taatcccaag aatcttccta gtgattaatc tgcaaatgga 300

aaccagcctt taagcatctg gggtctcatc tcattatt 338

<210> 1002
<211> 360
<212> DNA
<213> Glycine max

<400> 1002

agcttagcta agccaaagtc agagatcttg gcattcagat ccttgtcaag taagacattg 60

gttgccttaa tgtccctgtg tactattttc aaccttgact cctcatgaag ataagccaat 120

ccccttgcta tccccacaca gatcttcatt cttgtgggcc aatacaagtg cagcttctgt 180

tcatgttcac ctacgggaaa tgcgggggga aaggaaataa gctttttctg ttatatattg 240

attttgaagc agaaacatac acacacaaac acaaggtata tgttgcccgt aaagcattta 300

ccgaaaagtg cacgagcaag actggtggtc tccatgtatt catatataag tagcaactgg 360

<210> 1003
<211> 222
<212> DNA
<213> Glycine max

<400> 1003

agcttgacca ggaattattt gtatgggttg gatgttgaat tccggttgtt cctggtgcgg 60

agatgatggt acagcgggtg aaccaaaagc ggaagtttct tttggtgagg tagccatgga 120

aaagcagagc gtttggaatg atttcgtaaa tctcagaagg ctattgggaa atgctggtaa 180

aaacacgaat gccaagcaga tataaatttg aatgaaaaat gt 222

<210> 1004
<211> 296
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1004

agcttctatg atccgtcaaa atttcaatgt ggtgccccaa taggtattgc ctccacttct 60

taacagcagt ggtaatggca gctagttcac gaacataggt gaaggagctg agtaacttat 120

ggcaaaactg tttgctaaag aaagctatta agtgtcttcc tttgtgacaa cactgtgccc 180

attcctgagt cggaggcgcc tgtttccacc acgaagggtt tggtgaaatc aggaagtgct 240

aatactggng aattattcac gacattcttc aagttttgga aggcaactgt agcttc 296

<210> 1005
<211> 279
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1005

agcttcagag tgatgctntg cgtgaagcca tttcangaat catggcttat tcccaggaga 60

agaatcgcaa atttgtggag accatcgaac tccaaatcgg gttgaaaaac tacgatccac 120

agaaagacaa gcgtttcaag ggctctgtca agctgcccca cattcctcgc cccaagatga 180

aaatttgcat gcttggtgat gctcancatg ttgaagaggt ctctatttgc catattcatc 240

aagactctta atggatcata actatttcat gataattag 279

<210> 1006
<211> 386
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1006

tcaaacttgc aacaaaggag ttgagcaggt aaaaaagatt cgtcttcaaa ctcttagagg 60

tgactntgag cgtttgttta tggaggaatc cgagtcaatt tctgaatatt tttctcgagt 120

attggccgta gtcaatcaac ttaaaaaaaa tggtgaaaat gttgatgagg tgaaggtcat 180

ggaaaaatac ttcgaacttt aaatccaagt tttgacttca ttgtaccaac attgaaaaaa 240

caaggattaa agaccatgac tattgagcaa ctcatgggtt ccttacaagc atacgaagag 300

naataaaaga gaaaaattaa acaaaatgag gctactgagc aactactaca actcaacgta 360

agggagcaaa ctatgcaaat tacaag 386

<210> 1007
<211> 274
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1007

tactcaagct tctttcgaat tcaaactgcc ataactttct gctcggatgt ttgattgcag 60

accataatat ttcaagatgc tcaaaattgg agatggaagt cccagataaa ttcaaactgc 120

cacaactttt gactaggatg tctgactgcg gcccatcata taacgagacc ctcngaaatg 180

attatggaag ctccgagcan attcaaattg tcataacttt tgaatcggat gtctgactac 240

agaccatact atatcgagaa actcgaaatg aaca 274

<210> 1008
<211> 371
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1008

cgggatcctt aagcacctga gctgcagctt atgcttatta tgtatggcaa aacttcatta 60

ttggtggtca agacatacaa gtgagcttgt aaaaaatctt ctacacttga agtgatcaca 120

tgcaatcctc ttgaaccctt accacccact ctgtcatcat gccgagactt angaaggcca 180

acaggtttag ccttctcaat ttattctgaa caaaattcaa tggcttcttt agcaatgtac 240

ctctcaacaa tagatgcttc tggatgataa agattctttg tataccctt caagatcatc 300

atgtatcgct caaccgggta catccaccat atgataacag gaccacaaca tttgatttct 360

ctgactagat g 371

<210> 1009
<211> 377
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1009

agcttggggg agccttgatg ctctcatatg gaggcttang gctgcttatg aggaaaatgg 60

tgggtcccca gagactaacc cttttgcaag gggcttcatc aaggtgtatc tcaaagaggt 120

tagggagtgc caagccaagg caaagaggta tcccttacaa gaagaaaaag aaggcctcaa 180

atcanagcaa gggaaatgat gaatcatcct ccaccatgca cttctcttga acaacatctt 240

cagtatcgat ccctttggac ctttcaagtc atggtaatta attaattaac taatcttgct 300

tgccatcaca ctcatgatca taaactatgc ttaactagga tgattaactc aatgcggtgc 360

taggatctag ttttttt 377

<210> 1010
<211> 314
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1010

agctggctta aagacgtctt tgatcaatta attattntan aacctagtga aatattaact 60

aaaaaaagaa acttataaaa tttagtatga gtaatgtaca aatccaaaaa taattgataa 120

acaaaatcat attaaattca agtcattaaa acacaaagta tataaaaaaa atgaacaaaa 180

gagagcataa tattaaaaaa tacatacaaa gacaaggaat gactntaact angatgggta 240

agactatttg gtgtagatac aagaacttag agaaagaaaa tgaattaaaa gagtgagaat 300

gcanagggat gtgt 314

<210> 1011
<211> 258
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1011

cactaagcaa tcactacgca tagctctcaa ctcgaaggtg gaagacacat gaacgataac 60

gcaattcatg gggctccgaa atgatngaga atggagaatg gcactaagca atcactacgc 120

atagcttcaa aatggaaggt ggaggacaca tgaacgaaaa cgcaattcat ggggctccga 180

anaaggttga gaatggagaa ttgcactaag caatcactac gcatagctcc aaactcgaag 240

gtggaggaca catgaatg 258

<210> 1012
<211> 439
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1012

agcttggtca ctctaatgtt tggggaccaa catctgtatc ataagttggt gggaaacaat 60

actttgtgac ttttgtagaa ggtataagtt tactttctaa aacacaagtc aaaattattt 120

aaggctttta agatctaaaa agccatggtt gaaaatgaga cagggttgaa gatcaaaacg 180

ctcaaaactg acaatggtgg taaatatgaa gacacaaaat ttaagaggtt ctgctataag 240

tatggaatca aaatgaaaag gatngtatca cgtactcctc aacaaaatgg tgaagctaag 300

catgtgaaca gagaacattg acctaaagaa acagcctcag aagtgaagtg ttgaggagca 360

acnaaaagct cggcacgagc ccgagcttgg cttaaagaaa cagccttagc aacaacattc 420

ctattgcggc atctggtgg 439

<210> 1013
<211> 289
<212> DNA
<213> Glycine max

<400> 1013

agcttgtgag caattcaaat ggtcataact ttacactcgg tggtccgatt catgcgcata 60

atatctcgaa atgctcgaaa ttctacattg gacgctcttg agcaatatat atggccataa 120

ctattcactg ggacgtgcga ttcaagcgca taatatatcg agatgctcca aattgaacaa 180

cacaagctct cgagaaattc agacggtcat aacgtttcac tcagaggtcg gattcaggcg 240

cctaatatat cgagacactc agaattgaac aacgaaagct ctcgagaaa 289

<210> 1014
<211> 429
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1014

agcttataaa attntccaac cgcanatgga aaaagtagtg ttagcaggga tgttcactnt 60

gtggaagatg aagaatggaa ttgggataat ccaaggatga taaatcaagc ccctggacat 120

ttgaacttaa actttcctgc accaagttca aaaaattggc aagatgagct tgttgatgat 180

gttctagtaa gaggtactag acttctctct gatatttatg acaggtgcaa tattgttgta 240

tgtgaacctg aaaactatga agaagccaag aaaaatcaaa tttgggttgc tgcaatgaag 300

gaggagctct caatgataga gaaaaatcaa acttggcatc ttgtagaaag aacctcagac 360

aggaatgtga ttggagtcaa atgggtatat agaactaagc ttaatgctga tgggtctatt 420

aataaacat 429

<210> 1015
<211> 452
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1015

agctntgtag agattgttcc aactcccaac aagctataac agcttccatg gcatgaacac 60

ggacatgttg ttgcaattgt tctttgaaag cacagagcag tataacataa tgcgtctaca 120

acgaaaataa gagcaaaact tgtaaattaa ggagcatcat gtgaaataat tgagcccatt 180

gtcctgaaaa ctaaattcaa tcatgggaat tcatgaaaat tagagaaatt ctaacaataa 240

aaacacaatt ttagtgaatt cacctctcat ttaatgagtt ttcttaattn tatagttntc 300

aatggattnn taattattga tcaaatattg ccttgctagc cgtcctttta agaatatcca 360

aaccaacatt cagaagaaag gaactggagt atatgatnaa cagataacca tgagtgctaa 420

cttaacaata atctttatct attttttttt tt 452

<210> 1016
<211> 429
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1016

gctataccct accgggatga aaaagcttta atagaagtca agagcatgaa agtgtaacga 60

taccgttaac tagccagtag gttcttgggc gggttgagga catcaatagt atatttggaa 120

agaccaaaaa gaaggaaaaa aagtaaaact tggatatgga agaagaggtc gatattgttt 180

gatcttccat aatggtttga tctaggtgcc tgacattgta ttgatgttat gcatgtggag 240

aaaaatgtgt gtaatagtgt catcgacatg ttttttaaca ttcaaggaaa gacaaaggat 300

agtttgaata ctcgtcaaga tctagttgag atgggtgcat cctctagctt gtcatactnt 360

gtccagaana gagaagataa gtttttgtta gtgtctgtaa catgtgaaag tgtcacaagg 420

atactcttc 429

<210> 1017
<211> 156
<212> DNA
<213> Glycine max

<400> 1017

agcttcttct caataggatc atagaacctg tgactaaatt cattctcacc ataaccaatg 60

aagataccac tgccttgact ttgcatccaa cttggatctc ttatcctttg gaacatgcac 120

aaaagccttg cagccaaaaa ctcaaaagtg atcaca 156

<210> 1018
<211> 286
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1018

atggcttatt ccttatgcgc ctgaatcgaa catccgagtg aaaagttatg accattctaa 60

tttctcgata tcttccgttg atcaatatcg agcgtctcga tatgtgatgt tcctgaatcg 120

gaccttcgng tgaaaagtta tgagcatttg aatttctcga gagcttacgt tgtgcaatta 180

cgagagtctc gacatgtgat gtgcctgaat ccgaccaccg tgtgcatagt atgaccattt 240

gatattctcg agagcttctc gccgttcaat tgcgagggtc tcgata 286

<210> 1019
<211> 387
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1019

agctggcact aagaattctg attcaagttc ctaatgtatc gagacattgg ttattgaaca 60

atggaaactc ccgagaaatt aaaatcgtca ttacttttca ctcggatgtc cgattcaggc 120

acttcagata tcgagacgct cgaaattgaa caacggaagc tctcgagaat ttaagatggt 180

cattacttta cacatggagg tncgattcat aaacatcaca tgtcgagatg ctcgaaattg 240

aacaacggaa gctgaagaga atttcagatg gtcataactt ttcacttgga tgtccgattc 300

aggcgcatca tatatcgagg cgttggttat tgaataattg aaactctcca gaaaataaaa 360

tggtaataac tttcactcgg attccga 387

<210> 1020
<211> 384
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1020

agctnttcct ctagttgctc tggtaaggtt tccaaatgtt agagaatgaa aagagattga 60

agccttcatt ntgtactgtc ttcgtgcgat tcacttttct ctcttgataa atagtatttc 120

gtaaatccca acggtagaag tgtttacaat tgaatcggga accaggtgtc caaatttcat 180

gacgatccaa tggttaatga ttccgggatc gtagttttac tggacaggtt ttgagtctcc 240

gtgggaaaag agaaagctac aatgcaaagg agatttctct tagctccgac attctttcgc 300

aatttctgat ggngagaatg ctcggaactg agttgaaatc agtgctgaat atacaacgat 360

ccacggttaa aagttgagat cgtg 384

<210> 1021
<211> 406
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1021

ntataattga attgtgaata tttgattgga atcattctat ttagaaattg atttaagtaa 60

aatatgtaat tcaattaagt tgatttataa aagttagtaa tataaaagag aaatattnta 120

ctcaaaaaaa ggaaaatatt ctttgaatta aggttaatat ataatacttt aattgttatt 180

attattntat ttattaaatt attaacatgt aatcaattaa tatttattta atgttaatac 240

taatagtaat agtaacatat tattctgatt ggaatttatt tttaattatt ttaattatta 300

ttgaatcaaa taatctaaca taatgattca acatctaaaa aataatgagt tttgtataat 360

aatngatatt atatataaca attcattaaa tattaatata cacata 406

<210> 1022
<211> 439
<212> DNA
<213> Glycine max

<400> 1022

agcttctaaa ctttgtacaa gaatgaagct ctgttaccac ttgttggaca agtggcctca 60

gatatcttaa gaaggggaag ttgaattaag atattacaaa ttattttccc aattaaaaat 120

tctatttaac tttctattca agttattaat tcccttaata atgaatttct taaatattga 180

ttcaaataga acaatttgaa tatgaatata aaacaataat aaatgaagga gtttaaggaa 240

agagaaagtg caaactcaga tttatactgg ttcggccaca cccttgtgcc tacgtccagt 300

ccccaagcat cccgcttgag agttccacta tcttgtaaat tccttttaca agttctaaac 360

acacaaggac aatccttcct ttgtgtttag aattctttca caacaagaga ccctcggtct 420

cttaatccct tttcagaat 439

<210> 1023
<211> 271
<212> DNA
<213> Glycine max

<400> 1023

agcttccatc aagttatgac catttgaatt tctctgagat cttccgggtt caatttccgg 60

cgtctccata tgtcatgtgc ctgaatcgga ccttcgtaag aaatattatg accatttgaa 120

cttctctaga gcttccgttg tttaatttcg agcttctcga tatctgatgt gcctgaatcg 180

gacatccgag tgaaaaggtg ggacaatttc aatttctcca gagcttcccg tgttcaatat 240

tgagcgtctc gatatgtgat ggtcctgaat c 271

<210> 1024
<211> 403
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1024

agcttagctc caaactctnt gggtggagga tgaatgaaca gcgcttggca atgacattca 60

tgggtctccg aataaaagtg gagaatggag aattggcgta tagagctagg caatcacatt 120

cgcggngctc cagactcgaa ggtggaagac acatgaacag cgctaggcaa tgaccttcat 180

ggggctccga aaaaaagtgg agaatggagg attgcactat agggtccaca cttaggcaat 240

catgaagcat agctcaaaac acgaaggtgg aggacacatg aacagcgcta ggcaatgaca 300

ttcatggggc tccgaataaa agtggagaat ggagaattgg cgaacagcgc taggcattga 360

cattcgtggg gctccacact cgaaggtgga ggacacatga aca 403

<210> 1025
<211> 404
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1025

gtggcattag agcacaagag cttcaagtag gtgctcctta aacctccatt aattnttttt 60

ctttaccttc tcttccattg ntgtttcttc atttttctcc atgtatctcc tcacatgtct 120

tgttctaaat gttgttaaca tgattcttta gagtttccac cgattaaact tgctatagaa 180

gctagatttg attttctatg gttcaaattt cttgttcttg ttcttgaacc atgaattgtg 240

ttgagtttaa gttcctttga gtcttgtctt ggtatatctt gtggctgatg ttagtgtttg 300

gctctactga gctntaaaag aatggctaag aatttgttaa acataagcac ttagacaatg 360

aaggaaagct ggagttgctg cacatgatgt ccaacgttat gtca 404

<210> 1026
<211> 355
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1026

ggctgaaagt cggaaatnta ttntattaaa tcataaatgt tttgtaaaat tatatattga 60

agtagctaaa aaatgtaata ttacataatg ggcatatnta tgtaatgatt tatacaaatt 120

nntaattgat tnntgtgaca aaatatattt tgtagtattt ataattttgg tattaaatta 180

attttaaaca cttgtagctt tttatttata aaatatccaa agaataaaca aaaactacat 240

aaacttatta tatatcatta tcactatcat atngttnttt tatanattca atatcatata 300

taataaaagg gtaaaatgag taatcatata tatgtaaaaa ggataaaata ataag 355

<210> 1027
<211> 425
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1027

cgcttggtaa aatagagaat ggatccatct catttgagat attcacatgt gaagagagca 60

tcctatctaa gatatttgtt tcattctgcc atatgaatat atcatgtgaa agtctatata 120

tgatcaatta ccggtcaaat atttgaagcc aaaaaaagag aaagggaaat ggtaacaata 180

acgcacctca atttgatcaa atgaccttaa tcttctaaaa caaggagaat ggctaatttc 240

ataatttgtg tgcaggttgc taaagaaagt gcagatgtca taattctgga tgataatttc 300

tccacgatag tgacagtagc caaatgggga cgttcagttt acataaatat tcaaaaattc 360

gtacagttcc agcttactgt aaatgtgngt gcattactgg tgaactnctc atcagcatgc 420

atgac 425

<210> 1028
<211> 284
<212> DNA

<213> Glycine max

<400> 1028

taagcttggg ttttcaactg caagtccagg tggtatttgc atatacactt cttcttcaag 60

ctctccatgg aggaacgcat tgttgacatc caattgtcgc aagtgccatt gattttgcgc 120

agccaatgcc agaagaacac caaccgtagt gagttttgcc accggagaga atgtgtcgag 180

gtaatctaac ccctccatct gagtgtaacc cttggcgacc aagcgtgctt tatacctttc 240

tatggaacca tcagcccgat atttaatctt gtaaattcat ctgc 284

<210> 1029
<211> 309
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1029

ggagattcgg tcctatggtt gctaatggag gagttggaat ggatgatgga gggatgtcat 60

ctgctctagc ccattttctt gatgccatct gtaactaaaa agaactcaaa attccttaga 120

ccaaatttat tcaagtttaa aaatagaaat aaaggctgaa attaatgatg gctgatgcaa 180

tcctactccg caagggcatt ggatagaagg ctctaagaag aatgggccag agatgcaaga 240

gaagacctta nggttcccat gagccttatg gtagattntg ggcaaatggg ctaagtatga 300

gcccgctta 309

<210> 1030
<211> 284
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1030

actcggatgt ctgattgagt cccgtaatat atcgagacgc tcgaaattga ataccgaagc 60

gctgagcaaa ttcaaacgac aataaccttt tactcggatg tctgattgag tcccgtaata 120

tatcgaaaag ctcgaaatcg aatgttgaag ctctgagcaa attcaaacga caataacttt 180

ntactcggat gtctgattga gtcccgtaat atatcgagac gctcgaaagt gaatgtcgaa 240

gctctgagca aattcatacg acaataactt tntactcgga tgtc 284

<210> 1031
<211> 418
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1031

agcttgcctt acctgcaaag tctttggcta aatgttatta aaacaacagg ctggcgtcca 60

ccaccatact caatttctcc acttgattct tgtgctattt gtcttatatg ttgcaaggcc 120

tgcatagtta atttcacaat tgtcactcac taagttttga aaaagttaaa catatctaat 180

tcatttaaca agcaactaat taatcttaca acaattgtca acttttgagt caagaattct 240

gatgattcat acagaagcct gagtacttca agtacactct agagcttcat tcaataagtc 300

aaacaattga gggactatag gtctacaata tnaaattcac aaaatgactt ggatatatat 360

tacacatcta aatcaatatg catttaacaa gtactagtta tttagttctc ttcaattc 418

<210> 1032
<211> 373
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1032

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anggaagaat ttctccatga acaccctctt aaggtcattc cagctgaaaa tggacctang 120

agcaaggtag tatagccaat cttttgtcac tccctctaga gaatgaggaa aatcctttag 180

aaagatatga tcttcctgga cattangggg cttcatggtg gaacananna tatggaactc 240

cttaagatgc ttataaggat cttcacctgc aagaccacga aacttgngca gcanatgtat 300

tagtccagtc ttgagaacat atggaacacc ctcatcanga tattgaatgc acaagctttc 360

ataagtgaaa tca 373

<210> 1033
<211> 449
<212> DNA
<213> Glycine max

<400> 1033

tatgaggaga agcataagaa gaagcaagag atcaccaagc tactctttaa gttgctactg 60

aaggagaagg aagaaagtca atgaaatgaa agaagtcatt gacgccgagg tagaggttga 120

ggtcacggtc gacgatacgt tggaggtggc aatagtgtac gaggttcaaa tttcatcaac 180

aatagttacg agaaatgaaa tagctcaaga gaatgtggaa aaggctatac aagcacaagg 240

catgataaat ctcaaactcg atgttataaa tgtcaaaaga ttggccacta tgcttcaaaa 300

tgtagattcg ccaataatag agttgaggag gagactaact atgtggagca aaatgatgag 360

aagtttcaaa tagtgctcct agagtgtgga ataatgaacg tagccaaaaa acacatggta 420

ccttgacact agtgcaaaca accttatgt 449

<210> 1034
<211> 457
<212> DNA
<213> Glycine max

<400> 1034

agcttatgct gcaaacatct acaacagacc tcctcaacct tatcagcaaa atcagccaca 60

acagaataat taagacctct ccagcaacag gtacaatccc ggatggagga atcatcccaa 120

ccttagatgg tcgaatcctt cacaacagca gcagcaacaa caacagactt attttcaaaa 180

tgttgttggc ccaagcagac cacacgttcc tccaccaatc cagcagcaac aatagcaaca 240

gccctagaaa cagcaaatag ttgaggcccc tccgcaacct tcccttgaag aacttgtgag 300

gcaaatgact atgcaaaaca tgcagtttca gcaagagacc agagcctcca tttagagctt 360

aactaatcag atgggacagt tggctacaca gttaaatcaa caatagtccc agaattatga 420

tagattacct tctcaatctg tccagaatcc caaaaat 457

<210> 1035
<211> 345
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1035

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agagagcacg aaatgaagag ccaatggttg atacatggac ggagatgaaa aaaatcatga 120

ggaagcggta tgtgccggct agttactcaa gggacttgaa attcaagctc caaaaactaa 180

cccaaggcaa caaggggtt gaggagtatt tcaaggaaat ggatgtgctc atgattctgg 240

caaatattga acaacatgag gaggtaacta tggctcgatt tcttaatggt ttgactaatg 300

atatccgtga tattgntgag ctgcaagagt ttgttgaaat ggatg 345

<210> 1036
<211> 269
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1036

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ctatacaaga catcttgcca aacaaagtca ggttagccat aactcgcctg tgttttttct 120

tccatgccat atgtagcaaa gtcgttgatc ctaccaagtt tgatgagctg gaaaatgagg 180

ccgcaattat actgcgccag ttagagatgt attttccctc tgccttcttt gacatcatga 240

ttcacttgat tgtgcatctc gacagacaa 269

<210> 1037
<211> 416
<212> DNA
<213> Glycine max

<400> 1037

agctttcttc aatcgacgat acgggtgata tgctgtcaaa tttcttcggt gtctactata 60

tgctgatttc tttccatgtt tcagttggat gaagctggtg tttgtctcac atacagggca 120

tgcataatgt cctttcacac tatatccact taaattttca tatgttggaa agtcattaat 180

agtacaaaac accattgcgc gtaacctgaa gatctactac aaatttgcat cccacacatc 240

aactccatct tcccacaatt ttgtcaagtc ttcaatcaac agactgagat acacatcaat 300

atcattccta ggttgccttg gacccgctat cattagacaa aacataatgt attttcgctt 360

gatgcacaac caaggaggga gattgtaaat catcatcata acacgccatg aactat 416

<210> 1038
<211> 448
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1038

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caccatctca tttgctacaa gtacactatc atgcatgtgt ctccccccca acccacccca 120

caattgcact ctgcttatca tcaataattt tttcaagcac catctccatc cttttggcaa 180

acactttgga tataattttg taaacacacc caatcaagga tatatgccga aactccacaa 240

gctcttgtgc gttgtctctt tttggtatca aagcaatgaa ggaggaatta ccacctcttg 300

gaatagcatc attctcccaa aattcatgca tcatactcaa tactcctagt attaacagtt 360

cccaacatct tttaatattt attgataatc taacgaactc attaaattaa atcatcttat 420

ttaacccatc taattgtaaa taataata 448

<210> 1039
<211> 458
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1039

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cgctctataa cagcagtagn tatagcttta agtattgaat tattaaagcg tctctggtgt 120

tcaaaaagac caattcttgc atcagtatga tacttataat taagtataag aagcagtggt 180

taacttatat agaataatcg aaaaaactct ttctctctga accctgctgg aatctgtatt 240

tgtgagttgt tattcacaat ttgattatga tactatgcta gaattatata tagagttaac 300

caagtttgct tcataaaata tattatatac aatcagaaat tttggctgat gcatgattat 360

tcgcctaatt atattattta tgtaactatg ttttctcttt atgtttgtta caacattacc 420

taattgattt tatacttttc ttttttatgg ttcatata 458

<210> 1040
<211> 418
<212> DNA
<213> Glycine max

<400> 1040

ctgcagctag cagatataat ttttagatgg aatatacttt aacataattt atgcaggtat 60

ccatcacaat ccagaagaac attgatgctt ctattaaaga tctagaagtt caagttggac 120

aactgtaaaa atagctatct gaacatggaa gtggatcttt ctcagcaacc acacaggtca 180

accaatatga acattgtaat ttaattacaa caaggtgggg gactgtggtt ggtttgaagg 240

ataataatga gaaaaagaat aaagaatgag ttgaaaagga aaacgagaaa aatgatgatg 300

tggtgactag tgaaaaagtg gtaagtgaag aagacagaag acatctatga acaaccacta 360

ataaaagtga tctatagtaa atcatccacc attgagcatc tttcttatcc acatgctc 418

<210> 1041
<211> 294
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1041

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ctctcgcaga ttcccatccc acatatctac cctgtgttcc caatttttg tcaagtcttc 120

tatcaacaga gtcaagtaga cgtcaatatc attccctgga tgtcttagat ccgctatcat 180

catgcacagc attatgtact tttgcttcat gcacaacgaa ngaggaaggt tgtaaatcat 240

tatcaaaaca ggccatgaac tgtgattgct gcttaagtta ccaaatggat tcat 294

<210> 1042
<211> 424
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1042

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tggggatcat ctagagtgaa aactcatggt ggaagctcat actttctcac tatcatagat 120

gatttctcaa gaagagtatg gttgtatgtt ttgaaaaata agtcaaaagt ttttcaaaaa 180

ttcagagaat ggcatactct agttggaaat caacttggta caaaattaaa agttttaaga 240

actgacaatg gcctagagtt tttttcagag cagttcaatg agttttacag gaaaataggc 300

atcaaaaggc ataaaatagt ccctcacact ccacaacaga atggcttggc agaaagaatg 360

aatatgacca ttntggaaag agtgaggtgc atgcttctaa gtgtacgact gccaaagacc 420

tttt 424

<210> 1043
<211> 362
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1043

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tctgaaaccc atcaaacact aaaaccccct cgtcccaaaa ctttctcaag tcttcaatca 120

acggacttag ataaacatca atgtcatttc ctgattgtct tgggcccaat atcatcatag 180

acaacatcat gtantttttgc ttcatgcaca accaaggagg caaattggta attactagca 240

aaactggcca tgaactgtgt tgagtgctta aactgtcata tggattcatt ccatcactag 300

ctagtccaag cctaagattt cttgcctctt agccgaaatc cggatacana ctatcaatct 360

tc 362

<210> 1044
<211> 415
<212> DNA
<213> Glycine max

<400> 1044

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agaagaatgt ggcatttaac tggggtgaaa aaccagagca cgcctttgct ttgcttaaag 120

aaaagcttac taaggcacct gttctagctc tgtctaactt ttctaaaact tttgagctag 180

aatgtgatgc ctctggagtg ggagtcggag ctgttttgct gccaggaggg caccctattg 240

cttattttag tgaaaaactt catggtgcga cccttaacta caccacctat gataaagagc 300

tttatgcctt aataagagca ctccgaactt gggaacatta ccttgtttcc aatgaaatgg 360

tcattcatag tgatcaacaa tcacttaagt tcattagacg gcccatcaag ttaaa 415

<210> 1045
<211> 292
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 1045

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ttgttcaatg gcgagcaccn cgacacgaga tgcgctctaa tcggacatcc gtgtgaaaag 120

cnatgaccac ncgagagtct cgagagcttc cgtggttcaa tttcnagcat ctggtcatat 180

tatgtgcccg aatctgacct tcgngngaaa aaggatgacc atttgaattt ctcgagagcc 240

tccgatgttt aatttcgagc gcctcaatat attgtaggcc cgcctcggag ct 292

<210> 1046
<211> 427
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1046

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ctcagggagt tatgccaggg accaagggta caggtggctt cggtttcttt attntatcca 120

ccaaaatagc ttgagtagtt agaatgacac cagcaacaga aactgcactt tgaagagcac 180

atcttgcaac acgactagga tccgctactc cagcattcaa aagatcttca tacgtgcctg 240

tcattgcatt atatccagtt ctccaatcat gtgttctagt cttccggaca acaatgtctc 300

catcaactcc ggcattagtt gcaattgatt ttgcaggttc aaggagtgcc tgcaacgatt 360

catgtgcaac cgcttacata tgttaaaagc actccagagt ccagacaaag tcatacttca 420

tatggaa 427

<210> 1047
<211> 416
<212> DNA
<213> Glycine max

<400> 1047

agcttatgca gcaaatatat acaatagacc ttctcaacct cagcagcaaa atcaaccaca 60

gcagagcaat tatgaccttt ccagcaacag atacaaccct ggatggagga atcaccctaa 120

cctcagatgg tccagccctc agcaacaaca acagcagcct gctccttcct tccaaaatgc 180

tgctggccca agcaaaccat acattcctcc accaatccaa caacagcaac aaccccagaa 240

acagccaata gttgaggccc ctccacaacc ttccctcgaa gaacttgtga ggcaaatgac 300

tatgcagaac atgcagtttc agcaagagac cagagcctcc attcagagct taaccaatca 360

gatgggacaa ttggctaccc aattgaatca acaacagtcc cagaattctg acaagc 416

<210> 1048
<211> 446
<212> DNA
<213> Glycine max

<400> 1048

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aaagttatta taatacactg aagctccatt aaaaactgaa ccatgagtac ataattatta 120

tactacattg cagctgcatt aaacatgtta ttgttattta atttcaggac ctaaaggacc 180

ccttccctta tttttgagaa aactagctta atataatcta cttctataat taactaagga 240

gttgagagaa gctaacccaa aaacgcaata tcaccttctt atgtttgttc acaaagttca 300

attagagaat cttgataaag agaatagtat ataatcacta attaatagta aatattatag 360

aggttcaaac ctagttccag ctttcacaat gattgcgagg gtttcccaaa agcaagcagt 420

agacaagatg gcttcaactt atgata 446

<210> 1049
<211> 487
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1049

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ataatttatt gtcgtttgaa ttggctcaga gcttcaacat tcaatttcga gcgtctcgat 120

atatgacagg actcaatcag acatccgagt aaaaagttat tgtcgtttga attagcttag 180

agcttcaaca atcaatttcg agcgtctcga tatatcacgg gactcattca gacatccgag 240

taaaaagtta ttgtcgtttg aattagctca gagcttcaac attcaatttc gagcgtctcg 300

atatgtgacg ggactcaatc agacatccga gtaaaaagtt attgtcgttt gaattggctc 360

agagattcaa cattcaattt cgagcgtctc gatatatgac gggcctcaat cagacatccg 420

agtataaagt tattgtcgtt tgaatnggct cagagcttca ccattcaatt tcgagcgtct 480

cgatata 487

<210> 1050
<211> 431
<212> DNA
<213> Glycine max

<400> 1050

agcttcttag tttcagatga tgcagatgag tttgtggcta cctcatgcac tcctctaatg 60

actatagcct catttatggc gctaaactgt tgggagtcgg aagccatctt ctcaattaaa 120

ttcctggctt cagcaggggt catgtctcca agggctccac cactggcagc atctatcata 180

cttctctcca tgttactgag tccttgataa aaatattgga gaagaagctg ctcagaaatc 240

tggtggtgag ggcaactggc acatagtttt ttaaatctct cccagtattc atataggctc 300

tctccactga gttgcctgat gcctaaaata tcctttctaa tggtcgtggt cctggaagca 360

gggaaaagtt ttctaaaaat actctcttga ggtcttccca gctcgtgatg gaccttggag 420

caaggtaaca t 431

<210> 1051
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1051

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catatccctg caccttttgg gcgtgttctt tgaatgatcc gttccccttt ttgcacatgt 120

tccgtagttg ccttctatcc agaaccatat caaaattgta ttgatactgt ctaacaacgg 180

caaccattac gtccttgcta taatggactc tggaagattc caagttagtg taccacgtaa 240

cagctacccc aataagactg tcttggaagg aatgtatcan caattcctca tcttttgagt 300

attcccccat cttctgacaa tacatcttta gatgggtctt gagacaagta tgtcccttgt 360

acttgtctaa gttcagcacc ttgaacttgg gaatgaccat gtttgggt 408

<210> 1052
<211> 412
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1052

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gagcctcact ttgagcctcc agatctgcta tgaccttctt cagttgtgct tcttgccgaa 120

gaaccatctc actattgacg cgtaatgctc tatccgatgt aacaagctca tcaaaagtga 180

tgtgcactgt ctgtatcact tgaatcttca gcagactcta atctcccagt gagtgcatgc 240

acatcgctga cagagtcgct ttattgttca ctctctgcat cggatcgacg tacaaaaagt 300

cctttcctcc gcttcttgag atgagcggga cattcatctg tgatgtgccc atgggcttca 360

cacccatggc atagaattca cttgctgtga ctgangttta catctgacct tt 412

<210> 1053
<211> 438
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1053

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ggttgaaatt tttttaaaac tacaaaatca ggagagagac tcattagata agaaacggga 120

gccacatatt tgtgattttc aataaatttg cgacctattt ctcattcatt tgtctatagt 180

ttatgcattt tcaaaaatct tcaatccata tttggactgt ggatctcact aatgctatga 240

cctgctttgg tttcaaaatg cagtggttac ttggcaccag agtatgcaat gggtggccag 300

ttaaccatga aggctgatgt atacagttnt ggggttctta tacttgaaat aatcagtggc 360

aaaagcagtg caaggacaaa ctggngaggg tccaacaaat ttctattgga atgggtatgt 420

aactttcagc ttcccata 438

<210> 1054
<211> 240
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1054

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acccttatga ccccctggag gaacttgtcc ttttgtgaca acagagctgt ggaggacccc 120

atctgtgcct caagctgttc ccaacccacc aaacactctt cttgtaccaa gaggttgatt 180

gttacgcgct ttggtgatgc tcaaacgtaa aaaaagatga gaatggctcc attcaacatt 240

<210> 1055
<211> 272
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1055

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ctattctggt tgttgtggac aggctgacca aatatagcca ttttgttcca ttgaaacacc 120

cttatacttg ccaagggaat tgttgagatt ttcgtaaggg aagtagtgag gctacatgga 180

gttccaaaat ctctcgtgag tgatagagat cctttattta tgagtttgtt tggaagggaa 240

tttttaagtt acaagggacc atgctcaaga tg 272

<210> 1056
<211> 418
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1056

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ttaagacatc cgagaanaaa gttattggtc gtttgaatgg ctcagagctt caacattcaa 120

tttttagcgt ctcgatatgt tacgggactc aatcagacat ccgtgaaaaa agttattggt 180

cgttgaattg gctcagagct tcaacattca aattcgagcg tctcgatata ttacgggact 240

caatcagaca tccgagtaaa aagttattgt cgttggaatt ggctcagagc ttcaacattc 300

aatttcgagc gtctcgatat attacgggac tcaatcagac atccgagaaa aaagttatgg 360

tngtttgaat tggctcagag cgttcacatt caatttcgag cgtctcgata tgttacgg 418

<210> 1057
<211> 421
<212> DNA
<213> Glycine max

<400> 1057

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caattcatca gtgggctttc cttctgtgtc cagcatcttg ggatgttccc agcctttgat 120

gacagctttc caggttctgc tatccagtga tttgaggaag gccaccattc ttgctttcca 180

gtattcatag ttgcttccat caagaattgg tggtctgttc actggtcctc cttctttctc 240

catgttcatc agaatttatc tccccagatc tcactctgtg atttcgagtg ttggctctga 300

taccaattga aattctgata ccaggggaca gatgtcgtac aggatgtcac gacatcacgc 360

ttcagaacat gcagtttatg tgtgtccgta tgaacagatt aaacaagtaa taacacaaga 420

g 421

<210> 1058
<211> 289
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1058

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tattatgcgc ctgaatcggg cctccgagtt aaaagataac ccaaatcgca ttttatgaga 120

gctttcgtct gttaatttca agtgtctcga tatattatgc gcctgaatcc gaccttcaag 180

tgacaagtta cgaccattag aattgctcga gagcttacgt ggaacaactg ctagcgtcac 240

gataaattaa gtgcctgaat cggacttccc tgtgacaagt tattacgat 289

<210> 1059
<211> 300
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1059

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ttctcaatta aatttctggc ttcagcaaga gtcatgtctc caaaggctcc accactggca 120

gcatatatca tacttctctc catattactg agtccttcat aaaaatattg gagaagaagc 180

tgctccgaaa tctgatggtg agggcaacta gcacatagtt ntttaaatcg ctcccagtac 240

tcatacaagc tctctccact gagttgtcta atacttgaga tatctttcct gatggatgtg 300

<210> 1060
<211> 338
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1060

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ctcaattaaa tntcttgctt cagcaggagt catgtctcta aaggctccac cactggcagc 120

atctatcata cttctctcca tattactgag tccttcataa aaatattgga gaagaagttg 180

ttctgaaatc tgatggtggg gcaactggca catagtttct taaatctctc ccagtactca 240

tacaagctct ctccactgag tagtctaata cctgagatat ccttcttgat ggctgtggtc 300

ctggaagcan ggaaaattnt ttctaagaat actctctt 338

<210> 1061
<211> 364
<212> DNA
<213> Glycine max

<400> 1061

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gaattatggg aatgtcagca tcttcttcaa tgtctatcac tattgaaatc aacttgtgat 120

ggagcgatta gccaactgga gggtcatgcg tgtgggcatt atctctatct ctccaagtca 180

tcgacacata gagagaggca ttaaattgat actaggtccc aagtctatga gagctttacc 240

cacagcaaca ttgccaatag aacacagtat agtgacactt ccatggtctt tgtgcttcac 300

gggaaagatg cgttgaatga cagcactaca atttccttcc acaactattg tgtcactgtg 360

tatg 364

<210> 1062
<211> 426
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1062

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taacagcagt ggtgatcgca acgagatcac gaacataagt ggaagaggtg agtaacctgn 120

gacaaaactg tttgctaaaa aaagctatca gatgtcttcc ttgggacaac accgcaccca 180

tacccgaacc caaggcttct gtctcgacca tgaaaggttt tgtgaagtca ggaagtgcta 240

agaatggaga atgtgtcata gcatgcttca atttgttgaa ggcaacgtca gcttcaaggg 300

tccaatggaa ctcttccttg gttagcaggc ttgaaagtgg tgctgccaaa gtagcgtagc 360

tccttataaa tcttcgataa aagccagcaa ggccgaggaa cccacggagg gctcgtgtca 420

tgcgtg 426

<210> 1063
<211> 439
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1063

agcttctaaa ctttatacaa gaatgaagct ctgataccac ttgttagaca agtggcctca 60

aatatcttaa gaaggggggg gttgaattaa gatatcacaa actatttccc caattaaaat 120

tttattcttc tttaatgata atgtcaatgt tcccttatta tgaattacta taattcaatt 180

caaactaaac ttccttaatg caaaagataa ataacaataa ataaatgagt ttatggaaag 240

agaaagttca aactcagttt tatactggtt cggccacacc cttgtaccta cgtccagtcc 300

ctaagcaacc cgcttgagag ttctactatc ttgtgaaaac cctttacaag atctgaacca 360

cacaaggaca acccctcctt tgtattcaga tcgctntaca aaaagagacc ctcagtccct 420

taatcactnt ccttaagta 439

<210> 1064
<211> 394
<212> DNA
<213> Glycine max

<400> 1064

agcttattaa ctgtacttta taagatataa aagcatcatt aaaaatataa tgcccaattg 60

tttagtaaac ataaattagc tagaattaag gtataacaac atttataacc aaccaaatag 120

tgtttatatg ttagttaaaa agttgattct gtcatacatt aaaaaaaaaa aacctttgat 180

tgttataaga aatcattata aacttttaa aatttctcga ttgaactatc ttaccataaa 240

aaaatgttat actaataata gcatattcct gtattaaaga gaaaaaaatt atgaaacata 300

tagcaaatat gacaacttat ttatttatag ttaatggaac atttaaaatg ttttcactat 360

ttagatacaa aatataaaga ttattcttaa attt 394

<210> 1065
<211> 288
<212> DNA
<213> Glycine max

<400> 1065

tgtttacctc tacttttctg aatgtctcga agatctcttt ctctgcctct tccatttttt 60

tgttggaaac tgctcttgga gggaatggaa gatgagggat gtgctgcttc tgcaaatcgg 120

aattaccagt ggaagattca ccttgcacat aaattgttag ggaaattttt gtcatcacct 180

ttttctggag tagagtgaag tttggcaagt tcatttgcag atgaagaagg tgctacaggt 240

tgaggtccat gacattgctt tcccgacgtc aatgaaatgg cactgaca 288

<210> 1066
<211> 401
<212> DNA
<213> Glycine max

<400> 1066

ctcggatgtt cgattcatgc gcatatatat attgagacac ttgatattga ataacaggaa 60

gcttctcgag aaattacaat ggccataact tttcacaccg atgtccgatt ccggcgcata 120

atatgtcgag acgctcgaaa ttgaacaacg gaagctctcg agaaactcca atggccataa 180

cttctcactc ggaggaccga ttcaggcgca taatatatcg agacgctctg aattgaacaa 240

cggaagctct cgagaaatca aacggtcata acttttcact cagaggggcc attcaggcgc 300

ataatatatc gagacgctcg aaatgaacat cgaaagcttc tagaaactca catggtcata 360

acttttcact cggaggtcca attatgcgca taatatatcg a 401

<210> 1067
<211> 416
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1067

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gagttctcat gtagataaac caatccttca gctgtcccga tgataatttc atatctattt 120

tcccagttca attctttgcc cttgttttta tcttccatgt ataaattgag aaatattata 180

tttagttcac attatgatga attgataatc acttttagtg acccaaatga ggtgttatag 240

gtgaaaaggg tagtcaagcg tactgcatca gttcagtaat taccaaaaat gtagcggtca 300

agacttcggt tgggtagaaa ttcatataca agcaggcttt caggtcctga acaactgcat 360

cctaacagtc tgactagatt cttgtgctcc acgctactaa ttatgttgac ttcatt 416

<210> 1068
<211> 370
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1068

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ccttaactgc ttttgagagg agtctatttt gcaagaaaat ggctgtatga gctgcttctg 120

cccaaaactt cttgggtaga ttttttttcat gcaacatgca cctagtcatc tctaggatgt 180

atttgtttct cctttcactc accccattct gttgtggagt atanggagtg gttagctgat 240

gctcaatgtc agcttcctca caaaactgat tgaattttat tgaggtgtac tccttgccat 300

tatcagatct tagaatctga atttgcttgc cactgtgatt ntctactgcc tttttgaatt 360

ccaaaaagct 370

<210> 1069
<211> 431
<212> DNA
<213> Glycine max

<400> 1069

agcttcgacc aagagaggat ggtccatttc atgtacttga aaggataaat gacaatgtgt 60

acaagattga attgaccggt gagtataatg tgagtactac atttaatgtg tcagacttaa 120

ctctttttga tgtagatgga gaagccaatt tgaggacaaa tccttttgaa gagggagaga 180

gtgatgagga caaggcaagg aacctttaga aggacttgga ggacctatgg caagggctag 240

aacaaagaat gccaaggaag ttcttcaaca agtgttaacc atgctatttg aatttacgcc 300

caagttacaa atggagaagc ttcggattgt taattgcacc atgttccaag aagagtagag 360

ggtgccactt ttgttgagtg gttttattag cattctgtta gttgaaataa aggctcaaac 420

ttgtgttaaa g 431

<210> 1070
<211> 424
<212> DNA
<213> Glycine max

<400> 1070

agcttgtcaa gcattgtttt aagtccaaag tcatcaagta cagcaccaaa tttattcatt 60

gtattcggac gcatgatccg aaatttagtt tcattcaccc acttctcaaa attttcaatc 120

tagggagacc acaaatacat tttaacatac acaaaacata agtatacaaa cagccatctg 180

cttacaattt ccaatttaaa agatgagata ctgcttgtat cataggtaat gatagttaaa 240

atgatgaagt acctcagata gcaataactc acaaaagtgg gtctgaaata tgtcaaatat 300

aaaaatgcct ggagagggct cagacactat acttctaata ctttgttccg tattatcatt 360

aattgctctc agaaatgtgg ggacaaagaa tgtagcagga tccacagagt acaactcccg 420

atgt 424

<210> 1071
<211> 402
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1071

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aaaaataaat cattcacgag agcaccatat tttagagaaa caatatactc atgccaaaag 120

taatttcct tgtaatcgaa aatgaagggc aggatgtcaa catttagctt ttaaatgaac 180

attcagggga aacgtcgggt caaactgaaa ctaggaataa aatcactcat agtgtataaa 240

aactcacaca ggtaagtgtt ttaccctaat cccaaaccat agctgcacca tgactttatt 300

ttgcacatga tttcctatcg aaccaaaaga tcacacgcac aatcatggat caataggatt 360

ttctcgaggg tagtgttttt ggagaggaag ttgggtgttt cg 402

<210> 1072
<211> 253
<212> DNA
<213> Glycine max

<400> 1072

acatcttttt acttgattct tgaatggctg tcaaaggcct atatatgtgt gacttgggac 60

acgaatttgc taagagtttt tcataacaaa atagtcttat cctcttaaaa agcaaagtcg 120

tttatcctct tacaaattcc ttggccaaat tacttgtgat tcaataaggg aatatttgag 180

tgctcaaatg gttcaatcta tctctttaaa gagagattac ttcttttctt cttcttcatt 240

ctgaaaaggg atc 253

<210> 1073
<211> 388
<212> DNA
<213> Glycine max

<400> 1073

acagcaaaat cagtcacaac agaataatta tgacctctcc agcaacaggt acaatcccgg 60

gtggaggaat catcccaacc ttagatggtc gaatccttca caacaacagc accaacaaca 120

acaacaacct tattttcaga atgcttctag cccaagtaga ccatacgctc ctccaccaat 180

ccagcagcaa tagccccaga aacagcaaac agttgaggct cctccgcaac cttcccttga 240

agaacttgtg aggcatgact atgcaaaaca tgcaatttca acaagagact agagccttca 300

ttcagagctt aactaatcag atggaacaat tggctacaca gttaaatcaa caacagtccc 360

agaattctga cagattacct tctcaatc 388

<210> 1074
<211> 364
<212> DNA
<213> Glycine max

<400> 1074

tagctttgca gcaaatgcca ctctactcta aattgttgaa agatatgtta acaaggaagc 60

ataaatatat tcatcaggaa aacatcatag cggaaggatg ttgcaatgct gtgatgaaaa 120

agatccttcc acccaagcat aaagatcttg gtagtgtaac tattccttgc tcaatcggag 180

aagtcaatgt gggaaaatat cttcttgacc tgggagccag tctcaatttg atgccactat 240

ctatgtgcac aagacttgga gagttggata tactgcccac tcgaatgact atacaattag 300

ttgaccgctc cattaccacg ccatatgcag taattgaaga tgtgctggtc atagtataac 360

attt 364

<210> 1075
<211> 365
<212> DNA
<213> Glycine max

<400> 1075

gagagtttcc gatgtttaat ttcgagcgca tcgatatatt ataagcctga atcggacatc 60

cgtgtgacaa gttatgacca tgtgaatttc tagagaggtt ccgatgttta atttcgagtg 120

tatcgatata ttataaacct gaatcggacc ttagtggtaa aagatatgac catttgaatt 180

cgcgagagct tctggtgatc aattcgagtg tcactatatg tgaagcgcca aaatcggaca 240

ttcgagttaa atgttatgag cattcgaata tctcaagagc taccaattgt taatactgag 300

cggctgatat gtgatatgcc tgaatggaca tccgtgtaaa agtatgacat ttgaattctc 360

aagag 365

<210> 1076
<211> 426
<212> DNA
<213> Glycine max

<400> 1076

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ccggatttgt atttttatg ggtgattgtg tttttacatg gagttctaag aagcaaggca 120

ttgtgacact ttctacttgt gaagccgagt atgtagctgc aacttcttgc acatgtcatg 180

ccatttggct aagaagattg ttggaggaac ttcagttgtt gcaaaaggaa agcacaaaga 240

tctatgttga taatagatct gcacaagagc ttgccaagaa tccggtgttc catgaacgaa 300

gtaagcatat agatacaagg tatcatttca ttagagagtg cattaccaag aaagaagtag 360

aattgactca tgtgaaaact caagatcaag ttgcggatat tttcaccaag cctctcacat 420

ttgaag 426

<210> 1077
<211> 349
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1077

gagacaagga ggancnnnga gtctctgagc accctgcgac tctcgaaaca ctcgcaatga 60

agccgaaaga gaaagagtgt atcatcaatg accttgtgaa gttcaagagt gggaaaactt 120

attatgccaa aattgggaaa gcttggaaaa gaaggtactt gctgtatggc cctccaagta 180

ccgggaaatc taccatggtc gcggctatgg ctaatttcat gaactatgat gtgtatgatc 240

ttgaatagac agcggggaag gacaattcag atntgagaca gctgttgatt aacacttcaa 300

gtaagtcgat tatggtgatt gaagacattg attgctccct tgatctcac 349

<210> 1078
<211> 280
<212> DNA
<213> Glycine max

<400> 1078

ctactgcatc aatattccca gggttcactc tgattgctcc acttaaagat ggggaacagc 60

caatgaattc agacacaact aacatgcttt tcttcttatg ggaggaagct agacccaaaa 120

ctttatccaa ggtttcattt ccttgacgac tgatgatata ttcatacggt atgagattca 180

ttccatccct tactgcagtg actaaacaac actccgcgac aacatagtaa gcaactctct 240

cataaaactt gagaggctcc tcgatcagaa tgacgggatc 280

<210> 1079
<211> 374
<212> DNA
<213> Glycine max

<400> 1079

agcttcaacc tagaggagac ggaccattcc aagtgttgga gaagatcaac gacaatgcct 60

acaagattga cttgcctagt gagtataatg taagtgccac tttcaatgtg tctgatctat 120

ctctttttga tgcagatgga ggagccttgg atttgaggac aaatcctttt caagaaggag 180

ggagtgatga ggacataacc aagggcaagg accatgaagc acttgaaggt cccatgacca 240

gaggcagact taaacaagcc caacacgtca tagagacaag gctggtcatt tgtatagctg 300

ccattgatga tgattgaacg cccaagtgga gaaagatgaa cgcccagagg cagacgcact 360

accaagacta ctaa 374

<210> 1080
<211> 313
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1080

cgagcggntt atatcgagac gctcgaaatt aaccaacgga agctctcgag aaattcatat 60

ggtcataact tgcaactcgg aggtccgatt cacgcgcata atatatcgag acgctcgaaa 120

tagaacaacg gaagctctcg agaaattcaa atggtcataa cttttcacac ggaggtccga 180

ttcaggcgca tcacatatcg agaccctcta aatntaacaa cggaagctct cgagaaatac 240

caatggtcat aactnttcac tgggacgtcc gattcatgcg cataatacat tgagacgctc 300

caaattgaac aac 313

<210> 1081
<211> 439
<212> DNA
<213> Glycine max

<400> 1081

agcttatata agtaatgggg gagtttatca gataattata tatcaggtaa aattttatat 60

tatttttctt atgtaaatat ataatacatt attttcttgt cacggataaa aaaataacat 120

tttcttgccc ccactaaaca atttttctag attcgtccat actcatggtt gcctttgttt 180

atgtttcttt aattattttg ttggtataca tttataaatc attgattgat atttaatgac 240

tatggctggc attttttttt ttaaatcatt cctataataa atacaaatat taatttattc 300

ttggaatatc ttaatgtagt aaatatgtat tttgtgtcag tttggccgat gctaactcga 360

gtgaaaatat tctttaaagt gtattaagtg tgttggagtt aggggtagga ataggccagg 420

tcaggcttta aaaggcctg 439

<210> 1082
<211> 299
<212> DNA
<213> Glycine max

<400> 1082

ttgagtttga atatatcgag acgcttgtga tggaaaacag aagctcgtag aaaatgcaaa 60

tcgcaataac ttttaactcg gatgatcgat tgagtcccgt aatatatcga gacactcgaa 120

attgaaagca gaagctctga gcaaattcaa acgacaataa ctcttgactc ggatatccga 180

ttgagtcatt taataattcg agacgctcaa aattgaatac agaagctcta tgcaaattca 240

aatgacaata acttttgact tcggatgtcc gaatgagtca ttatataatt tgagacgct 299

<210> 1083
<211> 437
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1083

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aaaactaaaa ctttggagta tctgattaga gctgatgcta gtaaagtgaa caactttagg 120

attctggagg aggagggcat gcatatgtcg accaacacga ggatgaaagc ttcaaatttg 180

cttatgcaac tgatctcatg tggctcaata ttagtgaaaa accatagttt tggccttatt 240

ccttcctata agcccatgtt ttatagttca aaatgtcctt tcttttgtgt tgggggagtt 300

tgattgctta gtgattgagc atttgtagtt taatattttt ctattctttt tatctcaatt 360

gacatctctt tgacttttat tttttcacct taactcagtt ntggtctaag gcaaatgatt 420

gaggttaatt gagaact 437

<210> 1084
<211> 412
<212> DNA
<213> Glycine max

<400> 1084

agcttctgtt ttcaatttcg agcgtctcga tatattaccg gactcaatca gacatccgag 60

tataaagtta ttgtcatttg aattttgtga gagcttctat attcaattcc gagcgtcttt 120

aattattaaa tgactcaatc ggacatttga gtgcaaagtt actttcgctt gaatctgctc 180

agagcttctg ttttcaattt tgagcgtcta gatatattac gggactcaat cggacatccg 240

agtaaaaagt tattgtcatt tgaatttggt aagagctcct gcattcaatt ttgagcgtct 300

caaattataa aatgactcaa tcggacatcc gagtcacaag ttattgtcat ttgaatttgc 360

ttagagcttc tgcttcaatt ttgagcgtct caaattatta aatgactcaa tc 412

<210> 1085
<211> 440
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1085

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taatcaagta gtgaaatgtg tgtatattca atttttgaca atattcaaat ttcaatccat 120

aatcacgata acatttatca tgtctttgat ccaagagaaa ctcgttgaag tctctaaatt 180

aaaattgtaa attaagtctt gtagatagaa aaagtataat tgaaagtgaa gacctattat 240

aagtgattaa gttctcaaaa aagattattc ttgaacataa ataatagata tttcacacta 300

ataagtaaaa atattatagt aatatttaga atcttttgtt gttttaaaaa ttctagatgt 360

aaagagataa tcactctctt attaattagt aatcaagagt cattntctta acatagaata 420

catcattaca gatgaagtat 440

<210> 1086
<211> 412
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1086

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atacatatga ttctttcatg cagcatgatg ttcaagaact aaatcgggtt ctctgtgaaa 120

aacttgaaga caaaatgaag gtatggcaag agatttggaa tgtttgttca tgattcttct 180

tgatgagtga tcataccaaa tggttgttgt atgttatttt tcttcacgaa actgttgttg 240

agggaactat acaaaagtta tttgaaggac accatatgaa ttacattgaa tgcatcaatg 300

tagactacaa atcaactaga aaggagtcat tntatggtac ttncttatgc attttgaatt 360

caattatatg gttagttctt ctttgtatga attctattta gttttgcata tg 412

<210> 1087
<211> 440
<212> DNA
<213> Glycine max

<400> 1087

agcttcaaca tcagaccact tccagggtgc tggaactact tcacatgtac ttgatggggc 60

ctatgcaagt tgaaagcctt ggaggaaaga ggtatgccta tgttgttgtg gatgatttct 120

ccagatttac ctgggtcaac tttatcagag agaaatcaga caccttgaa gtattcaaag 180

agttgagtct aagacttcaa agagaaaaag actgtgtcat caagagaatt aggagtgacc 240

atggcagaga gtttgaaaac ggcaagttta ctgaattctg cacatctgaa ggcatcactc 300

atgagttctc tgcagccatc acaccacaac aaaatggcct agttgaaagg aaaaacagga 360

ctttgcaaga agctgccagg gtcatgcttc atgccaaaga acttccctat aatctctggg 420

ctgaagccat gaacacagca 440

<210> 1088
<211> 421
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1088

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caatagcatc atttctggca ctgaattgct gggagttgga agccatcttc tcaattaaat 120

ttttggcttc agcaggggtc atgtctccaa gggctccacc attggcagca tctatcatac 180

ttctctccat gctgctgagt ccttcataaa aatattggaa aagaagctgc tctgaaatct 240

ggtggtgagg gcaactggca cataattttt taaatctctc ccagtattca tataggctct 300

ctccactgag ttgtctaata cctgaaatat cttttctgat ggttgtggtc ctggaagcag 360

ggaaaatttt tttaagaaac tctcttaggt catccagctc ggatggcctt gaacaaggta 420

t 421

<210> 1089
<211> 410
<212> DNA
<213> Glycine max

<400> 1089

agcttgacgg ccatgagcca tgggcgcttg tatcaacaaa gaatgaagaa tgtgtttgac 60

aagaaggtgc gcttgcacaa gttccatgag ggggaccttg tgctgaaaaa gatgtcccac 120

gctgttaaag ataatcgagg gaagtgggcc ccgaactacg aaggaccttt cgtcgtgaaa 180

aaggcttttt tcggaggggc cctagtgctt accaacatgg atggcgagga gctaccttta 240

cccgtaaact ctgatgttgt cagacgatac tatgcttaga atctggggca attgaggata 300

tcgctgcatg ttcttttatt tttatgtgtg ttcttcttgg tttcccctag ggattcctgt 360

ctgctgtata tttcttgtca cagactttta aaagaagaga acatgagttt 410

<210> 1090
<211> 412
<212> DNA
<213> Glycine max

<400> 1090

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tcggctaaac ggacttcata cttgacttga ttgttcatcg tcccaaactt gaaccttagg 120

gattgctcta ggattatttc atttgggctt tctaggatga caccagtcct actccctttt 180

tcattggatg aacccatctg catacaaatt ccaccactcg gattgtagtt ctgtagtcgc 240

tgtcaattcc acgatgaagt ctgctaagca ttgagccttc gttagatccc ttggtttgta 300

cttgatccca aactcgaaca actagaccga ctaacatatc attcgcgttg caagttctgg 360

gttcatcatg actggtaaga tatggtgcgt tggttaaact atcatttgat ga 412

<210> 1091
<211> 425
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1091

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caccccccct ataatagcta agctcacccc tatgccaaaa aaacatgaaa aaaacaaaaa 120

aagtcgttgc tacaaagact actcaaaatg ccccaaaata caaggctaaa accctatact 180

acttgaatgc ccaaaataca aggcccaaac gaaggaaaaa cctattctaa tatttacaaa 240

gataagcggg ctcatacttg gtccatgggc tcgaaatcta ccctaaggct catgaagaaa 300

aatgcctaaa attattacac acaaatggaa gtttggaacc tattggaagt cctaacacac 360

ttccatgana aggcctttgt acaaacttga agcatgaagt agtaattgca ataaaaatac 420

aacac 425

<210> 1092
<211> 442
<212> DNA
<213> Glycine max

<400> 1092

agctctgacg atttagatag attataagat taattcttag tccgatattt aatcaaattt 60

aaagctttca aattggtttc ttattgtctt tattgtacac aaaaatatta ttaagatata 120

aatttatgat ataacctcgc atgaaaactt attaaataag tatttaatta aatttagggt 180

tggccaacat tattccaatg caaactttgg agtgagcttt tacaaaagtt ttatattttg 240

atttacgctt aaatgtaatt ttaatcatct tatcttattt aatatgtaat cttgattcct 300

ttatttaaa atagatattt ggtctcctta ttttaaaaaa taactaattt taatctctct 360

attctaatat ataaacattt ggtcctctta ctttaaaatt tttataattt ttgtcaaatc 420

tttaattcta catatatttt at 442

<210> 1093
<211> 440
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1093

agcttgcatt ccctaaggat ccattaggaa attacttgtg aaagagagcc atgagggtgg 60

gctcgtgggc cactttggga tagacaagac ccttgtctta cttaaagaaa agttttattg 120

gccccatatg aagaaagatg tccataagca ttgcactaga tgtgtggctt gtttacaagc 180

caagtctagg gtgatgcctc atgatctata cacacccttа cccatcccat ttgcaccttg 240

ggtagacatt agtatggact ttgtccttgg gcttcctaga acccaaagag gtgtagactc 300

tatctttgtg gtggaggata ggtttagcaa gatggcacac tttataccat gccacaaggt 360

ggatgatgct tcctatatct canaactctt ttttagggaa gttgtgagac tccatggttt 420

gcctaggacc attgtgtcag 440

<210> 1094
<211> 360
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1094

agcttaatga ccctcaatct ttcaatgatt atagacccat ctccctcata gggtgtgtct 60

ataaaatcgt ggctaaagtt ctggccaaga ggctggccct tgtgttacct caacttatac 120

atgaaaggca gacgactttc atgaagggaa gacacattct tcatggtgtt ttgattgcca 180

atgaggctat agctgaggct aaggctaaaa ataaaccttg catggttttc aaatcggatt 240

tcgaaaaggc gtatgattcg gtttcttggg gttttgtcaa ctacatgctc atgaggatgg 300

gcttttgtga naggtggagg aaatggatta atggttgtct gtccattgca acccatatca 360

<210> 1095
<211> 325
<212> DNA
<213> Glycine max

<400> 1095

ctgcaagctt tcatcggtgg gatttcatgg gatacgacgg aggacaagct caaggagcat 60

ttcggtaact acggcgacgc tttgagcact tccatcatgc gggagaagaa cactgggaag 120

ccaaggggct tcggtttcgt cgtttttgca gatcctaaca ttctagatag ggttttggaa 180

gacaaacatg tcatagatgg cagaaccgga acgcttctat catttttttt gtcatttctt 240

tacttcatgt tccgattgaa aatattgtat tgtacttttt agcgtgattg gtgctggttc 300

tgaattgggg ataatcttga aaccc 325

<210> 1096
<211> 392
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1096

aattccttca tctgacttat catcaaattt tcctaattnt tcttttccat tgtttaatac 60

aaagcatttg caaccaaaaa catgaaggtg tgaaatgtta ggtttttttt atcattaaac 120

agttcatata gagttttctt taaaatgggt cttattaaag ccctattcat gatatagcat 180

gcagtattaa cggcttcagc ccaaaaatat nttggaagag gagtgtcatt taataaggtt 240

ctagcaatat cttccaaaga tctattnntt cctttcaaca actccatttg ttgaggggtt 300

ctaggtgcaa aaaagttatg ttcaatgcca tgcttatcac anaataattc aaatttttta 360

ttttcaaatt caccccccatg atcgctccta at 392

<210> 1097
<211> 404
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1097

agcttgtagg aggaagaaac cagcaatgat tttcaaggtg gactntgaga aggcttatga 60

cacagtctca tggtctttcc tggactatat gctgtataga ttgggctttt gtcataaatg 120

gagaaagtgg atctcagctt gtcttcactc agcaaccatc tctatcctta ttaatggcag 180

ccctacaaag gagtttaccc catctagagg cttgaggcaa ggggatcccc tagcccctct 240

actctttaac atagttgggg aaggcatctc aggcctaatg agggaagcag ttaggaagaa 300

tctatatagc agctacaggg ttggtatgaa ttatgagccc acaaatattc tgcagtatgc 360

agatgatact gtttttgtgg gtgaggcttc ttgngaaaat gtct 404

<210> 1098
<211> 286
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1098

agcttaagct ccttttttctg cacttggctc ttataanncg aagagcatcc ctgtggaacc 60

tttacccgac gaagacactg acaaaaactt atcttcttct ttgtggacaa agtatggtaa 120

gctgggggca acgaaatctt cttcccatca aaccttggat gcaaatgtga tcgtatgccc 180

atatcagcta gaacttgacg ggtattcaag ccatccttcg tctcgccttg aatgttaagg 240

agccgcccaa tcacactgtc gcacactatt ttcttcacat gcataa 286

<210> 1099
<211> 441
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1099

ggtctaaact nttcactcgg agctctgatt atgcacatca catatataga cgctcaagat 60

tgaacaacgg aagctctcga tatattcaaa tggtcataac tnttaacttg gaggtccgat 120

tcacgcacat aatatatcga gacgcccgat attcaacaac ggaagcactt gagaaaatca 180

aatggtcatt acttttaact cggaggtccg attcangcgc atcacatata gagacgctcg 240

aaattgaaca acggaagctc tcgagatatt caaatggtca taactcttaa ctcggaggtc 300

cgattcatga gcataatata tcgagacgct ccgaattgaa acacggaagc tcttgagata 360

ttcaaatggt cataactttt cactcggagg tctgattcaa gtgcataaca catcgagacg 420

cttgaaatta acaacagaag c 441

<210> 1100
<211> 434
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1100

gctntgacca tttgaattgc tcaagcgctt tctttgttca atatcgagcg tctcgatcta 60

ttatgcgctt gaatcggacc tccgagtgaa aagttaagac catttgaatt gctcaagagc 120

ttccattaac caatttcgag ggtctcgata ttttatgttc ctaaatcaga cctccgagtt 180

aaaagttatg tccatttgaa tatctcgaga gcttccgttg tttaatttcg agcgtctcta 240

tatgtgatgc tcctgaatcg gacctccgag tgaaaagtta tgaccatttg aatatctcga 300

gagcatccgt tgttcaattt cgagcgtttc tatatgtgat gcgcttgaat cggacctccg 360

agttaaaagt aatgaccatt tgattttctt aagagcttcc gctgttcaca ttcgggcgtc 420

ttgatatttt atgc 434

<210> 1101
<211> 448
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1101

agtagggtta aagtctcacg attgtcatgt gttgatgtaa cttcttgtca tacaaagtca 60

ggttagccat aactcgcctg tgctatntct tccatgccat atatagcana gtcgttgatc 120

ctgtcaagta tgatgagctg gaaaatgagg ccgaaattat actatgccag ttggagatgt 180

atttttcccc tgctttcttt gacatcatga ttcacttgat tatggatctg gtcagagaaa 240

tcaaatgttg tgggcctggt tatttgtggt ggatgtaccc ggttgagcaa tacatgaaga 300

tcttaaaagg gtatacaaag aatccttatc atctagaagc atctattgtt gagaggtaca 360

ttgcaaaaga agtgattgaa tcttgttcag aattcattga gaaggctaaa cctattggcc 420

ttcctgagtc tcgcgatgat gacagaac 448

<210> 1102
<211> 468
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1102

gctttaagaa aaaccttatt tatcactcac tagacgacat tcttttgtgt taaactaaaa 60

ctaattttct atcactagat gatatagttt atcttgttat cttgtgaaaa actcttcttt 120

gtgaaaaaag cttatatctt tggttaacac acttttcgac ccctttctaa tatgatcttt 180

gatatttcaa aagtgtacta gtcttcttcg tatattggct tatgactcac ctgctgatag 240

tgtggacatg tatattcaga ttactaaaag cactgtagtg gaatgcttac aaaaaattgt 300

atcaaacatg tgtgcaatat ttggggatga gtacccgagg aggccaaata ataaagacac 360

atgaagacta caaattgaag cagtacatgg ttntctaggt atgttagggt tcattgattg 420

tatgcaatgg gaatagaaaa aaaatgtcca gttgcgtgga aaggtcta 468

<210> 1103
<211> 459
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1103

tataatatat tattacactc gaaattaaac atcagaagct ctcgtgatat tcaaatggtc 60

ataacttttc acccggatgt ccgattatgg cgaatcacat atcgagacgc tcaaaattgg 120

acaacggaag ctcttgagaa attctaatgg tcataacttt taactcggat gtccgattca 180

cgcgcatcac atatagaggc gctcgaaaag gaacaacgga agctctcgag aaattcaaat 240

ggtcataact ttncacactg aggtccgatt cacgattata atatatcaag acgctcgaaa 300

ttgaacatcg aaagctctca agaaattcaa ttggtcatca cttttcacac ggatgtccga 360

ttcggcgcat atatgtcgaa cgcttgaaat gaacaacgga agctcttgga aattaaatgg 420

tttaactttc acacggatgt caattcaacg catacatat 459

<210> 1104
<211> 224
<212> DNA
<213> Glycine max

<400> 1104

agcttgccgc cacggagttt tccgactatg ctcttgtgtt gtggaacaag ctacaaaagg 60

agagagcaag aaatgaagag ccaatggttg atacatggac ggagatgaaa aagatcatga 120

ggaagcggta tgtgccggct agttactcaa gggacttgaa attcaagctc caaaaactaa 180

cccaaggcaa caaggggttt gaggagtatt tcaaggaaat ggat 224

<210> 1105
<211> 328
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1105

tanagataaa ctaagaataa tgactagaaa tcttatctta gttcttgata ananaggcta 60

tcaaatacaa actgattagc taggctaaga ataccgatag aatatctcat catatattct 120

gagaatatat tctatcaaat attaactgac tagcttggct aagaaaaccg atagaatatc 180

tcatcatata gtctgataat atattctatg aaacacagac tggattagta agctaacaat 240

actaataaga tatctaatca tatattttat cattaggtag gcttagaata cagatagaat 300

atcttatcat atattgtgat agtatatt 328

<210> 1106
<211> 353
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1106

agctttccat tctttcggaa gtttatcatc tttattggct tcttgaggag gagcttcatt 60

gcttccttt ccttttcctt tacaatctng tccatgaata tgcatttgtt ctaaagattc 120

tgcaacatca tctaaaatat cctttcttga agaaatagca ttagactcat caaaggaaac 180

atgaatagat tattcaatag tcatagttct tttattatat attctataag ctttactatg 240

caaggaataa ccaaggaaaa ttccttcatc tgacttagca tcaaattttc ctaagttttc 300

ttttccattg tttaatacaa agcatttgcc accaaacaca tgttgatgag aga 353

<210> 1107
<211> 349
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1107

cggaagctct cgagaaaatc gaatnntcat atcttttcac acggatgtcc gattcggnga 60

cataactgat ctagacgctc gaaattgaac aacggaagct ctcgacaaat tcgaatggtc 120

ataacttttc acacggatgt tcggttctgg gacataacac atctagacgc tcgaaatgaa 180

ccaccaaagc tctagagaaa ttcgaatggt cataacttat tacacgaata gtcgattggg 240

aaaataatat atcgagatgc taaaaattaa caaccgaagc tctagagaaa ttccaatggg 300

cataactctt cacacagatg tccgattcgg ggatagaata tgttgagac 349

<210> 1108

<211> 373
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1108

agctntgatg caacattngg agaggttaat gtatcaacta tatgatgcgc tccatgagag 60

gttggatcaa atggagaata gagatcataa tgaagaagaa aggaggagaa gagggaatga 120

tggtgttcct agacaaaacc gaattgatgg tattaaactc aacattcctc catttaaagg 180

aaagaatgat ccggaggcct acttggagtg ggagatgaaa atagagcatg ttttctcatg 240

caacaactat gaggaggacc aaaaggtgaa gcttgccgcc acggagtttt ccgactatgc 300

tcttgtgtgg tggaagtgat tatgcaagtt gaagtggacg tttccattgg gaaatacaat 360

gataagggac ttt 373

<210> 1109
<211> 411
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1109

agcttgaggg aaaaattgat gccttggtca ttctagtaac tcagcttgcc atgaattaga 60

aatttgcatc tgcacttgtt gcaagagtct gtaatctatg ttttctgcag atcaccatac 120

agatctatgt ccttctttgc agcaatctgg agtcaatgag caacctgaag cttatgctgc 180

aaacattcat aatagacccc ctcagcagca aaaccaacaa aataattatg atctttcaag 240

caatagatac aatccaggtt ggaggaatca tccaaatctg agatgggcaa gccctccaca 300

acaacaacaa cagcctgtcc ctcctttcca gaatgttgcc ggnccaagca agccatatgt 360

tcctcctcca atgtagcaac aacagcaaca gtcacaataa aaacaacaag c 411

<210> 1110
<211> 427
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1110

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cctgaggaat ggtgtagtct tgctgctgac tacttgcatt gtggcccccc gcagctccca 120

ttcatatacc tagggatgcc tataggtgtt aaccctagaa ggaaggtggt gtgggagcct 180

ataatcagaa aatttgaagc caaattgaac aaatggaacc acagaagcat ctctatggct 240

ggcagaatta ccttaatcaa tgctgtcttg acagctntgc ccttgttnta tatgtctttn 300

ttcagggccc cttcagcagt catcaagagg ctcactacta tccaaagaca atttctttgn 360

ggtggaaact tggaaggaaa aaagatagct tggatctcat ggcagcaagt gtgtgctcct 420

agagaaa 427

<210> 1111
<211> 450
<212> DNA
<213> Glycine max

<400> 1111

cgattgtcac gtgctcatgc attatttgtt atccgtggct atacgagaca tcttgccaaa 60

caaagacagg ttagcaataa ctcgcctgtg ctttatcttc catgctatat gtagcataga 120

cattgatcca gtcatgtttg atgaaatgga aaatgaggcc gcaattatac tgtgccagtt 180

ggagatgtat ttcccccctg ctttcttaga catcatgatt cacttgattg cgcatctggt 240

cagagaaatc aaatgctgtg gtcctgttta tctacggtgg atgtacccgg ttgagcgata 300

catgaagatc ttaaaaaggt atacacagaa tctatatcgt tcacaagcat ttatcgttga 360

gaggcacatt gcagaagaag ccattgaatt ctgtctgact acttacagaa tgctaaacct 420

gttggacttc ttgagtctct gcatgatgac 450

<210> 1112
<211> 447
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1112

tgctctacat tacattgatg tttgtattta ttggaggatg ttgtatgcca ttnttgtttt 60

aagggtagca tttcttggta aaactaactt tccaaatgtt tgcattcgca ggaaacggcc 120

ccgaggaagt gatgcaatcc taccccccaa gggcattgga tagaacactc caataagatt 180

gggccaaaaa tgcaagagaa ggccctaggg ttctcatgag ccttagggta gatttctgag 240

cccatgggcc aaggttgggt ccaattatct ttgtacatat tagactagga tgtcattata 300

tttggtcctt gtatttaggg atccatattg taggtagggt accctagaaa tataggattn 360

ttcagccctt gtatttttgg gcacctagac tagttnttgt attaggggta gttntgtaat 420

ttcacatgca ctaagtggat atttgat 447

<210> 1113
<211> 346
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1113

tgtactatng gtcatatgca tatgatacaa tcaaagcctt ctcttcacca accaggattc 60

cgaatgcttg cagtgcaaac accgctgata tcaacgctcc gcgcgtcttg ttgctggcat 120

atttatacat gattgtggct gaaagagggt agtctccacc gatggcaaac gctagacaga 180

atctgaagaa gcatagagag gccatgacac cctgtggagc tgacccacag gagagttgct 240

gggcaaggga ccacactacc atgagaatga gcgttagtgc ccatactcta tatctcccca 300

tttaggcacc aagccaacca aataataatg gtccgtatta tgcgcc 346

<210> 1114
<211> 409
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1114

atgctttaat cagtgttttc tctaactcat cttttcttta aatcaacctc ccggtgtcaa 60

aaatcacttg atccatgaca tgcactctaa aatactttgt cttatgttta aggtgtttca 120

tggaaataca ttaaactgta cttcatcatc ttgtaccttg acagtgagtg ttccatcatc 180

cacatcaatc acaactttag aaatcttgat gaaagatcta ctaagaatca attgaacttc 240

attgccttca tccatatcca tcactgcaaa gttgactgga aagacagatt tgtcaacttt 300

tatcaataca tctacaacaa tgccataagg aagctgtgtt gttctgtcag ctaactgcaa 360

acccatcctt gntggtctga tttcaacttc tcctatctgc ttgatcatg 409

<210> 1115
<211> 474
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1115

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atgtgatgcc tctggagtgg gagttggagc tgtattgtta caaggtgggc accctattgc 120

ttatttttagt gaaaaaattc atagttcccc cctcaactac cccacctatg ataaagagcg 180

ttatgcctta ataagagccc tccaaacttg ggaacattac cttgtttcca aggaatttgc 240

cattcatagt gatcatcaat cacttaagta cattagaggg caaaacaagc taaacaaaag 300

gcatgcagaa tgggtagagt acctatagca attttcatat gttatcaaat accaaaaggg 360

aacaacaaat gtggtagctg atgccctatc tacgagacac acattgtntt gctccctang 420

agctcaaatt ttaggatttg atcatatcan ggacttggat gctttagatg aaca 474

<210> 1116
<211> 341
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1116

agcttgtaat cgattacaca tatactgtaa tttattacca gaagagagtt tcagaanaca 60

ttctcaacag tcacatcttt ttgtgtgatt cttgaatggc tatcataggc ctatatatat 120

gtgacttgag acacgaattt gataagagtt tttcaaaaca aaaaggtctt atcctcttat 180

aaagagaaat cgttttatcc tcttacaaat tccttggcca aattacttgt gattcaataa 240

ggaattattt gagtgctcac attgttcaat ctatctcttt caagagagat ttcttcttct 300

cttcttcttc attntgaana gggattaaga gaccgagggt c 341

<210> 1117
<211> 374
<212> DNA
<213> Glycine max

<400> 1117

agcttatgca gcatatatat actatatacc ttctctgcgc agcagcagac tcatacgctg 60

gctgacaatt atgacgtttc cagcagccga tacaaccctg gatggatgaa tgcccctaac 120

ctcatatgtg acaggacctc acaacaacca cagtagtctg gtgcttcctt acaaaaagct 180

ggtgggccaa gctgaccata cattcatcca ccaatccaac aacaacgaac cccccggaca 240

cagccaacag ttgaggcgcc tccacaagct ttcctcgaag aactagtgag gcaaacgact 300

atgcacaaca tgcagtttta gcaagagacc agagcctcca tttagagctt aaccgatcag 360

atgggacaat tagc 374

<210> 1118
<211> 423
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1118

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attntggaag caacgggtgc aactccgtga cccgaaacca catgacccaa gtactcaact 120

tgtggttggg caaatgacca tttagagaac ttgagcacga attggttgtg aaggagggtc 180

tcgaatgctt gctcaagatg aatgagatgc tcaggcaatg tacgactata aattaaaatg 240

tcgtcaaaga aaacgatgat gaatcgccgg aggtaaggcc ggaaaatgtc attcatggtg 300

gcttggaacg acgaatgtgc gttacacaaa ccanacggca tcactttgaa ttcatagtgg 360

ccgtggtgag tgcaaaacgc agtcttggcc acatcggatt catgcatnct tatctgataa 420

tat 423

<210> 1119
<211> 372
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1119

ctcactcgga ggcccgattc aggcgcataa tatatcgaga ctctcgaaan tgaacaacgg 60

aagctatcga gaaattcaaa tggtcaatac ttcgaactcg gaggtcctat taaggtgcat 120

aatatatcta gacgctcaaa attttacaat ggaagctcta tggctataca aatggtcata 180

actttttcact cgaaggtccg attaaggcgc ataatatatc gagacgctca aaattgaaca 240

atggaagctc ttgagcaatt canatggtca taacttgtca ctcggaggta cgactcagct 300

gcataatata tcgtgacgct cgaaattgaa aatggaagct cttgagcaat gcaaatggtc 360

ataacttgtc ac 372

<210> 1120
<211> 378
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1120

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ttggatcaaa tggagaataa agaccatatg aattgctcaa gagcttccat tgtttaattn 120

cgagcgtcta gatatataat gcgcctcaat cggacctncg agttaaaagc tatgaccatt 180

tgatatgctc acgagctttc attgttcaat ttcgagcgtc acgatatagt atgcacctga 240

atcggacctg cgagtgacaa cttatgacca tttgaatcgc tcaagagctt ccattgccca 300

atcttgacgc gcacgatata ttatgcacct gaatcggacc tgcgagtgac aacttatgac 360

cattcgaatt gctcaaga 378

<210> 1121
<211> 355
<212> DNA
<213> Glycine max

<400> 1121

ttctgctgga tcttcatggt ggaaaatcac cattaaagga cctcattgaa gctaaaagat 60

ccagcctcca tagaaacccc acaagcaagc tttcatcatc acgataccgg gttctattgg 120

tgaggttgat gtaagcaaag ctcttatact tgggagctag tatcaattta atgcctctct 180

ccatgtgctg gcgactttga gagatagaga taatgcccac acgcatgacc ctccaattag 240

ctgaccgctt catcacaagg ccatatggag tcattgaaga tgttttggtg aaaggtaaac 300

cccttatatt tccagatgat ttcattgcat agatatataa gaagatgctg acatt 355

<210> 1122
<211> 345

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1122

cggatcctta agcacctgct gcttgcaagc taacagtttt tttttcttag tgcatacttt 60

tcaaaattag tatcaaaata atcttcaaat gattcatatt ntagtgtatt ttaaatttct 120

ttgaattttt atctacatat gaattaatta tcaaataatt gtttattaat gcaaaatttg 180

ataaatatga tatgcctgaa aggacacttt catctaattt gaacttttac aatagaatta 240

ttcaattaga agttattaaa aggtattaaa tgatgtgata ttgaacgcat tacattcatg 300

tcatctgatc tctcctatat atgcattaat tgttatatat taata 345

<210> 1123
<211> 402
<212> DNA
<213> Glycine max

<400> 1123

tgttactgca tgatggcagc aatttcgaca gatagatgac atgtaacatg ttgagtccac 60

ttctcaaatt tctggaaatc cagagggaaa actgaaagat gataagtaaa ttatgcagta 120

taaacctttt atgcagtaac aagccccaaa cacatgactt gtaaataaca atttgaatag 180

taaaatttga ttacactgtg aacaattata taatccagag aaattttgga actctcaact 240

tccatttcaa attgttatga caagctacta cttccatttc aaattgttat gacaagctac 300

tgtggtgaac catctgcttg aaaaaattaa attaaatgtc atatgagcca atggcccaca 360

tatcacatat aaaactgcta agaacagata tgcacttgat ct 402

<210> 1124
<211> 214
<212> DNA
<213> Glycine max

<400> 1124

gagcacctcg atgtattatg cgcctgaatc gaatctccta gtgaagagct actaccattt 60

gaattcctgc agagctttca ttgttgaatc tcgagcggat cgatatatta tgcacaagaa 120

tccgacctat gagtgaaaag ctatgaccag tttaattgct ggagagcttt cggtgatgaa 180

tttctagcac ctcgatatat tatgcgcctg aatc 214

<210> 1125
<211> 463
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1125

cactaagctt ctttgagaga cttgcttgag aagctagagc ttagctacac acacccctct 60

cataactaag ctcacctcct tgagaagctt ccttaagaag attcctaaag aagctagagc 120

ttagctacac atacctctct aatagctaag ctcacctcct tgagatgaga agctagagct 180

tagctacaca ccccctataa tagctaagct caccccccatg acaaataaca tgaaaataat 240

ataaaaaaag tccttattac aaagacaact cacaatgccc cgaaatacaa ggctaaaacc 300

ctatactact agaatggcca aaatacaagg cctagacgaa ggaaaaacct attctaatat 360

ttacaaagat aagcgggctc atacttagcc catgggctcg aaatctaccc taaggctcat 420

gagaacccta nggcctttcc ttggatctct agcccaatct act 463

<210> 1126
<211> 331
<212> DNA
<213> Glycine max

<400> 1126

ttctggcttc aattcatcag tgggcttgcc ttgtgtgagc aacatcttgc gatgtatcca 60

ggctttgatg acagcgttgc aagggctgct atccactgat atgatgaaag ccaccattct 120

tgctttccaa tgtacataga tgatgccatc atgaattggc ggactgatca ctggtgctcc 180

ttctatctgc atgttcatca gaattgaact gcctagatct cactcgagga tttctagtgc 240

acgctctgat accaattgaa attctgatac tgaagacaga tgccgcacat gatgccacga 300

cattactctg aatgacatgc agattgtgat g 331

<210> 1127
<211> 413
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 1127

gganactgag cagccatcat tccanatctt ggtgggaagc caaagacaaa accatcagca 60

tcacggagct catttctggt gatgattggt acatcactct tgggcggtgc tctcaatgcc 120

tcaagctcct cagttgatag tgtctcgggt acctgctcat atgtttagtt aagtaaaaaa 180

ggaaatcctt taaataccct attnttattc tcaataatga agttgttttc taccccttgac 240

taaatgaatg cttacaacat ccctttagct agagtaaatt tgggaaatta agtcttagtc 300

acagagatca tacagaatan agcacagggg ccattggact aaaagtgaca taagttgaat 360

taatgcatat acagcattag gaattntgat ggattaaaaa tgaaaattac atg 413

<210> 1128
<211> 445
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1128

cttctctatg gatcaagctg gtgaggaaag aaagttgcaa ctgagtgagt tagatgaaat 60

ccgcctagaa gcctacgaga acgccaagtt ctacagagaa aagaccaaga agttccatga 120

tagcatgata gttaaaaaag acttcgtggt tgggcaaaaa gtgttattgt ataattctag 180

gcttggactc atgagtggta agttgaggtc taagtggatt ggtcctttct gtgttactaa 240

tgttnttcct tatggtacag ttgagatcag aagcgactcc acaaacaaga gcttcaatgt 300

caacagacat cgacttaagc cattcctcac gaacccttct ttagtggacg tagtggtgga 360

agagacttct tactcccccc actctttctc accatgactt agggagtttt atttctatct 420

ccttttttgtt ttattacact gctga 445

<210> 1129
<211> 411
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1129

tgcagcttaa cattcaattt cgagcgtctc gattatgacg ggactcaatc agacatccga 60

gtaaaaagtt attgtcgttt gaattggctc agagcttcaa cattcaattt cgagggtctc 120

gatatattgc gggactcaat cagacatccg agtaaaaagt tattgtcgtt tgaattggct 180

cagagcttca acattcaatt tcgagcgtct cgatatatga cgggactcaa tcagacatcc 240

gagtaaaacg ttattgtcgt ttgaattggc tcagagcttc aacattcaat ttcgaggcgc 300

tcgatatatt acgggactca atcagacatc cgagtaaaaa gttattgtcg tttgaattgg 360

ctcagaggtt caccatttca ntttcgaccg tctcgatata ttacgggact c 411

<210> 1130
<211> 480
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1130

ctaagcttta gccaatgaac tntgttagtg cttagctcta ctggagttta taagattggc 60

taagattttg ttaaaacata agcacttaga caatgaagga aagctggagt tgctgcacat 120

gatgtccaac gttatgtcaa agaataagat cgggctgcac aatgcacaag gcaagatgaa 180

atgtctaatg aagaattgaa gctgcaggat tcacgatgtc ggatacaatg tccaggacat 240

cctgcctgaa aatactggaa ttgctaaaag cattgaagct gcaggatcca cgatgtcgga 300

tacaatgtcc aggacatcct gcccgaaaat actagagttg ctaaaagcat tgaagctgca 360

ggatccacga tgtcggatac gatgtccagg acatctggcc cgaaaatact ggacatataa 420

atctgttata tctttaacag attattgtgc agttagcaag agataagatg atctattctt 480

<210> 1131
<211> 357
<212> DNA
<213> Glycine max

<400> 1131

tcttgtacgg taaagtctca cgatagtgac ttgctcatgc aacaattgtt agtcgtggct 60

atacgataca tcttgccaaa caaagtcagg ttagcgataa ctcgcttgtg ctttttcttc 120

catgctatat gtagcaaagt cattgatcca gtcaagtttg atgagttgga aaatgaggcc 180

gcaattatac tgtgccaagt ggagatgtat ttcccccctg ctttctttga catcatgatt 240

tacttgattg tgcatctggt cagagaaatc aaatgttgtg gtcctgttta tctacaatgg 300

atgtacccgg ttgagcgata catgaagatc ttaaaagggt atacaaagaa tctatat 357

<210> 1132
<211> 496
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1132

actcagctta cacaatntaa ttttctcaaa cctcgagttt ggaagaccaa ttactaagtc 60

tttcttaact agatgattaa gatgatgcat gtttatgtgt gcagtcctac aatgccacaa 120

ccaagagtca tctatcttac caaacaactc agctcctaaa atgatgcatg ttcaatattt 180

aacatataga tattacctac tctcttgcca atatggacat cctgaccaga catagcttca 240

ctaataagac aataattctt gttgaattca attttgaagc ctttgtcaca tagttgacta 300

atacccaaga ggttatgctn tagtccatcc acatatagaa ctntctttat ctgagttntg 360

tactgatttc caatatttcc ttcttccatt atctttcctt tgttattggc tccaaaagtg 420

acatatcctc cttcttttga cacaaagtaa tgtagctcca tgtggagctn gtaagccttg 480

gatcttcttc atcaac 496

<210> 1133
<211> 388
<212> DNA
<213> Glycine max

<400> 1133

agcttgtagg cctaggatct tcttcatcaa tggattcctt tgcttcttgg aaaatgaatg 60

gcagcggaat ggagaatgat acgagagaag gagacccact tcaggagaag atgagtctag 120

aagaagctca ccaccatagg aggccatgga taatagcttg ggggaagaac gagatgaatg 180

aagggagagg gagagaagac acgaaatttt gtgctccaaa tgagctctga aatctgaatt 240

gtaatattct aatgatcaaa gttgaaaaaa attcacacac atgacctcta tttatagcct 300

atgtgtcaca caaaaattgg acggaaattc agattctctt gaatttgtgg agccaaactc 360

tggcagccaa attcactaat tatgatta 388

<210> 1134
<211> 450
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 1134

tcagcttagc tacacaccac ccctctcata actaagctca cctccttgag aagtttcctt 60

atgaagattc ctaaagtagc ttgagcttan ctacacatac ctctctaata gctaagctca 120

cctncttgag atgagaagct agagcttagc tacacacccc ctataatagc taagctcacc 180

cccatgacaa aaaacatgat aatacaaaaa agagtcctta ctacaaagac tacttataat 240

gccccgaaat acaaggctaa aaccctatac tactagaatg gccaaaatac aaggcccaga 300

cgaaggagat acctattcta atatttacaa agataagcgg gctcatactt agcccatagg 360

ctcgaaatct accctaaggc tcatgagaac cctangacct tcccttggat ctctagcnca 420

atctacttgg agtcttctac ccaatgccct 450

<210> 1135
<211> 305
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1135

tacttcacat ggacttgatg gggcctatga agttgaagcc ttggagaaaa aggttgccta 60

tggtgttgtg gatgatttct ccagatntac ctgggtcaac tttatcagag agaaatcaga 120

cacatttgaa gtattcaaag agttgagtct aagacttcaa aaagaaaaag actgtgtcat 180

caagagaatc aggagtgacc atggcagaga gnttgacaac agcaagttta ctgaattctg 240

cacatctgaa ggcatcactc atgagttctc tgcagccatt acaccacaac aaaatggcat 300

agttg 305

<210> 1136
<211> 441
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1136

tgcttctcac acgttactct gatgacaaca tctcttcctg agactcttgc ttcaactctg 60

ggacatatct tgataggtgt atcatcacat gcgcaaacgt tgtcagcaac attggttgta 120

tttattttga aacatcctac ggattctgtc tttctcttct tgttatcttt ttccaaatcc 180

tttacacgct gctgaagata tttcacatgc tctatagcgt tgganagaac agaagccttg 240

tccatctaca cattagagat atcttacata ttattttata agctaatgat ggattggtgt 300

gatctaaatn tcttaagttt ggctttgaaa ttacaataac aacaagaata aattttattc 360

cagtggatga ctcagatata tgaatatcga tcacaagaga tcattaaact agcttaaaat 420

caaattctgg gaatatatta t 441

<210> 1137
<211> 384
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1137

cctcttcacg ttaggaatat gaatgtagca tatatatcca tagattctta cgtgctntgc 60

tgatggcttc ttcccgttcc aagcttcaat tggagtcttg acttttacag acttagttgg 120

acatctgttg agtatgtaaa cagcagtgta gactgcttca gcccagaatg tgttaggtaa 180

tcccttctcc ttgagcattg atctagccat tatcataact gtgcgattct ttctctcgaa 240

cactccattt tggtgaggag aatatgcgac tgntagttgt cgcttaatgc cttcatcctc 300

acataatctt tcaaactcgc gagaggtgta ctctttgccg tgatcacttc ttagtacttt 360

tatacatttt ccactgtgat tttc 384

<210> 1138
<211> 422
<212> DNA
<213> Glycine max

<400> 1138

gacaatataa tccatatctt gtgataaata ataatgtata atatataaag agacatctaa 60

ttacttagca gatcatagtc cattaggtaa cattatatga tataagcaat ttatttcatt 120

ttaccttcct taaatttctc acattcctta tttggaagca ttagtaatgg tgcctctttt 180

aaccaatctt gagtgcaaat aatagtatcc actatttttg gtgttaggga gttgcagtat 240

ggatcaagca ctcttccacc attgctgaat gttgacttag aagtcacaat ggtgacatgt 300

atagccagaa catctctcgc aatatgttca aggaccaaga attgcccaca ctttaatctg 360

caccaatgtg gatatccaaa gccttagcct ctaaggattc cttcatgtat ctatctaact 420

ca 422

<210> 1139
<211> 421
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1139

tgacaatgac tntntactcg gatgtctgat tgaggcccgt aatatatcga gacgctcgaa 60

attgaatgtg gaagctctga gccatttcaa acgacaataa ctatttactc ggatgtctga 120

ttgagtcctg tcatatatcg agacgctcga aattgaatgt tgaagctctg agcaaattca 180

aacgacaata actntttact cggatgtctg attgagtcct gtcatatatc gagacgctcg 240

aaattgaatg cggaagctct gagccaattc atacgacaat aacttttac tcggatgtct 300

gattgagtcc cgtcatatat cgagacgctc gatattgaat gttgaacctc tgagctaatt 360

caaacgacaa taacttctta ctcggatgtc tgattgagac tcgtcatata tcgagacgct 420

c 421

<210> 1140
<211> 390
<212> DNA
<213> Glycine max

<400> 1140

tctctctctt gtgcaactgt ctcatcctat tctcaggtgt ataatgaagc tttgcaggtt 60

caggtgcagg tgttgctact ggtggaggca cttgaatttg gttgctatac ctcaacgtga 120

tggcactcac atgtttcgga ttttgcacag tttgtgaatg caatttgtca gaattctggg 180

actgagctcg gttcatctga gtagccatct gccccatctg atttgtcaga ctttgaatgg 240

aggctcttat ctcttgctga aattgcatat tatgcatggt cattgtgcct gactaacttc 300

tttaagggag gttgatgacg agcctaaata gttgttgtct ttgtgggact gctgctattg 360

ctgatgctgt tttgaggatg aacatatggc 390

<210> 1141
<211> 428
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1141

tggatntcct gttagtacgg aatctttcct tcctaagatg gagccaaacc cagtcccccct 60

cattaagaac tagctccttt cttcctctat tgcccttagt tgaatacacc ttctgttgga 120

tctctatttg tgtcttaacc ctctcatgca acttctttac aaactctgac ctagattccc 180

cttctatatg tataaaagaa gtgtcaagtg ggacgggaat gaggtctaat ggtgttaatg 240

gattgaaccc atagacaacc tcaaaaggcg attgcttggt ggttctatga accctcctat 300

tgtacgcaca ttctacatga tgaagatact catcccaaga ttatggntgc cttttagaag 360

agcccttata agaggggata aagacctatt cactacctct gtttgcccat cagtctgtgg 420

atgacaac 428

<210> 1142
<211> 475
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1142

tattaggacc tataatactc agcttatgag agagtcaaag atcaaattga gagganaaat 60

ataagctatg ctaaacaagc caacanaggg agaaagaagg ttgtcttcga acccggagat 120

tgggtttggg tgcacatgag aaaagaaagg tttccggaac aaaggaaatc aaagcttcaa 180

ccaaggggag atggaccatt tcaagtgctt gaaagaatca atgacaatgc ttacaaagtt 240

gagctgcccg gtgagtataa tgttagttcc accttcaatg tctctgattt atctcttttt 300

gatgcagatg gagaatccga tttgaggaca aatccttctc aagagggaga gaatgatgag 360

gacatgacca agagcaacgg caatgatcca cttgaaggac ttggaggacc tattgatgat 420

gacatgccaa gagcaatggc aacgatccac ttggaggact tggatgacct atgac 475

<210> 1143
<211> 284
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1143

agcttgaacc ctaacaatgg aagctctcta tattttcaaa tggnnntanc ttctcagacg 60

gatgtttgat ttggacacat aatatatcga gacgctagaa attgaacgat tgaacctgtc 120

gagaaattca attggtcata acgttacaca cggatgtgcg attcgggcgc attatatatc 180

gtgactgttg aaattgaaca atggaccctt ttgagatatt tcaatggtca ttactatatc 240

acacgaatgt gcgattcagg gactaaatat atcgagacgt gtga 284

<210> 1144
<211> 312
<212> DNA
<213> Glycine max

<400> 1144

agcttactgg gggacatctt gacttgcttt cctatctgac attcaccaca gattctgcct 60

tcttctattt tcagatagag gatgcctcta acaccacctt tgtgaatgat ttccttcatg 120

cctcttaagt gcagatgtcc aaatctttga tgccatattc tgacttcatc ttctttggag 180

gatagacatg tggaggagta cctggttttt tgaggtgtcc ataggtagca gttgctcttt 240

gatctgctgc ccttcattag aacttcactc tactcatctg tcaccaagca ttctgactat 300

gtgaagttac tt 312

<210> 1145
<211> 168
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1145

gtccgatncn ggcgcataag agatcgagac gcttcaaatt gaccatcgga agccttagag 60

aaatttcaat ggtcataact tctcactcgg aggtccgatt caggcgcata atctatcgag 120

acgcccaaat tgaatcatgg aagctcttga gcaattcaca tggtcata 168

<210> 1146
<211> 348
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1146

ctatgattgt cacgtgctca tgcatttatt gttcgtcttg tctatacgag acatcttgcc 60

taacaaagtc aagttagcca taactcgcct gtgctttttc ttccatgcta tatgtagcaa 120

agtcattata tcctgtcaca gttgatgagt tggaaaatga agccgcaatt atactatgtc 180

agntggagat gttttttccc cctgctttct ttgacatcat gaatcacttg attgtgcatc 240

tggtcagaga aatcaaatct cgtggtcctg cttatctacg gtggatgtac ccggtngagc 300

gatacatgaa gatcttaaaa gggtatacaa agaatctata ttgtccag 348

<210> 1147
<211> 367
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1147

agctatacat ttgctattac taatatttga ttttgtttta agcatctgct tacttgacaa 60

gacgtgcaac ttgagtaata aactgagaga ccgattcttg agttgccaac actgaagaag 120

atggttctgc taaaggcttt gcgggtggtt cctcctttga tttggctttc ataggaggag 180

aagtagcatt ggaggaacta tcaagggcaa ccttgttgaa gccaaaaaga tgagaccaat 240

atgtgtgtca caggagaaga ttttaacaag tttacacatt ctagtgatgt ttggatgaac 300

ttcttcaaca acacttgagg aagatattaa taaggtaaaa tggattaaac tanaatcaac 360

ttatgca 367

<210> 1148
<211> 338
<212> DNA
<213> Glycine max

<400> 1148

agcttctcaa tgatgtgagg tctgaatttg cttttctatc acgcgttggc gtcttccaga 60

atttgattgg atgaccacga gcggttgttg gaacaggatc tgactgagct tggtgagccc 120

aggtgcagcg tgatgtcaaa catggaaaat ttgaatgacg cacacattga agtggacagt 180

gagagaaaga aactcagggt tgcagagtct cctaacagac agcttgaacg ggatctgaat 240

atggaatacg agcttattgt gagtcggagg atgagctgat aaagagacga ctttttgga 300

gcaggcagtc aacgaagtgg ctttttttta gaggaatt 338

<210> 1149
<211> 352
<212> DNA
<213> Glycine max

<400> 1149

catgcaagct taccattcat agaatacctc ttctctattt tatattgacg taccacagct 60

ccatcttgaa catgtcctaa ttgcgcaaac gctgtaatat caattaacaa ggttctatca 120

tcacgcacca catgtgtcga ccttttcata taataaaata ttgtcaaagc ctcgatgcta 180

caaccattct gatcatatcc agccattatc gtattacaag aattaacatc tcctctgcgc 240

atttcatcaa ataaccgcgt ggctgcaaga acgctacccc gatttcgctt aaccatctat 300

caaactccac gccctttttc cacttaacat accctaccga cattgaattc ca 352

<210> 1150
<211> 385
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1150

tgagcgtctc gatatactac gggactcttt cggacatctc cagaaaaagn tattgtcgtt 60

tgattttgct cagagcttct gttctgaatt tccagcgtgt cgatatacca cttgtcacaa 120

tcagacatcc gagtaaaaaa ttattgtcgt ttgaatttgc tcagagcttt tggtttcaat 180

cttgagtgtc tcgatatatt acgggattaa ttcggacatc cgagtaaaga gctattatcg 240

ttagaatttg ctcagagctt ctattttcaa ttacgagcgt ctcgatatac tacgggacac 300

aatcggacat ccgagtaaaa agctattgtt ggttgaattt gcttcaagcc tttgttttga 360

attttgagcc gttctgttta ctatg 385

<210> 1151
<211> 386
<212> DNA
<213> Glycine max

<400> 1151

aaatttagga ggctggaggg gggtatccca tgaaagcaag ctgagaggac taccattatt 60

taatctcccc gctcgctatt gttaatgatg tgtacttgtc tagaagttta gaactaaatg 120

ctcacaagag ttcaacatca catctttcac gccccccgag ctattacacg ttttcgtccg 180

tgggccaaga taaccccaag ctcagtacga aataataaat attacctcta tatcattgat 240

tatttttcaa gataaacatg ggtctatttc ttaaagcaca aatcataacg tctttccacc 300

ttcaagaagt tcaaagctgc agtaacaaaa gatagtggct gagagatcac agtcattacg 360

actgatcgag gatgagaatt cacttg 386

<210> 1152
<211> 444
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1152

gcaaacttct tatatccata aggaaattca atcaataggc ctccaatctt taatggagag 60

ggttaccact actcgaaaac ccgaatgcaa atttttattg aggcaataga cttaattatt 120

tgggaagcca tagaaatagg gtcttatata tccaccacag tagaaagaat tacaatagat 180

ggaagcacat caagtgaaag cataacaata gaaaaaccta tagatagatg gtctgaagag 240

gataaaagac gagtacaata caatntataa gccaaaaata taattacatc tgccctggga 300

atggatgaat atttcacggt ttcacattgt aagagtgcta aggaaatgtg ggacactcta 360

cacttaacac atgaaggaac aacatatgtt aanagatcta ngataaacac attaactcat 420

gaatatgaac tatttacgat gaat 444

<210> 1153
<211> 404
<212> DNA
<213> Glycine max

<400> 1153

gatccttaga gataacctcc acgcatgcaa gcttgtagaa cttcccaaag gcaaatatgt 60

tgttggagca tagtgggtgg tcagaaacaa gctagatgaa atatgtaagg ttgtgaggaa 120

taaggctatg cttgtagcca agggttattg agaataagaa ggtgtaaatt ataccgaaac 180

ttttgctcat gttagtcgtc tatagacaat acatatttta ctatccttta ctgctcatca 240

tggtatgata ttttgtctat agaaaaaaga attgtatttt ttctatattt tgaaaaacgc 300

acaatggtgt gtataaatac ggttacaaga ctgattgtat acactaattc tgagctaaaa 360

ataaggaacc aaaatcccta taattgctgt aactatgaaa ggaa 404

<210> 1154
<211> 332
<212> DNA
<213> Glycine max

<400> 1154

gtagacaata taatcaatat cttgtgataa aaaaaaattt ataaaatata aagagacatc 60

taattactta gcaaatcata atttattaag taacattata ttatataagc aatttatttc 120

attttacctt ccttaaattt ctcaaattcc ttatttgtaa gcattagtaa tggtgcctct 180

tttaaccaat cttgagtgca aataagagta tccactattt ttggtgttag ggagttgcag 240

tatggatcaa gcactcttcc accagtgcta aatgttgagt tagaagtcac aatggtgaca 300

ggtatagcca aaacatattt cgcaatattt tc 332

<210> 1155
<211> 433
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1155

actaagctta atttacacca gattgttgaa gctgttaata aagataaagg tggtatgttt 60

tttctctatg gatatggagg tacaggaaaa acatacattt ggaaaacact tgcaagttca 120

ctaagagctg acaataaaat tgtaataatg gtagcctcta gcggcatagc ttctctacta 180

tttcctagag gtagaactgc acattcaaaa tttaaaattc tagttccagt ttttgaagac 240

tcaacttgca atatccatca aggaactcaa ttagctgaac tattaaatca gacaagtcta 300

atcatttggg atgaagcacc catggctcac aaattctgtt ttgaggcact tgatcacagt 360

cgtagagata tcatcaaaca caactcanag gacaataaaa tctttggagg taaagtcatg 420

gtctttggtg gag 433

<210> 1156
<211> 337
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1156

agctntggaa aatgatatct atacaaaagt tattttatga agcgactaac actcatgcct 60

cttgtccttc atcgtaagtt gatccttagc tacctatgaa gttgtttgag gatgcaacac 120

aaatttagcg ctaagatggg tgagggtaat ctcattactt aggtctttat aaatgacctt 180

cctatcaagc tgccatgacc ttactaaaag aatatgccct acctccatgg gaactatatc 240

ataattaaat tcatccttat atgtcctaat ggagaaaggc accttcactt gctggtaaca 300

atcattatcc ctttctcact gagccattaa agtttat 337

<210> 1157
<211> 397
<212> DNA
<213> Glycine max

<400> 1157

agcttgagct tggctcatta cttgtcatag gtttttttta aggctcggct cggcttatat 60

aaaagtctgg tttggcccac gagcctattt aaaagcttgc ttaaagacgt atttgattaa 120

ttaattattt taaaacctag tgaaatacta actaaaaaaa gaaacttata aaatataaaa 180

tttcgtataa ataatgtaca aatccaaaaa taattgataa acaaaatcat attgaattca 240

agtcgttaaa gcacaaagta tatcaaaaga aaataaaaag agcataatat taaaaaatgt 300

atggattaga gatgattggt agaaaatgaa ttctattcta cgtgaacagt gtgcatgaac 360

agtaataaaa actgaaattc taaaatccta aaattat 397

<210> 1158
<211> 305
<212> DNA
<213> Glycine max

<400> 1158

cactttgcat gtctaacatg agttctcata ctctcggtta catccctata agcgcaaaaa 60

ccattctcta ggtctttctc tactacatat ctacgacgaa cacattgagg aatcttcttt 120

tggtgatact tctccaaacc tgatttggca agggctatat caattatacc cagcttctgc 180

ctctctcttc tgcacccata tcatgcaata tggtgtatca gacacaattg tccttctttt 240

cttgtccttt tgagacctat aatcattgtg tactctatgt attatgatag actgaagact 300

atgga 305

<210> 1159
<211> 438
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1159

ctatgttcta atgcaggcac ttagagcttg tcatgatgct ctcaaatcat ttatattatc 60

atatggtttc acaaccagaa gaagcaaccc ttctctcttt atctacatct cgggtaacat 120

aactgtctat tttttggtgt atgttgatga cctccttctc acaggaaata acactacatt 180

catagacaca ttcattgagt tcttatctaa tcggttgtca ctcaaaaaca tgggggcacc 240

atactacttt atgggtattg aacttatacc catgaactca agcatgttcc tctcacaaca 300

caaatacatc aaggatgtac ttgagatatt tgagatgcan gatgtgaagt cgtcacccac 360

accacttgcc tcgacgacta cactcatgtn gcatgatggt acaccaacca ataatgctac 420

tcaatatcat agaattat 438

<210> 1160
<211> 429
<212> DNA
<213> Glycine max

<400> 1160

agcttgttta ccccatgttg aattcgctta caataaagtt gttctttttc accactaatt 60

gctctccttt tgaagttgtt tatggtttta acccactaac tcctcttgat cttttgccta 120

tgcctaatgt ttctgttttt aagcataaag aaggtcaagc ataggcggac tatgtgaaga 180

agcttcatga gagagtcaaa gatcaaattg agaggaaaaa taaaagctat gctaaacaag 240

ccaacaaaag gagaaagaag gttgtcttcg aacccataga ttgcgtttgg atgcacatga 300

caaaagacag gtttccggaa caaaggatat caaagcttta accaaggtga gatggaccat 360

ttctagtgct tgaaagaatc aatgacaatg cttacaaagt tgagctgctc ggcgagtata 420

atgttagtt 429

<210> 1161
<211> 377
<212> DNA
<213> Glycine max

<400> 1161

tgcaagcttg atgtttgtgt tgaatgcatt aaaggtttac aatctcaaaa acaagaaatt 60

aagtgcatat agggctacag acgtcttgga attgatacat acaaacattt gtgggccatt 120

tcatacacct tcgtggaatg gttaacaata ttttatatca ttcatagacg gttactctag 180

atatgcatac ttgtttctta tacatgaaaa gtcacaatct ctggatgtgt tcaaaacatt 240

taaagttgaa gttgaaaatc aactcaacaa aagaataaag tgtgtcaaat ctgaccgtgg 300

tggtgaatac tatggcaaat atgacggttc aggtgaacaa cgtctggcgt ctttttcctg 360

gtacctagat gaatgtt 377

<210> 1162
<211> 292
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1162

agcttatgaa tgcttactgt gaccgattat tctgtttatn tcaactacat tgcttttctg 60

tttgatggac accgcctcct agctgagcag actccagatg aggtttgtgt ttcctacatg 120

tattcatgaa ttccccttgt attctttatt cttataatct acatttttcg gtttgacttg 180

aatttctttt tgttgcagtt ggaaatggat gacggtgacg agattgatgc catgcttcac 240

caaacaggag gttctgttgt ctgaaggatg tgattacctt tgctcctcat ta 292

<210> 1163
<211> 430
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1163

tttgagcaat tcanatggtc ataactnttc actcggaggt tcgattaagg cgcataatat 60

atcgagacgc tcgaaattga acaatggaag ctctcgagaa attcaaatgg tcataacttt 120

taactcggag gtccgattca ggcacataat atatcgagac gctcgaaatt gaacaatgga 180

agctctttag caattcaaat ggtcataact tttcactcgg aggtccgatt caggcgcata 240

atatatcgag acgctcgaaa ttgaacaacg gaagctctcg agaaattgaa atgatcataa 300

cttttctcac ggaggtcaga ttcacgcgca taatatagcg agacgctcaa aattgaacaa 360

cggaagctct cgatatattc aaatggtcat aactcttcac acggaggtcc gattcaggcg 420

cttaatatat 430

<210> 1164
<211> 435
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1164

tgaaggcgtg tagcccacca tcttttcata gtagaatatt tgtaatgtgt ctactatcat 60

tgttatcatn tttttcttcg tcattgaggt gccacttgag ctgccagatc tctccacctt 120

tgggtgtatt ctttgaaaga accgtgcccc tttttgcaca tgttctatag ttgcatccta 180

tccgaaacca tatcaaaatt gtactgatac tgcctaacaa aggcaaccat taggtccttc 240

caagaatgga ctcgggaagg ttccatgtta gcgtactatg taacagctac cccagtaaga 300

ctttcttgga agagatgtat caacagttcc tcatcttttg cgtatgcccc catctttcga 360

caatacatct ttagatggtt cttggggcaa gtagtcccct tgtacttgtc aaagtccggc 420

accttgaact tggga 435

<210> 1165
<211> 429
<212> DNA
<213> Glycine max

<400> 1165

ctctatattt taacaatccc atcctccctc cagataatga gtttctggtg gagagtagat 60

ggcacagccc cgactccatg gatccattcc cttcctaata gcacgtcaaa attagccttg 120

gactgtatca ccaggaataa agttggtcga actatactgc ctacagcaac atctacttga 180

atggctccca cagaatagcc agtgttaccc tcataattcg aaagcacaat gttgtgggca 240

gatagatcag tgtcatgttt cccgatcttg tagagcatac atcgaggcat taagttaaca 300

gacgctcctc catctatgag cacatttgtg attccaacat tctcaactct tgccctgatg 360

aaaagaggtt cgagatgact tttcactcga aaatctggct tatgaagaac gctaattgtt 420

catccacac 429

<210> 1166
<211> 394
<212> DNA
<213> Glycine max

<400> 1166

tctagccaaa tggacttacc ttgaattaat tcctttgatt tctcctttga gccttgtttc 60

cctttccttg ttttgaagct cactacaagc cttaagtgaa aaaccatgat attaccatat 120

ccttaaggaa ttttggagct ctggaattgt tttgcgaata agtgtggggg gtatttgttt 180

cattggacaa cttgtgatgc aatcctactc cgcaagggca ttggatagaa aaactccaag 240

tagattgggc cagagatgca agagaaggcc ctagggttct tatgagcctt agggtagaat 300

tcgggcccat gggctaagta cgagcccgct tatctttgta aatattagat taaggtttca 360

ttatttttgg gccttgtata tagggcttca taat 394

<210> 1167
<211> 516
<212> DNA
<213> Glycine max

<400> 1167

agcttgtcaa tgcagcctta tcttgagata cacccaatcc ccctccttaa tctttgaagg 60

taggcgatga ttattggcat actatgtcat gtgattttgg gctctgttta gatgaaactt 120

caactgatta agtgcttcat ctctttctat aagatcctaa gccactgcct caactaggac 180

ttcccctaga atgaaccttg ccaaagatgg ggatggtcga ccataaccta tttcaaatgg 240

ggtacacctg gcagctccct ggtaatatgt attataccac tattctgccc acgggataaa 300

ctcaacccaa gatttggatt gctttgcaca catctcaaat atctctccat ggttatgttt 360

agtaccttag tttggccatt tgaccgaggg tgataagcaa tacttatttt caaagttggt 420

ccttgttttt tgaataactc ctgctaaata taactcaaag catccttgtc ccttcactat 480

tgaaaaaagg aattccaagc tgccttatta cttcct 516

<210> 1168
<211> 678
<212> DNA
<213> Glycine max

<400> 1168

tcccaagttt ttaagttctt cctcaaaact gtcctaagca aagttcccaa agtcctatta 60

acaacttccg tttgcccatc ggtttgtggg tgacaagtgg ttgaaaataa caatttagtg 120

cccaacttgc tccacaaagt cctccaaaaa tggcttagga acttagagtc cctatcacta 180

acaatgctcc ttggcaaacc atggagtctc acaatctcct tgaaaaacaa atcagccaca 240

tgggaagcat catcaatttt tttacatgga ataaaatgag ccattttaga aaacctatca 300

acaaccacaa aaatggaatc tctaccattg cttgtttttg gcagccccaa aacaaaatcc 360

atggataaat caatccaagg atactccgga attggcaatg gagtatacaa tacatgaggc 420

tttaccttag actttgcctt tttacataca atgcaatgtt cacaaaattt ctgcacatcc 480

tttttcatat gaggccaata aaaatgttct tgtaatgttt ctagagtctt ttggacccca 540

aaatgcccca tttaacctcc ttcatgtgct tcacaaacaa gcaaatttct agtagaacat 600

taggcacaca caattgtttt cttgaaaaga aagcttcatg tctaaaaaac atttctgaaa 660

aatttcacaa ttttaaaa 678

<210> 1169
<211> 578
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1169

agcttcttct tgtttctctc cccatttgaa accaacattt ttcttgagca cttcattgag 60

aggtgctgcc aatgtgctaa aatccttcac aaatcgtcta taaaaacttg ctaagccatg 120

aaaactcctc acctcggtca cagacttagg tgtaggccat tcttgaataa ccctaacctt 180

ctcctcatcc acttgcactc cttttgaact cacaacaaaa ccaagaaaca caacatggtt 240

agtacaaaag atgcattttt caagattgac atacaattgt tcttctctaa gcacagtcaa 300

gacagatttt aaatgatcaa tatgcaaatc aagtgaagtg ctatagataa gaatatcatc 360

aaagtacacc acaacgaact ttcctatgaa ctctctcaag atatggttca ttaatctcat 420

gaaagtgcta agagcgttag ttaggccaaa aagcataacc aaccattctt acaaaccata 480

ttttgttnta aaagccagtt ttcattcatc ccctttctaa tctaatttga tggatccctt 540

tttaaatcga ttttaaagaa tacatgcccc atgcaatt 578

<210> 1170
<211> 552
<212> DNA
<213> Glycine max

<400> 1170

atatgttata tttaatcatt ttaatatata atactatata tggagaaaaa tacttatttt 60

aatacataaa tattaaatta ataacattaa atgcaacctt aatatttttg tttaaatctc 120

gtttaaaatt ttaaatttaa ttacttaaaa aatatgtatt aaaaatattt tttttacata 180

tatagttaaa tataaattaa aatatttttt tggttaccat gcaatttata taaaatattc 240

acctgcttta actttaccga aaccttaaag tttttatttt ttaaatccgc aaacaaatta 300

tatatattag aagtaagtat cagagatacc ttaagaacaa aatataagcc caacattcag 360

caactcggtt aatcaatatt aatatctgat caaaagatat aagattaatt tgataaataa 420

aaattaaaat ttaagagtga aaagagaaat tgtgagttta aatttctgtc attaatattt 480

ctaacaaaac taataaaata actcatttac tgaaaaaaga acacctcatc cgattaaata 540

taaactaacc ca 552

<210> 1171
<211> 420
<212> DNA
<213> Glycine max

<400> 1171

tgcaagcaaa ctggatgcgt tggtcaactt ggtaacccag ctggccttga atcagaaatc 60

tttacctgtc gcaagggttt gtggtttgtg ctcctctgct gaccaccata cagacctttg 120

cccttccatg cagcaacctg gagcaattga gcagcctgaa gcttatgctg caaatatcta 180

caatagacct cctcaacctc agcagcaaaa tcaaccacag cagagcaatt atgacctttc 240

cagcaacaga tacaaccctg gatggaggaa tcaccctaac ctcagatggt ccagccctca 300

gcaactacaa caccagcctg ctccttcctt tcaaaatatt gttggcgcaa ccaaaccata 360

cattcctcca ccaatccaac aacataacca ccccataaac agccaacagt tgaggcccct 420

<210> 1172
<211> 496
<212> DNA
<213> Glycine max

<400> 1172

tgccttccaa gaatgatatt gcggttatca tgtacacaag tggtagtaca ggtctgccaa 60

aggtttgttt cttcgtcaag ttttgttaaa ggtgtccctt tctgtgtgtc tgtgaatgta 120

taatctctta ttcatatttg tgatttgatg caaagtgctt ttgtccagag tcatgcttgt 180

gaataatgat tttgggtgat aaaatatcaa caagaaccat atcaagacat tgtattaata 240

taatgaaaat tttcttgtct gcaacattga gaaccaatag gatctccctc agctcagttc 300

tatgattccc tttgatttga cagggtgtta tgattactca tggaaacatt gtagcaacaa 360

cagcagcagt tatgacaatt attccaaatc ttggtagcaa ggatgtgtac atggcctact 420

tgccccttgc tcatgttttt gaaatggcag cacaggtaat ttcttcttag ccttctaact 480

gtcaaagtag ttgatg 496

<210> 1173
<211> 486
<212> DNA
<213> Glycine max

<400> 1173

ctaattaacc taaaattgag agaaaatgat tttttaacac acaaaccgga agtactaaat 60

atttattacc aaataaattg gaataatctc atacaattta cacaagtttt atacataaaa 120

ggtagtgatt ttcaccgact aacagaggcc tctacaatca cctttcctcc ttctctatta 180

tactgccatt gatcttcaag aagcaaatga ctctattgat gaacaacatc caaagtctac 240

aagctccaca tgaagctaca tcatgtggga tcaagaacag cttcatctac gagaagctct 300

tttgcttcct ctatcttttg cttgggcaat tcaatttaat aacgtattct taacaatttc 360

tccatgtatc tgcttcattg ccttgcggtt tggttctgct gaaagtttat tccaataaac 420

acaccgattt aatcctacat ctacacttgt tattggattt ctatgggtca aatttatcca 480

tatact 486

<210> 1174
<211> 615
<212> DNA
<213> Glycine max

<400> 1174

gaaagataga acagccaaaa agactgacaa actgacatga ataatgtact attgttgtaa 60

gcttttcaag gaatcaccgc atcctgatga aaagcagagg caacaactca gcaaccaact 120

tggccttgct ccaaagcaag ttaagttttg gttccaaaat cgtcgaaccc aaatcaaggt 180

atctaaattt atttacctaa atattactca agaatatatg caaacttaat ttatttaatt 240

agaaattatg taagcattat gcaatattat tgccttttgc aggcaataca agagcgccat 300

gaaaattcat tgttgaagac agaattagac agacttaggg aggaaaataa ggccatgaga 360

gagaccataa acaaatcttg ttgccccaat tgtggcatgg taacggctac catagatgct 420

tccatgtcca ctgaagaaaa acaacttctt attgaaaatg ccaaactcaa agccgaggta 480

ataaatttgt ataaaactaa atctaaatac aaggaacatg aaactttaaa aaaagaaaat 540

gtattaatgc tagaataatg gtggatctat gtgtcaaagt acaaactaca atcttaatga 600

aaagattccc taata 615

<210> 1175
<211> 684
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1175

tatatcgttg ctagcaagca gtatatcatc gacatataac accaagaatg agtatttact 60

cccactaaac ttgtggtata cacaatcatc aactgcattt gcctcaaaac catatgaggt 120

aatgacttga tggaacttgt aataccattg acgggaacct tgcttcaaac catagatgga 180

cttatttagt ttgcaaacca tagactttga gtcacctgat acaaagtttt ctggttgcat 240

catataaatt gtttcttcaa tgtcaccatt tagaaacata gtcttaacat ccatttgatg 300

tagctctaaa tcataatgag ctaccagtgt cattattgtt ctaaaagaat cctttgaaga 360

tattggagaa aaggtttctt tatagtcaat gccttccttt tgggtaaatc cttaggcgag 420

ccttatatct ctcaacattg ccctttgaat ccctttttgat tntaaatatc catttgtaac 480

caataggttt cacactttta ggcaattcga cgagatccca aacgtcattg tcttgtatag 540

atttcatctc atctttcatg gcattgatcc aattttgaga gttagaacta cgcatgactt 600

gtgataactg ctaaataatt gtgaataaat gtagaaaatt agccaaattt ttgctttaaa 660

atattattta gcagttattt gtga 684

<210> 1176
<211> 506
<212> DNA
<213> Glycine max

<400> 1176

agcttgagct tggctcatta cttgtcatag gtttttttta atgctcggct cggcttatat 60

aaaagtctgg tttggcccac gagcctattt aaaagcttgc ttaaagacgt atttgattaa 120

ttaattattt taaaacctag tgaaatacta actaaaaaaa gaaacttata aaatataaaa 180

tttcgtataa ataatgtaca aatccaaaaa taattgataa acaaaatcat attgaattca 240

agtcgttaaa gcacacagta tatcaaaaga aaataaaaag agcctaatat taaaaaatgt 300

atggattaca gatgattggt agaaaatgaa ttttattcta cgtgaacagt gtgcatgaac 360

agtaattaaa actgaaattc taaaatccta aaattattct cctctccgaa aaaaaactcc 420

ttacctaaaa cttgggggct ggtatataag tccacggtcc tcaaacttac aaatttattt 480

aagttccacc ccttaacgaa atttaa 506

<210> 1177
<211> 559
<212> DNA
<213> Glycine max

<400> 1177

agcttctaaa ctttgtacaa gaatgaatct ctgataccac ttgttagaca agtggcctca 60

gatatcttaa gaaggggggg ttgaattaag atgtcccaaa ctgtttcccc taattaaaaa 120

tctatttcac tttttactca agttatgaat tcccttaatg acaatcttct taaatattaa 180

ttcaaatgaa gcaacttgaa tatgaatata aagcaatgat aaataaagga gattaaggga 240

agagaaaatg caaactcagt tttatactgg ttcagccaca cccttgtgcc tacgtccagt 300

ccccaagcaa cccgcttgag agttccacta tcttgtaaat tccttttaca agttctaaac 360

acacaaggac aatccttcct ttgtgtttag agatccttta caacaagaga ctcacagtct 420

cttaatccct tatagaatga aaaaaagaaa aagaaccaat ctctctagaa agagatggat 480

tttacagatt gaccactcaa ataattcctt aatgaattgc catttgaatg gccaacgaat 540

tctttagaag attaaatga 559

<210> 1178
<211> 369
<212> DNA
<213> Glycine max

<400> 1178

tctattctga atgtcaagcg tctcgatata ctacaggaca ctatcaaata tccgagtaaa 60

aagttattgt cgcctgaatt tgcttagagc tttcgttttc aattttgagc ttctcgatat 120

attacgagac tcaatctgac atccgagtta aaagttatcg tcgttagaaa tttctcagag 180

ctttcgttat caattacgag ttactcgata tattatggga ttcattcgga cattcgagta 240

aaaaattatt gccgtctgat tttgctcaga gattccgtta tcaatttcga ggatctcaat 300

atatcacagg attcatttcg acatctgagt aaaagttatt ggcctttgat ttgctaacag 360

cttctattc 369

<210> 1179
<211> 511
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1179

ntatgcttgc tctcttattc acaccaaaaa aaggagacca aatctaccaa agccaaaatc 60

tcctacaggt ccaaactcaa aaagacccat tgatctgtga tgattatgcg cattacccct 120

tgatttgatg ggaaatgact tgcaaaatcg atttatgacg tgtttgtgat ttggaattga 180

gaggagacac ttgccagtgt gagattttat acacctttga gtggttttcc tccattttat 240

tgaatctagt gtttcttcta atgtttctgt agaaaagaaa tgcaaaatgt cttaatctca 300

ttcttggtta tgagaaattc tatctttgtg ctttcattcc tcattcgtgg cattattttt 360

gaaaaaaaaa gtgtgttctg atcggtttgg gagtttgatt tctttaccaa gtgtgttcgc 420

attttaatgg aagttttcac aaactccaat gccttctgtc ttttacattt caaagactgt 480

aatgtcttca gtcttttaca atttcaaaga c 511

<210> 1180
<211> 531
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1180

tcctcaattt ttttggattg atgctcttaa gacggttgcg tatatattaa accgagttcc 60

aaccaaaatt gtctcaaaga caccttttga gctattcaag ggttggaaac caagtttgcg 120

acatatacgc atttggggat gtctgtctga agtaagaatt tataatccac aagagaagaa 180

actagaccct aagaatatta ctgggtattt cattggatat gctgaaaggt ctaaagggta 240

taggttctat tgtccatccc acaacactan gattgtggaa tcaaggaatg caaagtttct 300

tgaaaatgac ttgatcagta ggagtgatca atttcagaac atttcttctg aaagggatca 360

ctatgaagct taaccttcta ggacaagtaa taggttggta gtcattccca cccctcaagt 420

taaaatgggt gttagacaac cagtgattga agttccacaa gctgttgaaa gtgatcatgt 480

agatcaagtt gtttgtgagg aacaaaatga tgatattgaa acaactagtg a 531

<210> 1181
<211> 361
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1181

tatagagctc tgtagtgggt tgtaaatgga ataacgattt aaacaaatga attaatatat 60

tcttggactt gannagaaga ttannaaata gtaccatatt ttaatttaag atgcccgaaa 120

cttcgacaaa ataccgacaa caatttattt aacgaaaaaa ataagtattt ctattaaaaa 180

aacttgtttt attcaaatat tatattttat caaaaacaag aaatttggaa aagtaagtaa 240

ttgaatttct ttatccaagc ataaaattct aaaaatgaag caatttattt tattaatcca 300

agcacacaat tttgaaaatg aaataatttc atatgaagca tttaaaattc tatagaattt 360

t 361

<210> 1182
<211> 444
<212> DNA
<213> Glycine max

<400> 1182

ggataatgtg agtgtatgta tacatgattt tgatgatgtc aaaagaacaa tcagacgaag 60

gtgcttcaaa ggataagcat ggcttcaaga ttaatacaag actgattcaa caaacaaagc 120

cttgcttcga gattaactca aagatcaagc cttgccttaa aacaaatagc tttcaagaca 180

tgcaaggctc tagtaatcga ttaccaggcg ttgtaatcga ttaccacgca gtgtaatcga 240

ttactagcag acagggttga aaaatagctg gtgaaaagag ttttacattt gaattttcaa 300

catgtaatcg attaccatat gtgtgtgatc gattaccagc aacgaaactc ttgaaattca 360

gattccaaag tcatgaccct tcaaattata actgtgtaat ccattacacc aacattgtaa 420

tcgattacta gtggagagtt ttca 444

<210> 1183
<211> 494
<212> DNA
<213> Glycine max

<400> 1183

agcttgctaa cccatggaag ctcctaatat ctcccacact ttttggggtg ggccattctt 60

ggatggcctt gattttctca gggtccactt ggaccccatt tctaccaact acaaaatcta 120

agaaaactat attatctaca caaaaggtac acttctctat atttgcatag agggtgtttt 180

tcctaaggac taaaagaact tgcttgagat gtcctaagtg atcatctagg ctcatactat 240

acactaaaat atcatcaaaa taaacgacta caaatctacc tatgaaatcc cttaagacat 300

gatgcataag cctcataaag gtgcttggtg cattagtgag cccaaaaggc atcactagtc 360

attcatacaa accaaacttg gtcttgaaaa cggttttcca ttcatcaccc tttttcatcc 420

tgatttggtg ataaccagtt ttaagatcaa ttttttgaaa aatattagca ccatgcaact 480

tatcaagcaa atca 494

<210> 1184
<211> 597
<212> DNA
<213> Glycine max

<400> 1184

tcatgatgat gaatcaagtt gattcaagta tttttgataa tgacaaagtt gatgacaaaa 60

atcccaaaga atgatttcaa gattaagtca acaagaagaa atcaagaaga ttcaagaatc 120

aagtgaagtt tgatttcaag attcaagaaa agatgaattc aagattcaag agaagaaatc 180

aagaagactt cacaagggaa gtattgaaaa gttttttcaa aaaacaaaca tagcacaatt 240

ttgttttttc aaaagagttt tctcaaaatt ttctaagtta ccagagtttt tactctctgg 300

taatcgatta ccagtttctt gtaatcgatt accaatggca aagtttgatt tcaaaaagct 360

ttcaactgaa tttgcaacgt tccaattgat ttcaaaatgg tgtaatcaat tacaagatat 420

tggtaatcga ttaccagtgt atctgaacat tgaaattcaa aatcaattgt gaagagtcat 480

atcctttcat aaaaagcttt gtgtaatcga ttgcatggtt ttgggtatcg attaccagtg 540

acaagtttga ataaaaatca aaggatataa ctctttccat gggttttagt ttttttt 597

<210> 1185
<211> 590
<212> DNA
<213> Glycine max

<400> 1185

tcataaggct atctatgggc taaggcaggc acttagagct tggcatgatg ctctcaaatc 60

atttataaca tcatatggtt tcacaaccag aagaagcaac ccttctctct ttatctacat 120

ctcgggtaac ataactgtct atttttttggt gtatgttgat gacctccttc tcacaggaaa 180

taacactaca ttcatagaca cattcattga gttcttatct aatcggttgt cactcaaaaa 240

catgggggca ccatactact ttatgggtat tgaacttata cccatgaact caagcatgtt 300

cctctcacaa cacaaataca tcaaggatgt acttgagaaa tttgagatgc aggatgtgaa 360

gtcgtcaccc acaccacttg cctcgacgac tacactcatg ttgcatgatg gtacaccaac 420

caataatgct actcaatatc aaagaattat tggtgcatta caatacctta ccctaacaag 480

acctggcctc tcattctcca tcaacaaact ctcaatatta tgcacaaacc aaccttcctt 540

catcttccac atctcaggcg ccttctcgaa tacttgaagc cactattaac 590

<210> 1186
<211> 424
<212> DNA
<213> Glycine max

<400> 1186

agcttgtacg gccagccgct ctaacatcta atccatgaaa ggaaggggaa agtgatccat 60

ccttgttgcc ttgttaagat ttttataatc tatgtacatt ctccatccgg tcattgttgt 120

tgtgcgaatt aattcatttt tctcattctt aacaattgtc atgccaccct tcttcagatc 180

cacttgcact caactaaccc atgcactatc caaaattggg taggtcattc tagcttctag 240

aagtttcaaa acctctttcc ttacccttc cttcatcaca agattcaatc ttctttacga 300

ttgagccact agtttaaagt cttcctccat aaaaatttta tgcatgcaac aagaaggatg 360

atgtagctcc atgtagagct tgtatgcatt ggatattctt catcaatgga tttctttgtt 420

tctt 424

<210> 1187
<211> 436
<212> DNA
<213> Glycine max

<400> 1187

tctggtggga catcttgact tgctttccaa tctgacattc accacagatt ctgccttctt 60

ctattttgaa actgggaatg cctctaacaa caccttttgtc aatgatattc ttcatgcctc 120

ttaagtgcag atgtgcaaat ctttgatgcc atattttgac ttcatcttct ttggaggatg 180

gacatgtgga ggagtaactg ggttcttgag gcgtccataa gtagcagttg tcctttgatc 240

tgctgccctt cattagaacg tcattcttct catttgccac caaacattct gactatgtga 300

agcttacatt gaatccttca tgacacaact gactgatgct gatcaaattt gcagtcagtc 360

ccttcaccag cagaactttg tttagactag gaactacatc ctggactagc tctaccattg 420

caggatcttt ccttta 436

<210> 1188

<211> 514
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1188

tcattctaca cctgaaaaag aggatgagat agttgcacaa aaaaaaaagc ttcttaacaa 60

aaattttcat gcaggtggac cttcttctag taattccgac ttacagcagc ctcgtatccc 120

tcttccattc ccacctagag cgattccaaa caaaaaaaat ggaagaagtg gaaaaggaga 180

tcttggagac cttcagaaaa gtagaagtga acatacctct gctagatgcc atcaagaaga 240

ttccaagata tgccaagttt ctaaaggagt tatgcaccca caaaaagaag ctcaagggca 300

atgaaaggat tagcatgggt agaaatgtgt cagcattgat aggtaaatct gttcctcaca 360

ttcctgagaa atataaggac ctangtactt tctgtatacc ttgcatcatt gggaacatta 420

aatttgagaa tgccatgcta gatctangag catcagttag tgtcatgcct ctgtccattt 480

tcaattcttt atctcttgga tccttgcaat ctac 514

<210> 1189
<211> 511
<212> DNA
<213> Glycine max

<400> 1189

agctttgaga atgcaaattt agctctattg tctctttgtt tgcattcgct gaacctttga 60

tgtattatct gatatgttat cgaagatttt cttgtttact aacttactct ccctttatat 120

ctcaattttt tatgtgtgca cgtgagctga tgagcatgcc aatgactgat tactattgtt 180

tgaattttac ttgattgaga tataggaggt gaagatgtcg accccggcaa ggaagagact 240

gatgagggat tttaaaagat tgcaacaaga tcctcctgct ggcatcagtg gggctcccca 300

agacaataat attatgcttt ggaatgctgt tatctttggg tgtgtaggag tatataaatc 360

atgaaatttt tgttttctta agagtgtgtt tctcttaact ttgggggttt ggatgattta 420

aggtatgata acaatctaat tgtgcctttc ttggtctttt tttccagacc agatgacccc 480

ccttgggatg gaggtacaat tttatctatc t 511

<210> 1190
<211> 363

<212> DNA
<213> Glycine max

<400> 1190

agctttgcag tagatgccac tctactctaa atttttgaag gatatgttga caaggaagca 60

catgtacatt catcaggaaa acatcatagt ggaaggaaat tgtagtgctg taatccaaaa 120

gatccttcca cctacgtgca aagatcctgg gagtgtaacc attccttgtt caataggaga 180

agtcaatgtg ggaaaggctc tgattgatct gggagccagc attaatttga tgccactctc 240

tatgtgcaga agactgggag agttggagat tatgcccact cgaatgactt tgcaattagc 300

tgaccgctcc attaccaggc cctacggagt gattgaagat gtgttggtca ggggtaaaca 360

ttt 363

<210> 1191
<211> 498
<212> DNA
<213> Glycine max

<400> 1191

agctttgatg tttgtgttga atgcattaaa ggtaaacaga ccaaaagcaa gaaattaggt 60

gcatataagg ctacaggtgt cttggaattg atacatacga acatttgtgg gtcatttcat 120

acaccttcat ggaatggtca acaatatttt atatcattca tggacgatta ctccagatat 180

gcatacttgt ttcttataca tgaaaagtca caatctctat atgtgttcaa agcatttaaa 240

gttgaagttg aaaatcaact caacaaaaga atcaagagtg tcaaatttga ccgtggtggt 300

gaatactatg gtagatatga cagttcaagt gaacaatgcc cagggccttt tgccaggtac 360

ttagaggaat gtggaatcgt cccaccatac accaagtctg ggtcacctta catgaatggt 420

gtgggtgaaa gatgaaacca aattcttaag gatatgggaa aaaatatgaa ttgtcatttt 480

aactgtacca aagtcact 498

<210> 1192
<211> 440
<212> DNA
<213> Glycine max

<400> 1192

agctttagtt cactacttca agtagtgcac gatatgcttc cagaggaaaa cacgttgcct 60

aaaagttatt atcaagcgaa gaagatactg tgtccgatag gtatggagta tcaaaagatt 120

catgcttgcc tgaattattg catattgtac agacatgaat ttgaagaatt gtccaaatgc 180

cctaggtgtg gggtatcacg gtacaaagtc aaggatgatg aggatcatag tagtgatgaa 240

aactcaaaga aggccccccc cagcaaaggt gttgtggtat ctatcgatcg ttccaaggat 300

taagcatctt tttgctaatg gagacgacgc taaagacctt acatggcatg caaatgggag 360

aaactgcgat ggaatggttc atcatctgat tgattgctcg tagtgcaaga aaatagaacg 420

tttgtttcgg atttcgggaa 440

<210> 1193
<211> 621
<212> DNA
<213> Glycine max

<400> 1193

aaatggattt taaaccccca aaattgtaat actaaatatt tattacctat acttaataga 60

aaatacttat aacactacaa aataaccatt aattggaaga agttgataca atttacacaa 120

gttttataca caaaagttag tcgtattcac cgactaacac cttttacata acaaaaatat 180

gtttatgctt tataattttt ttataaaaaa attgcgatta attgcataaa taagtttttt 240

atctatagga attaaacaca atgccaaagg atttataata ctcacatcct gctcaacaaa 300

aatatgtttt tgatttataa ttttttacaa aaaaaaaatt gttattaatt acataaatat 360

gttgctttat ttacaattga tgatataagc taccctttt aatccttctt gaattaatta 420

tgatacacga cacaaactat cttaataatg actcattact tttttaatag taatagaata 480

aaatggtcga taattatttt tatttaaatt tgtattatta atgacactta gtacccttta 540

tttataatca attaattgac gtacaaaatt aagtaactat gatacaatta gttgtattca 600

ataaaaaaat tactcttttt a 621

<210> 1194
<211> 526
<212> DNA
<213> Glycine max

<400> 1194

agcttatgtc gcaaacatct acaatagacc tcctcaacct caacagcaaa atcagccaca 60

acaaaacaat tatgacctct ccagcaacaa atacaatccc gggtggaaga atcatcccaa 120

ccttagatgg tcgaattctt cacaacagta gttacaacaa caacaacctt attttcaaaa 180

tgttgctggc ccaagcagac catacgttgc tccaccaatc cagcagcaac aacaacaaca 240

gccctagaaa caacaaacag tcgaggcccc tccgcaacct tcccttgaag aacttgtgag 300

gcaaatgact atgcaaaaca tgcagtttca acaagagact agagcctcca tttagagctt 360

aactaatcag atgggacaat tggctacaca gttaaatcaa caacatgttg gatcgagtgg 420

cctcagaata ttaagaaagg gggttgaatt aattattcct aaacctttac ccaattaaaa 480

attactcttt taaggctttt acttatgttg ttaagaaaat atggag 526

<210> 1195
<211> 347
<212> DNA
<213> Glycine max

<400> 1195

tctcgatata ttatgtcccc gaatcagaca tctgtgggaa gagttatgac catttgtatt 60

tctcgagagc taccgtagtt caatttcgag tatctcgata tactattttc ccaaatcgga 120

tatccttgta ataacttatg accaatcgaa tttctcgaga gcttgtgttg ttaaatttca 180

agcgtgtcga tatattatgt cctataatca gacatccgag tgaaataata tgactagtcg 240

attttctcga gagcttgctt tgtccaattt cgagcgtctc gatatattat gttccaaatt 300

cggacatgcg tgtgaaaaga tatgaccatt ctaatttatc gaggagc 347

<210> 1196
<211> 469
<212> DNA
<213> Glycine max

<400> 1196

agctttcgag aaattcgaat ggtcattact tttcacacgg atgtctgaat ttgggacgta 60

atatatcgag aggctccaaa ttgcacaacg aaagtactcg agaaattcga atggtcataa 120

cttttcacgc ggatgtcaaa atttgggaga taatatatcg agatgctcga aatggaacag 180

cggaagctct cgagaaattc gaatggtcat aactattcac acagacgtcc gaatttgcga 240

cataatatat cgagacactc gaaattgaac aacggaagct caccagaaat tcgaatgagc 300

cataactttt cacacggatg tctgattcgc ggacataact catctagacg ctcgaaaatt 360

gaccacggaa gctctcgaaa aaattcaatg ggcattaact tttcaaaccg atgttccgaa 420

ttgggggggac taattatttt gaaaccccccc aaaatttgcc ccacggaaa 469

<210> 1197
<211> 371
<212> DNA
<213> Glycine max

<400> 1197

agcttataat atatcgatac gctcgaaatt aaacatcgaa aactctcgga aaattcaaat 60

agacataact attcacacgg atgtccgatt cgggcgcata atatgtcgag aggctcgaaa 120

ttgaacaacg gatgctcttg ataaattcaa ctggtataac ttttcacacc gatattcgat 180

tcgggcacat aatatgtcga gaagctcaat attgaacaac caaagttctt tagaaaatca 240

aatgggcata acttttcaca cggatgtccg attcaggctt attatatatc gatacgctcg 300

aaattaagca tcggaactct tccgaaaatc aaaagggcgg aaattttcac accgaaattt 360

ccctttgggg c 371

<210> 1198
<211> 494
<212> DNA
<213> Glycine max

<400> 1198

agctttggag tttccaagtg ccaattcgtc ttcttcttta gtccagtctt cttctagctt 60

caatccatca gtgggctttc cttctgtgtc cagcatcttg ggatgttccc agcctttgat 120

gacagctttc caggttctgc tatccagtga tttgaggaag gccaccatcc ttgctttcca 180

gtattcatag ttggttccat ccaggattgg tggtctgttc actggtcctc cttctttctc 240

catgttcatc agaatttatc tccctagatc tcactcagtg atttcgagtg cctgctctga 300

taccaattga aattctgata ccaatgacag atgtcgtacc ggatgtcacg acatcacgct 360

tcagaacatg cagattatat ttgactgtat gaacagatta aacaagtaaa taacacaaga 420

gaattgtaac ccagttcggt gcaacctcac ctacatctgg gggctaccca gccagggagg 480

aaatccacta aaat 494

<210> 1199
<211> 535
<212> DNA
<213> Glycine max

<400> 1199

taataaatct atatatggtt taaaacaagc ctcctgtcag tggtaccttа agtttcatgg 60

gataatttct tcatttgatt ttgatgaaaa ccccatggat taatgcatat accacaaggt 120

aagtgggagt aaaatatgtt ttcttgtttt atatgttgat gatattttac ttgacaccaa 180

tgatcgaggt ttgctacatg aagtgaaaca atttcaatct aagaattttg acatgaaaga 240

tatggatgat gcatcttatg tcatcgacat taagattaat agagataaac ctcgaggtat 300

tttgggtcta tcacaggaaa cctatattaa caaaactcta gagagatttc ggatgaaaga 360

ttgttcacga agggttgctc ccattgtgaa gggtgatagg tttagtttga accagtgccc 420

aaagaatgac tttgagaggg aacaaatgaa aaacatttct tatgcttcag ttgttggaag 480

ccttatgtat gctcaagtgt tcacaaggcc tgacattgct tttgcaattg gaatg 535

<210> 1200
<211> 463
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1200

tgtataagcg agtgcaagaa tgcaggatag ttttgaaacc agtgtctgtg acacgacaaa 60

agccaccaag gcatatgctc tccatgtttg cacacttgtc agccattaga agtaatccca 120

gatcattcac tcttcggaag taagtaattt ggaactcttg gcttcgaacc aatgaaagat 180

gtttcaatct cccaagttga ttaatttgtt gaagaccagc attggttagg tcaaatgtaa 240

ttcttggttc aatcagtggt gcatcttgaa gatccaaatg ggtcaaaagc atgagacctt 300

tggatattgt accaaccata gcatcagtta tatagtctac attaagacac agtttctgaa 360

tgcttggaag tatggatggt tgagcangat ttgagggcag ctgggatccc aaatttgggc 420

taagcagttc agtcactgtc actgaagaaa tgtagccaat ctc 463

<210> 1201

<211> 439
<212> DNA
<213> Glycine max

<400> 1201

tggaatgatc tgcaaaagct aaacccttct tgctggacaa tgtctgcttt taaagtaaac 60

acaaagtgtg atttgcaagt aaataacatg tataaagcat tcaataatgt aataatgtag 120

tacagacata agccaattat tacactattg gagggaattc aattttacat aagttctaga 180

attgtgaagt tgaggactac cttgatgaag tatgaggggt caatctgtcc taaaattaag 240

caaatcatgg aaaagaataa aaaagcatgt gaaccatggc gggcacattg gtgtggtgat 300

gataatctgt ttttgtttga agtgtcaaaa ggcatggaaa aatatgttgt caatcttaaa 360

caataaacat gttcttgtac aaagtgggag tgtactggaa ttccatgcac tcattccata 420

acatgcatgt ggatcaatg 439

<210> 1202
<211> 395
<212> DNA
<213> Glycine max

<400> 1202

agctttggaa agacttctta gttcttttca gtcttgcttt ggtcattggg cctttcatcc 60

attgcaaaag atatttgaag tcattggact cttgttggat catatcaaca agactttgga 120

cattttcat gagattttct tttggcctaa aatgaaacat gatgttaata aatattatgc 180

caaatgcatt gtatatcata aagctaagtc taaggtctta aaccatgaat tgtatacccc 240

tttgcctatt cccacctctc cttgaactaa catatccatg gattttgctc ttggtcttcc 300

aaggtccaag agaggtaaaa attctatttt tgttatggtt gataggttct caatgatggt 360

tcactttatt ccttgccata aaggggatga tattt 395

<210> 1203
<211> 238
<212> DNA
<213> Glycine max

<400> 1203

ttcgagaaat tcaaatgggc aaaacttttc acactgtagt cctattcatg cgcataatat 60

atcgaaacgc tcgaaattga acatcggaag ctctcgataa attcacatgg tcataactct 120

taactcggat gtctgatctt ggcgcataat atatcgagac gctcgacatt gaacatcaga 180

agctctcatt ggtcatatac ggtcactcgg gggtgataaa aaagcgcatt atatacct 238

<210> 1204
<211> 437
<212> DNA
<213> Glycine max

<400> 1204

agctttccct ctttgaacaa ataccctca gccaaataga atccatcttg ggccttttc 60

ccacaactct cataaatggg agagaaatgt tcatctaaag catacaagtc cctaatatta 120

tcaaatccta aaatttgagc tcctagggag caaaacaatg tctgtctcct agagagggca 180

tcagctacca catttgtttt tccctttttg tatttgataa catatggaaa ttgctctagg 240

tactctaccc attttgcatg cctcttgttt aacttgcttt gccctctaat gtacttaagt 300

gattgatgat cactatgaat gacaaattcc ttggaaacaa ggtaatgttc ccaagtttgg 360

agggctctta ttaaggcata aagctcttta tcataggtgg ggtagttgag ggtggcacta 420

tgaaattttt actaaaa 437

<210> 1205
<211> 461
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1205

agcttcataa cctgtcttgg cacctctgga ggatttgcac aacggatcag tgcccagtta 60

acattctgaa agaatggatg ctgttttatc tctgtcgcac cacgtctata ggcaagacga 120

tgctgaggct ctttcacaag caagcccctg atcaagtccc tggcagcaaa gctgacacta 180

ggagattctg gaaaccgtag aggctgccca attacgttaa acagtgttgc acgattcact 240

gaacctttga atggtgttct gccaaacaaa agctcataca agaatatccc aaatgtccac 300

cagtccacgg cacttccgtg cccttcaccc ttgatgatct ccggcgccaa gtactcgtgt 360

gtccccacaa aggacattga tctggcattt gttggctcan caattagctc aggaagaggg 420

gtcacttggt gatgcatgtc attctttggt ttgaactttt t 461

<210> 1206
<211> 527
<212> DNA
<213> Glycine max

<400> 1206

agcttgacat taagaaaaga taaacatctt atatgtctga gtataatcat aaacaaaaat 60

attaattttg gataaagaaa aaatacttag taaattttac ttgtcttaaa aaaatagcat 120

tatctaattt ttatgttcac gtttcattat actttctttc ttctctttat tttatttcat 180

tttttacaag taaatgtcta ttaaatagtt aataaacttt aaaatacttc aaaaatatat 240

ttgataaatt agaataatca agttataaat gagtaacaag ctaaatttaa aacttttttat 300

ttgtataact tcgtttattt aaattaattg aacttcaaca taatatctta caagtgaaac 360

ttgaatatta aatactcaac catgttcaaa acatttacgc catagatgca gtcactcaaa 420

ttaattagca ctagatcgtt tgaatttaac cgatagtttt gagccaatat tgattatatt 480

tgattgaaca taactatata tgtgatagaa ctggagcagg caaaatg 527

<210> 1207
<211> 503
<212> DNA
<213> Glycine max

<400> 1207

ttactatgca aggaataacc aaggaaaatt ccttcatttg acttagcatc aaactttcct 60

aagttttctt ttccattgtt taatacaaaa catttgcaac caaaaacatg aagatgcgag 120

atgtttggtt tcctgccatt gaacagttca tatggagttt tctttaaaat gggtcttatt 180

aaatccctat tcatgatata gcatgcagta ttaacggctt cagtccaaaa atattttgga 240

agaagagtgt catttaataa ggttctaaca atttcttcca aagacctatt tctcctttca 300

acaactccat tttgttgagg agttctacgt gcagaaaagt tatgttcaat gccatgctta 360

ccacaaaata attcaaattc tttttttcaa attcaccccc ataatcactc ctaatagata 420

taattttgag atttttattg tcttgaatga tttatgctag tttcctaaat acttgaaatg 480

catcattctt atgagtgata aat 503

<210> 1208
<211> 511
<212> DNA
<213> Glycine max

<400> 1208

tgagggaaaa cttgatgcct tggtcaacct aataactcag cttggcatga atcataaatt 60

tgcacctgtt acaagagtct gtggtatatg ttcttctgca gatcaccata cagatctttg 120

tgcttctttg cagtgatctg gagtcaatga acaacctgaa gcttatgctg cctacattta 180

taatagaccc cctcacagca aaaccaacat tagcgaacta attatgatct tccaagctac 240

agatacaatc cacgttggag aaatcattca aatatgagat gggcaagtgc ttcacaacaa 300

caacagtctg tccctccttt ccagaatgtt gctggtccaa gcaaaccata tgttcctcct 360

ccaatacagc agcaacaacg acaacagtca caacgaagac gacaagcaac tgagacttct 420

ccttaacctt ccttagaaga gttagtgagg catatgacca tccagaatat gcaatttcag 480

catgagacaa gagccttcat tcagagtctg a 511

<210> 1209
<211> 570
<212> DNA
<213> Glycine max

<400> 1209

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tgcacagctt ttgagctcat tcctttactt gcacataaga aggcaagtgt ccttaggtgc 180

ccagactctt ctaacatctg ctccaattcc tcctgaaaaa gagatgtatt tcacacggtc 240

atttttcagg caacccccag gtaattacca ttatgtcatg caaccaaagt tttctttaag 300

gagcagcatg gatttaaaaa agggaatttt tttcattttc ctgtatatgc ttgtgcttga 360

cattcaaaga aggttaggtt ttgggttttc atgtttattt tgctgctgag gctattctct 420

ttctgcagag cttcaatatg atcatatcag gaaaaggaaa aaagtatttc tcaaatctac 480

atagaaataa tgggtataat tcaattcacg acatatttat tttacagtat taattatgaa 540

aaatgtattg aaattacttc attcaataac 570

<210> 1210
<211> 561
<212> DNA
<213> Glycine max

<400> 1210

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ttcctcgatt ggcacaacca tgtgcttgaa tttgggatct atcgagtgta gagtcttctc 120

cataattctt acatcttcta acttctcacc atttatttttt agtttatttg aaacagcgag 180

aattcctgaa aaataatcgg aaatggacgc tgactctttc atatgtaagg attcgaactc 240

acctcttata gtttggagat gcaccttctt tactttgtct tctcctttgt gagaggtttg 300

aagcttatcc catgcctcct tagcagatgt tgcataagaa atcttctcga atgcatcatt 360

ctttaatgct tgatacatga agaagagagc tttattgtct cctcttttttg agtcccttaa 420

tggctccttt tgtacttggg ataatgaaag cccatcttgg gactcctttt agcatttttc 480

aacctttccc caacattatg tgcttcaaga aaggcccttc ttttgatgct ccatttgcaa 540

tagggcctcc ccttttgaag t 561

<210> 1211
<211> 504
<212> DNA
<213> Glycine max

<400> 1211

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atgacatcca ctccacaagg tttgaagttg aggagacctt caatcctatt acacaacgtg 120

gccgacaaaa gtgggcagtt aacttgaatg gtcattattg tcaatgcaga aggtattctg 180

cgcttcacta tccatgttca catattattg cagcttgtgg ttacgtgagc ctgaactact 240

accaatatat agatgttgtt tatacaaatg agcacatcgt aaaagcttac tccgcacaat 300

ggtggcctct tgggaatgaa gcgactattc ctccttctaa tgacgcatgg acacttatcc 360

ctgacccaac agcaattcgt gcgaaaggtc ggcctaaatc aacaaggata aggaatgaga 420

tggattgtgt cgaacccctt gagcaccgac aaaaatgcag tagatgtgga gccgaagcgc 480

ataacaggcg tcgatgtcca atgc 504

<210> 1212
<211> 364
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1212

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attcaggccc ctaccattct gctccttctt gggatatgga caatctctct gaatattgtt 120

ggatcaagtg gcctcagaat aattaagaag ggggggttga attaattatt cctaaacctt 180

tactaattaa aaatttactc ttctaaggat tttactatgt tgttaaataa atgaagaata 240

gaaaagaaac ttaaccaaaa gtaaaagcgg aaattaaagt gcacagcgga aattaaaaga 300

gtagagaaga aggagacaaa cacacaagag ttttatacta gttcagcaac aacctgtgcc 360

taca 364

<210> 1213
<211> 390
<212> DNA
<213> Glycine max

<400> 1213

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ggatcatgag aagacgacct tcacatgccc ttttggtgtc tttgcctaca gacagatgtt 120

gtttggatta tgtaatgcac ctgccatatt tcagatgtgc atgttggcca ttattgcaga 180

tatggtggag ttggagcata aagcctaatg ggccctcaaa ctgcttaact ttgattaagc 240

tacatctaga gagaagatga agttacagtt gctagagtta gaagaaataa ggatgaacgc 300

atatgaatca tccaagattt ataagcaaaa gatgaaggcg tatcatgaca agaagttact 360

aagacaaaac ttccagccag gacaacaagt 390

<210> 1214
<211> 244
<212> DNA
<213> Glycine max

<400> 1214

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aagttattgt cgtttgcatt ggctcagagc ttcaccattc aatttcgagc gtctcgatat 120

atgacgggac tcaatcagac atccgagtaa aaagttattg tcgtttgaat tggctcagag 180

cttcaacatt caatttcgag cgtctcgata tattacggga ctcaatcaga catccgagta 240

aaaa 244

<210> 1215
<211> 314
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1215

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atatatcgag acgctcgaaa ttgaatgttg aagctctgag ccaattcaaa cgacaataac 120

tttntactcg gatgtctgat tgagtcccgt aatatatcga gacgctctaa attgaatgtt 180

gaacctctga gctaattcaa acgacaataa ctttatactc ggatgtctga ttgagtgccc 240

gaacatatcg agacgctctg aaatgaatgg tgaacctctg agccaattca aacgacaata 300

acttttttact cgga 314

<210> 1216
<211> 406
<212> DNA
<213> Glycine max

<400> 1216

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ctcaatctca tgggtttttt tggattatat gctgcaaaga atgggttttt gccacaaatg 120

gagacactgg atgtctgcct gtctcaagtc agcaagcatt tctattctta tcaatggcag 180

tcctacaaag ggaatttgct cctactatag gtttgaggca aggggatcct ttagcccccc 240

tactctttaa tatagttgga gaaggcatca caggattgat gagggaagca gttcataaga 300

acttatatag aagctatatg gctggaaaga aaaaggaacc cattaatatt ttgcagtatg 360

cggatgacac aatttttgtg ggtgaggctg agtgggagaa tgttat 406

<210> 1217
<211> 221

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1217

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acctaattga ttcattttgc aaggcangca tgacactgga agcaaataaa ttttttgtt 120

gacatgatac atgttggtct tcaacccaat gaatntacgt atacatctct aattgatgca 180

aatcgtaaaa tacgtgatct caatgaagca ttttatctgg a 221

<210> 1218
<211> 260
<212> DNA
<213> Glycine max

<400> 1218

tcaacctaga ggagacgaac cattccaagt gttggagaag atcaacgaca atgcctacaa 60

gattgacttg cctagtgagt ataatgtaag tgccactttc aatgtgtctg atctatctct 120

ttttgatgca gatggaagag ccttggattt gaagacaaat ccttttcaag gagggagtga 180

tgaggacata accaagggca aggaccatga agcacttgaa ggtcccatga ccagaggcag 240

acttaaacaa gcccaacaca 260

<210> 1219
<211> 295
<212> DNA
<213> Glycine max

<400> 1219

tttgagctag agtgtgatgc ctctggtgta ggtgtgggag ttgtgttatg gtagggtgga 60

caccctatta cttaatttag tgagaaactt catggtgccg ctcttaacta ccccacatat 120

gataaggagc tttatgcctt agttagagcc ctccaaactt gggaacatta ccttgtttcc 180

aaggagtttg ttattcatag tgatcatgaa tcacttaagt acattagagg acaatgcaag 240

ttaaacaaga ggcatgcaaa atgggtagag ttccaagagc aatttctata tgtta 295

<210> 1220
<211> 370
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 1220

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tgtccgatgg gagttaacaa agtaccatgg tatttgccag ttaagaatgt cccatctaat 120

tgcacaagtg gcttgcaata tttgaagcct tcaatgcatg gattaaagtt gtgtgttcat 180

ggtttgggga ttaaggcttg aggtttagga tttagagttt actgatactt gaggtaaagt 240

tgtgtgttag gatttacgat acaatgagaa agatatttgg actattaatg agatatttaa 300

tcaaatggac ttattagata taaataggga aagaaggata tganatattc tctactatat 360

tatgaccttt 370

<210> 1221
<211> 374
<212> DNA
<213> Glycine max

<400> 1221

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cttcatttat gaatccattt ataaatgcac tcttgacatc catctgatat agtttaatgt 120

ctttgtgtgc tgcataggct aagagtattc tgacagcttc aagtcttgct actggtgcaa 180

aggtttcatc aaagtcaatc ccttctttgt tgattgtacc catgagcaac tagtctagcc 240

ttattcctaa ccacttctcc tttttcattg agcttgtttt tgaataccta cttagttcca 300

atcaccgact aaatcttatg agggggaaca tgattttaga ccttgatcta acgaactggc 360

tggttcttct tcat 374

<210> 1222
<211> 380
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1222

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agcccagttc tgtacttgga tcatggaatg tgtttcttcc acttccttta gtgtggcagt 120

caatggatcc atttatggtc acttcaaagg gcagcggggt cttagacaag gggatcttct 180

ctccccttat ctgtttgtgc tctgtttgga gtacttttcc agagatatga gcagcctcaa 240

ggaagatgcc aattntaaat ttcatcccaa ctgtgcaagt attcagctat ctcatttggc 300

ttttgcagat gatattatgc ttttatctag aggagatatc ccttctgtgt caactaatgt 360

tgccaagctt caacacttct 380

<210> 1223
<211> 398
<212> DNA
<213> Glycine max

<400> 1223

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aacaccatta gagtcctctt ataattggct gcaaatttag attggccatt acagcaactt 120

gacgtaaaga atgtcttttt aaatggggac ttagaggagg aagtctacat ggactcacct 180

tctggttttg aatctcagtt caatcaaaag atttgcaagc ttcaaaagtc tctctatggc 240

ttgaaacagt cacctatagc atggtttgag agatttgccc agtttattaa gaagctggga 300

tattctcagt gtcagagtga tcacaccttg cttgtgaaac actcttttga aggaaagatg 360

gttgtattaa ttgtctatgt ggatgatatt ataattac 398

<210> 1224
<211> 386
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1224

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tccttgatga acctccgata aaaacctgca tgtccaacaa aactcctgat acccttaaca 120

tttactggtg gtggtaactt ctctatgaca tcgatttttg ctttgtccac ctcaatgcct 180

tgggctgaaa ttttgtggcc caacattatc ccttcttgaa tcatgaagtg acacttctcc 240

caattcagca ccagattcgc ttcaacacat ctttgcagct gtcataccct aatttcgtcc 300

ggggactatc gtttgttgat cttttgatcc ttgctagtcg acttacgatg ttcaaacgcc 360

agttacagtg canaacagat gatcat 386

<210> 1225
<211> 321
<212> DNA
<213> Glycine max

<400> 1225

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tagtcccgaa aaagactggc ctcacagtga tcagaaatga gaaggaggag ctgattccta 120

ctcgggtgca gaacagttgg agagtctgca ttgactatag gaggctgaac caggttacca 180

aaaaggacca ttttcccctg ccattcattg accagatgct tgaacgcctg gcaggtaaat 240

cccactactg tttccttgat ggtttttctg gttatatgca aattactatt gctcctgagg 300

atcaggaaaa gaccacattc a 321

<210> 1226
<211> 458
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1226

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gggcttttaa gatcccgaac tcgaaggatt cccatcaaag catcattcag atttttctgc 180

aggagaataa aataagaaaa ttaaatctat gtttggtact tggtaggaca aagatttatt 240

ctttgcaatc gtccattcac agacacagtc agtagattga attttaaggg tttataatta 300

tcacatttac ttgctaaaat atcagtaccc aaaatcttat agaaacctat tggctgaagt 360

gtaagagaga atactaacct ttttcaagta gccaactcca aaagctcgag taaccttcaa 420

tttacctttc acttttcctn ctataacgat cttgggat 458

<210> 1227
<211> 306
<212> DNA
<213> Glycine max

<400> 1227

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aagtgaaaag ctattgtcgt ttgaatttgc tcagagcttc gatattccat ttcgagcgtc 120

tcgatatatt acgagactca atccgaccac cgagtgaaaa gttattggcg gttgaatttg 180

ctcagagctt cggcattcaa gttcaagcgt ctcgattatt acgggactaa atcagacatc 240

tgagtaaaaa gtattggcgc ttgaattgct cagagttcgg aatccatttt gagcgtctcg 300

atatat 306

<210> 1228
<211> 294
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1228

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accctattac ttaatttagt gagaaacttc atggtgccgc tcttaactac cccacatatg 120

ataaggagct ttatgcctta gttagagccc tccaaacttg ggaacattac cttgtttcca 180

aggagtttgt tattcatagc gatcatgaat cacttaagta cattagagga caatgcaang 240

tatacaagag gcatgcaaaa tgggtagagt tccaagagcc atttctatat gtta 294

<210> 1229
<211> 355
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1229

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tcttaagaag ggggggttga attaagatat tccaaattat ttcccctaat tagaaatcta 120

tttcactttt taaccaagtt atgaattccc ttaatgaaaa tcttcttaaa tattaattca 180

aatgaaacaa tttgaatatg aatataaagc aataataaat aaaggagatt aagggaagag 240

aaaatgcaaa ctcagtttta tactggttcg gccacaccct tgtgcctacg tccagtcctc 300

aagcaacccg cttgagagtt cactatcttg taaatccttt tacagttcta acaca 355

<210> 1230

<211> 361
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1230

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caacagtcac atctttttat ttggttcttg aatggctatc aaaggcctat atatatgtga 120

cttgagacac gaatttgcga agacttttg agaacaaaaa ggtcttatcc tcttaaagag 180

caaaattgtt ttatcctctt acaaattcct tggccaaaac acttgtgatt caataaggaa 240

ttatttgagt gctcaaattg ttcaatctat ctctntaaag agagatttct tcttctcttc 300

ttctttattt tgaaaaggga ttaagagacc gagggtctct tngtgtaaag aaatctgaac 360

a 361

<210> 1231
<211> 274
<212> DNA
<213> Glycine max

<400> 1231

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tttaataagt catccgcata tttttcttgc gagaaaaata tttgtccaag tctttgcttg 120

acttgcatct tcacatatag tgacggctca cttggacttt tgaggaatct atgctcgacg 180

aaggatttgt ctattttgtt gtccatgctc ggggagcttg tttgagacca taaaatgcat 240

ttttcaagcg atatactttg gcttcttctc cctg 274

<210> 1232
<211> 220
<212> DNA
<213> Glycine max

<400> 1232

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attactgatt cgactgatca tggtagagag ctagaaatag ttcagagaag actaaaagaa 120

aaattggcag ataaaaaatt tctcgtcgtt ttggatgacg tttggaacga aagcaggcct 180

aaatgggaag ctgtgcagaa tgctcttgtt tgtggagctc 220

<210> 1233
<211> 358
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1233

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ggccaatctg aggagtggtg tactcttgca gcagatatct tgaattgtgg tcctctgcag 120

ttcccattta tatacctagg gatgcctata ggtgttaacc ctanaaggaa ggtggtgtgg 180

gagcctctaa tcacaaaatt tgaggccaaa ctgaacaaat ggaaccagag aagtctatct 240

atggctggca gaattacttt aattaatgct gccttgacag ctttgccttt gttctatatg 300

tccttttta gggcccctac agcaatcatt aagaggctca ctgctattca aagacaat 358

<210> 1234
<211> 448
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1234

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ttcctgcaac aaaataaaac ttcaatcaga aacaatatct tgtttgcgga acatatacaa 120

taaccttctt ttactgaatg cacaataaac atttttaaga ataaaaaata ccaaccaaaa 180

acatttgatg caccaaccaa ggcacttgct gcaacatcag aagcaattcc agcactacgg 240

aacacagaag ttgaataata aactacagca tttattccag ccaactgctg gaacaagaaa 300

agtgctgccc caacactgac aactgaaaca aggcatantt taaggaagtg ctatatacta 360

tttcataaaa gaatacattt aatcaactaa atagtaaact aaaaaaaagt tgtcagtgaa 420

attaaaacat gaacaatgat aatattat 448

<210> 1235
<211> 310
<212> DNA
<213> Glycine max

<400> 1235

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tacgcagaaa tcccaacttg ttcaacttcc caatctctgg aggaatgtgg ccagaaaatt 120

tggcggtact taagtctaga tatgacaggt tggacaagtt tgctatggaa ttaggaattg 180

ctccacttag ttgaagacat tgggaaagat caagagcatg taaactcctt agtgaccaca 240

tttcttgagg gatggaacca tggaaagaat ctaaagaaaa attcacaaca tttactttgg 300

acatgttacc 310

<210> 1236
<211> 307
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1236

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taagatatta caaactattt tcccaattaa aattctactt tgattttaat gcaagttcca 120

agttcccttа atgacgaatt tctaaatgat gattcaaatt aaacaatttg agtgtaaatt 180

taaaacaaca atagataaaa gagtttaagg gaagagaaag tgcaaactta gttttatact 240

gattcggcca tacccttgtg cttacgtnca gtccccaagc agctcgcttg agagttccac 300

taacttg 307

<210> 1237
<211> 307
<212> DNA
<213> Glycine max

<400> 1237

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ataccttctt ggccatcaat tcatgatctt gactgatcac agaagtctta aggagctcat 120

gactcagatt gttcaaactc cagagcagca aatgtatttt gccaggctta tggggtatga 180

ctactccatt caatatcggt ccgggagcac taatttggta gctgatgcct tatcgcgctt 240

gaaggaggga tcagaaggaa ccatgttatt actatctgta ccttgcctga catttctaga 300

tgaattg 307

<210> 1238
<211> 346
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1238

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tattaagaac tagctctttt attcctttat tgcctttagt tgaatacacc tttgtttggt 120

tctctatttg gttcttaacc ctctcatgca acttctttac aaactctgac ctagattccc 180

cttctttatg tataaaagaa gtgtctagtg ggaggggaat gtgtctagtg ggaggggaat 240

gaggtctaac tgtgacatcc tggaaatatt tacctggaat tttgtaagcg atatattnta 300

aataaatata tatatgtatt attcagtgga tatatatata tatact 346

<210> 1239
<211> 293
<212> DNA
<213> Glycine max

<400> 1239

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ttgatgaaaa ccccatggat caatgcatat accacaaggt tagtgggagt aaaatatgct 120

ttcttggttt atatgtagat gatattttac ttgcaaccca cgattcgggt ttgctacatg 180

aggtgaaaca atttctcttc taaaattttg acatgaaaga tatgggtgat gcatcttatg 240

tcatcggcat taagattcat agagatagat ctcgaggtat tttaggtcta tca 293

<210> 1240
<211> 357
<212> DNA
<213> Glycine max

<400> 1240

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caacaacctc agatttcatt cctttcactt caatggctat aatcagtcgt ttatataggg 120

agaggcttaa catagacaca tcataaaacc accaatcatg gagttgagat ggtttctcag 180

aagaaattcc attccacaat gcactgttgt ctgcttgatt ttgcttgcaa ttgcttccaa 240

ccacaggcca gtggaataag gttggatctg aacaagcctt tatagccaag gaatcaatgc 300

atcttgaaac tatatggaga tcttttgtca agggctgcac ttccttcaca tgtttaa 357

<210> 1241
<211> 396
<212> DNA
<213> Glycine max

<400> 1241

tgttggttac agtgacaaca attgggctgg agatgaagat gattggaaaa gtaccagtgg 60

atttgtgttt ttcataggaa acacaacctt cacttggatg tcaaaaaagt agccgatatt 120

cactcttttg actcgtgagg cagaatacgt agcagctact tcatgtgttt gtcatgcaat 180

ctagcataag aatttattaa aagagttggg catgtcacaa gaagagttga ccaagatctt 240

tgtggataat aagttagtca ttgctctagc aaggaatcca gtgttctatg atcgaagcaa 300

gcatattgat acccccttacc actacataag ggagtgcata gcaagaaagg atgtacatgc 360

agaatatgtg aagtctcaag accaagaagc tgacat 396

<210> 1242
<211> 323
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1242

tcaaccctac gtcctgctct tacatctcta tatatagaga atgcttcttc cattatctta 60

gcttgngcca gcaattctgc tctctgtatt ccagaaggat gagtagagaa ataatccccg 120

aaggtagaat aaccagcaaa ttttcctaac tcctcataca ctttatgtgc cacccgggga 180

tcataaccgg ctaatgcaat tatgtactaa gttatgtcac gcctattttg aacactcagt 240

ccatctattt atcacttgct catttgctaa attcattcgc gtattaactc atgtagatgt 300

taattgtgaa gcatcgggat aca 323

<210> 1243
<211> 333
<212> DNA
<213> Glycine max

<400> 1243

tgtaggccta ggatcttctt catcaatgga ttcctttgct tcttggaaaa tgaatggcaa 60

cggaatggag aaggaagaga gagagagagg agacgccact tcaaggagaa gatgagtcta 120

gaagaagctc accaccataa gaggccatgg ataagagctt gggggaagaa ggagatgact 180

gaagggagag agagagaaga gcacgaaatt ttgtgctcca aatgagcttt gaaatctgaa 240

gtttgatatt caaatgatca aaagtgaaaa aaaatcacac acatgacctc tatttatagc 300

ctaagtgtca cacaaaaatg gagggaaatt cca 333

<210> 1244
<211> 376
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1244

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tttggaggga gatgntaaat tggctagaac tagtcctaag catagcactt cttatcatcc 120

ccaaacggat ggtcaaaccg aagttgctaa tcggtgctta aagacctatc ttaggtgctt 180

tgctggccct aagcccaaga cttggtttga atggttgcat tgggctgagt tctggtttaa 240

cagtaactac aatatctttg ctggaatgac acctttaaa cctttatatg gacgagatcc 300

tccattgttg attaagagct gcaccattcc atcaaagttg gatgatgtaa atcagttggc 360

ccaacaacga gatgat 376

<210> 1245
<211> 314
<212> DNA
<213> Glycine max

<400> 1245

tcaacctaga ggagacgaac cattccaagt gttggagaag atcaacgaca atgcctacaa 60

gattgacttg cctagtgagt ataatgtaag tgccactttc aatgtgtctg atctatctct 120

ttttgatgca gatggaggag ccttggattt gaggacaaat ccttttcaag gagggagtga 180

tgaggacata accaatggca aggaccatga agcacttgaa ggtcccatga ccagaggcag 240

acttaaacaa gcccaacaca ttatagagaa caggctggtc atttggatag ctgtcattga 300

tgatgattga aggc 314

<210> 1246
<211> 287
<212> DNA
<213> Glycine max

<400> 1246

ttgagaaaac tcaactttca taactttgga ctcaaatgtc tgattacgga ccataatata 60

tcaagacgct aaaaattgaa cacggaagct cgggcccaat tcaaactggc ataacttttg 120

acttagatgt ctgattgtgg accatattcc aactgccatg attggtgatt ctgatgtttg 180

actacggccc ataatatatc aagactcttg aaattgatta caaaagctcc tcacaaatta 240

aactaccata acttttgatt ggatgtctga ttgtggccga taatata 287

<210> 1247
<211> 384
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1247

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tgttctcaat tagctcagtt gcttcttccg gggtcttcag ttttatcttt ccccctgcag 120

aagcatctag cagttgcttg gtttgtggtc tcagcccatc tataaacata ttcaattgaa 180

ttagctcgga aaacccatgg gtgggagttt ttctcaataa acctttgaac ctctccaatg 240

cttcacctag agattcatca gggaactgat gaaatgaaga gattgcagct ttcccttcca 300

cagccttgga ctttgggaag tatttcttta ggaacatttc aacaacttca tcctangttn 360

tcagattgtt acccttaaat gagt 384

<210> 1248
<211> 272
<212> DNA
<213> Glycine max

<400> 1248

tggatttcct tttagtaggg aatctatcct tcctaagatg gagccaaacc cagtcaccct 60

tattaagaac tagctctttt attcctttat tgcctttagt tgaatacacc tttgtttggt 120

tctctatttg gttcttaacc ctctcatgca acttctttac aaactctgac ctagattccc 180

cttctttatg tataaaagaa gtgtctagtg ggaggggaat gtgtctagtg ggaggggaat 240

gatggctaac tgcgacatcc tggacatttc ta 272

<210> 1249
<211> 356
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1249

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agtctttgga tgaagcaaca atgatgtaag ctccattgga gcttgtaggc ctaggatctt 120

cttcatcaat ggattccttt gcttcttgga agatgaatgg cagcggaatg gagaaaggaa 180

gagagagagg agacgccact tcaaggagaa gatgagtcta gaagaagctc accaccatag 240

gaggccatgg ataagagctn ggaggaagaa agagatgaat gaagggagag ggagagaaga 300

agcacgaaat ttgtgctcta aatgagcttt gagatccgaa gtntaatatt caaatg 356

<210> 1250
<211> 414
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1250

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tgcactctgt atgccttgga caattcaaag tattcaagta agattctaga atcacactag 120

gagtcaaact ttccaagttt atccttggtg tttaagatga aacgctgaca tccaaatgag 180

tggaagtaag agatattggg cttacgtctc ttccataatt catagggact tctttaagat 240

aggccttatg taaattttgt tctataaata ccaggaaaca tttacagctt caacccataa 300

atctttggga gttgagtgat cgttaagcat tgttcatgcc atttcctgaa gagatattnt 360

tttcctctca acaacttcat tctgttgtgc tgttcttgga gtgggaaaaa tatg 414

<210> 1251

<211> 357
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1251

tcaataataa catagaattc ccaagtatat gtagatagtt tctgcattct accagacaat 60

tttttttag aaataagcaa taggatgctt gttttggctt aacacaacac caactcccct 120

ccctgaagca tcagtttcta atacaaaaag tttattgaaa ttaggaatag ccaagacagg 180

tgcagaagtc atggctatct taagtttttg gaaagcctgg gcagtagctt gaccccattt 240

gaaagagtcc ttcttcaata gaacagtcag aggtgttgca atggtagcat aggtcttaac 300

aaatcttcta taataacctg taagtcctag gaagcccctt aatntcttta gattcat 357

<210> 1252
<211> 419
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1252

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acatgaggca gcaatcacag gctatgtaga tgcagatttt gcaggaaatg tagacataag 120

aaagtcctta actggatatg tgtttacttt gtttggaaaa acaatcagtt ggaaagcaaa 180

taaacaatta gttattgctc tttcaacaac taaagtagag tacatggccc taattgaagg 240

agtgaatgaa gcaatctggc taanaggaat ggtaaatgaa cttggaatag cacaaccttg 300

tgtacaattc actatgacag ttagagtgct attcatttag canatcacca aatttaccat 360

gagaggacaa agcacataga tgtngaaata cacttcatca gagatctgat tgaatctga 419

<210> 1253
<211> 389
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1253

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atgggctaaa ttcctcattt ggttntgatg aaaaccccat ggatcaatgc atataccaca 120

aggtaagtgg gagtaaaata tattctctta ttttatatgt agatgatatt ttacttacag 180

ccaatgatca agttttgcta cataaggtga aacaatttct ctccaagaat tttgacgtga 240

aggatatggg tgatgcatct tatgttatcg gcattaagat tcatagagat tgtagaagca 300

ngcttcatga tgatgaatca agtagttttg atgatgacaa aaagcccaca agaatgatgt 360

caagattgag tcaacaagtt caagatcaa 389

<210> 1254
<211> 321
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1254

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gaacaattat gatctctcca gcaacagata caaccctgga tggaagaatc accctaatct 120

cagatggtct agccctcaaa agcaacaaca acagcctgct ccttccttcc aaaatgttgt 180

tggcccaagc agaccataca ttcctccacc aatccaacaa cagcaacagc ccctgaaaca 240

gccaacagtt gaggctcctc cgcaaccttc cctcgaagaa cttgtgaggc anatgaccat 300

gcagaacatg cagtttcaac a 321

<210> 1255
<211> 445
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1255

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acagcctccg taattgctac catatcctca tctacaatca tgtaaagaga tcctcacttt 120

tttccacgag ccccaacgag attgcctttt gttaccttcc aagctccatc tccaaaagtg 180

gtgtgatgcc cctcatcatc ctaccatcct atagatatta aatttttttt taaggcagga 240

atatgtctaa cattgtgcaa tgtccatagg gatccactag aggtcttgat gttgatatca 300

ctntttccaa caatgtcaag agattntcca tctgcaaggg aaactttccc aaatcttcca 360

gaaatatagt tagacaataa atctatagag ggagtagtgt ggaatgaggc acctaagtcc 420

attaatcatg aatcaacggg actat 445

<210> 1256
<211> 358
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1256

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agtaagataa gatcgcacct ctcacacgca agaggggtaa tgcaattgtg aaataacaaa 120

aaattttgca ggatctactt caatgcccct attggaaata atgtggccta aaactatacc 180

ttgctcaacc ataaaatgac atttttcata atctagaaca aggttagttt cagtgcatct 240

attcaaaacc ttttccagac tatccagaca aatatcagaa gagtatccat atacagtgaa 300

atcatccata aacacctcta tgcaattttc tcaaaaatca ctatnaatac taatcatg 358

<210> 1257
<211> 463
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1257

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tttatttcag gaaaaaatta gaggtagggc aggaagtttt actttttat tatgtgtggn 120

tgaatgaaat aaaaaatctt tgatttggtt tgtgctgaat ttgatgagtt tggttttcta 180

ttttttaaaa cattttcttg catttcttag ttgtcaaaaa tcatttaaca cattttaaac 240

aagtcaaaca attatatttt aaaaaatctt aacggtcaaa aaattaatcg caacaaaatg 300

caataaaagt ttaaggatta agattaatta aatntttggt taagaattaa aaatcaaaat 360

ataaaaaagt taatggatta naaacgtagt taatcttatt ntatataata natacanaga 420

atattttaac tattttattg taataaataa tgcatgaaat ata 463

<210> 1258
<211> 371
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1258

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tacttgctgt ctttttttag aatccctaan aaagtggtgc aaaagatagt tgctattcag 120

agaaattttc tatggggagg tgatattgag gccaacaaga tcccttgggt gaaatgggac 180

acagtttgtc ttcctaagaa caaaggggg ttagggatta aagacttgat caaatttaat 240

gaggttntgc ttggcaaatg gcgttgggag ttgactaata atcagaacca gctataggca 300

agaattctat tgtctaaata tggtgggtgg aatgcattgc tctctggtag aaatagtagt 360

gatctctccc a 371

<210> 1259
<211> 362
<212> DNA
<213> Glycine max

<400> 1259

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taattagctg acagtcggat catgctgata tatatcaata agttaaattt gatagtgata 120

ctgttgtata tattaaacta cattgagatt tggcaaaagc aaaaagctat taaacattgt 180

cttgtgttgc attctcattc aggaaacagg tttcaacttc tgtacaaaac agaaatttct 240

tacaataaaa gaagacggct tctgttcaaa attgcctcat ctgatctgtc tgtgtctcca 300

ttagcatgat ttacaggtca ttcaagtgac acgtgacagt taggaactca tccttcttac 360

at 362

<210> 1260
<211> 441
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1260

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cagganagcc ccatctttaa agttctaatt aaggttagat taagaatttt aaatgcaaat 120

tacattatta taagtaatat tgaataccta attaaattat atttttaag gaacctaaat 180

aatctaatta gatttattct atttaatttt aattaatatt cattagttaa agttgatctt 240

agttgattgg ataattaaaa ttagtttcaa gtgagaataa ggacttacat tntttgttta 300

agttaaaatc attctanatt actatgcttg gagaacctga aataactaat taatacatnt 360

tttatgaatt aaatanacca cacttatant tctattaaat ttgagttaac ttttttaag 420

agaaatttga gttactaagt a 441

<210> 1261
<211> 404
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1261

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gatggccttg atttcccaag gtccacatgg accccatttc taccaactac aaaacctaag 120

aaaactatat tatctacaca aaaggtacac ttctctatat ttgcatagag ggtgtttttc 180

ctatggactg aaagaactta cctgagatgt cctaagtgat catctangct cctattgtac 240

actanaatat catcaaaata aacaactaca aatctaccta tgatatccct taagacatga 300

tgcataagcc tcataaaggt gcttggtgca ttagtgagcc caaaaggtgg tcttgaaagc 360

gattttcact catacccttn tcatctgatt tcggatacca cttt 404

<210> 1262
<211> 305
<212> DNA
<213> Glycine max

<400> 1262

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atcctccgag gtaaagatgt ccagactaca actattggct acaaaggtcg aaaatctgaa 120

gatgaatgag gaagagtgta ttcatgactt ccacatgaac attcttgata ttgccaatgc 180

ttgcactgcc ttgggagaga agatgacaga tgaaaagctg gtgagaaaga tactcagatc 240

cttgccttag agatttgaca tgaaagtcac tgcaatagag gaggcccatg acatttgcaa 300

catga 305

<210> 1263
<211> 444
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1263

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gtcttttaat taatttacaa gtgaattttc aatactaaag taatggttca tacttcttaa 120

tctaacaact attntgatac attattattt tttattttac gaaaattaca aacaacaaag 180

attaattaaa aattagaaga catataaaca agttgcatag aaaaataata cggtagattn 240

tacaaaagtt taaactgttt gacacttctt atttactttc acacataaat acaacaaaaa 300

tgtgtattat cttgaaaatg attacaagta tgacaactta acataagttg tctatcacat 360

taatacaaat cggaatacct aagaagtata taagaaatga taaattaatt ttcacaagag 420

ttcctctcag tgtcaccaca agca 444

<210> 1264
<211> 426
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1264

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agaagttgga aggtattgga caagggaaga aagaattcag ggccgaagtt agcatcattg 120

gaagcattca tcatcttcat ttggttaggc ttaggggatt ctgtgctgat ggaactcata 180

ggctccttgc ttatgagtac ttgtctaatg gctccttgga taaatggata ttcaagaaaa 240

acaaaggtga gtttctgttg gattgcgata ctangttcaa tatagctctg ggaacagcac 300

aaggacttgc ttaccttcat gaagattgcg actctaagat tgttcattgt gacatcaagc 360

ccggaaaacg tgcttctgga tgaccacttc atgcgcatgg ttcggatttc gactggctaa 420

ctcatg 426

<210> 1265
<211> 350
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 1265

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gaatatcgag acactcgtaa ttgaaaacgg aagttctgag aaaaatcaaa cgacaataag 120

ttttaactcg gatgtcctat tgagccctgt catatatcga gacgctcgta attgaagacc 180

gcagctctga caaaaatcaa acgactataa tctgtaactc ggatgtgcga tagagacccg 240

taatatatcc ggactctcat aattgaaaac taaagctctt aacaaatatc aacgactata 300

caatcttgac tcggatgtcc gactgtgtcc cgcaagatat acagacgctc 350

<210> 1266
<211> 384
<212> DNA
<213> Glycine max

<400> 1266

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cttctatctc ttttaagtgc ttatttttta cctgaataat gttagttaaa ttcgagacaa 120

gcttatcttg ccttcgagct tcttcttcca taagctcaga tatggttttg acatcgccca 180

tccttcgcag atgttctcca tagatactat tgatcttgta gtcatctgcc cgggcaaccc 240

atgcataaag gccagacttc agcccagaat tagtaaacca atccttttt ccatgatgat 300

ctaattcata tgctctttca aatgccaatg cattatgtaa gcctggccaa gttttattga 360

attccacaag agcagtttca gagt 384

<210> 1267
<211> 346
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1267

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ttagattgng agcttccatt tgaatttatg tgtgatgcct ccaattatgc acttggggat 120

gttntgtcgt agagagttga tagactatca catgtcattg cttacgcctc accactctgg 180

atgcaaccca agtcaactac accaccaccg aanaagagct tttagctatt atttttgcat 240

tagataaatt cagatcttat ttgtttgctc ctatattact atttgtactg accatgcagc 300

cttgagatac ttgttgaaga aacctaatgc taaacccaaa ttgatc 346

<210> 1268
<211> 392
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1268

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cgcaagggtt tgtggttggt gctcctctgc tgaccaccat acagaccttt gcccttccat 120

gcagcaacct ggagcaattg agcagcctga agcttatgct gcaaatattt acaatagacc 180

tcctcaacct cagcagcaaa atcaaccaca gcagagcaat tatgacctct ccagcaacag 240

atacaaccct ggatggagga atcaccctaa cctcagatgg tccagccctc agcaacaaca 300

acagcagcct gcttcttcct tcaaaatggt gctgggccag cagaccatac atntctccac 360

caatcaacaa cagcaacaac cccagaaaca ac 392

<210> 1269
<211> 405
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1269

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tcagggtcca cttggacccc atttctacca actacaaaac ctaagaaaac tatattatct 120

acacaaaagg tacacttctc tatatttgca tagagggtgg ttttcctaag gactgaaaga 180

acttgtctga gatgtcctaa gtgatcatct aggctcctac tatacactaa aatatcatca 240

aaataaacaa ctacaattct acctatgaaa tcccttaaga catgatgcat aagcctcata 300

aaggtgcttg gtgcattagt gagcccaaaa ggcatcacta gccattcata caaaccanac 360

ttggtcttng aaagcagttt acactcatcn acccttttat cctga 405

<210> 1270

<211> 418
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1270

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gaggtccacc attgcgcgag ttgcttaaac aattccaatc agcttctctt acccgggaag 120

aaccgataat aactatttat actggaacca atgggtatct tgattcctta gaaattggac 180

aggtaaggaa atttcttggt gagttacgtg cctacttaaa caccaataaa cctcaactcc 240

aagaaatcat atcttctacc aagacattca ctggggaagc agaagtcctt tttgaggaag 300

ctattcaaga acagatggaa ctctttttac tacaggaaca ggtagaaaaa agatgattaa 360

tcatttaata actttataat tcactctcaa ttcttataat angnatcttt taatatct 418

<210> 1271
<211> 402
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1271

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gatcatcgat ggtcggcaag tatgatggtc ttaatgatga tcctacacgt attttcgtgt 120

gtatctcaca ggcggtttta aaaaacctcg ccaattaact tgggttacgg gtgtagttat 180

ggctgtattg actgcatctt ntggtgtaac cggttattcc ttaccttgtg atcaaattgg 240

atatagngca gtcaaaattg taacaggcgt acccgacgct attcctgtaa tangatcagc 300

tttggtaagc tattacgcgg aagtaccagt gcaggacaat ctaccttaac tcgttgttat 360

aggttgcata cttgttgcat acctcttcta ctgctgtatt at 402

<210> 1272
<211> 341
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1272

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aaacctaatn ttggtcacgt aaggaaaagt angacaaact tacctaatgc aaaatggcaa 120

ggtaaaggtg tgccacatct cttcaatgtg gtcatttcat catctgttag tttacgattc 180

acaccatatg gaagaaggca aaagggctta ctataaccat gaataacagc aggcagaaga 240

tcagcatcaa caggcaaagg atcacactcc caccaatcaa tatatcgagg cccaagccct 300

gttagcaaac agtctgtatc ttctgcaagc tctgcttcat c 341

<210> 1273
<211> 328
<212> DNA
<213> Glycine max

<400> 1273

tggttacccc atgttgaatt tgcttacaat atagctgttc atagcaccac taattggtct 60

ccttttgaag atgtttattg gtttaaccca ctaactcctc ttgatctttt gcctaatgtt 120

tctgttttta agcataaaga aggtcaagca aatgcggact atgtgaagaa gcttcatgag 180

agagtcaaag atcaaattga gaggaaaagt ataagctatg ctaaacaagc caacaaaggg 240

agaaagaagg ttgtcttcga acccggagat tgcgtgtggg tgcacatgag aaaaaaaagg 300

tttccggaac agaggaaatc atagcttc 328

<210> 1274
<211> 339
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1274

agctagcaac aaacataatg tcttgtcttg ttgctgacag atacaacaaa ctaccaatta 60

tacttctata aacaaaatca tccgctttat caataccatc gttcattgat aacctttcat 120

tcacaacaat tggagaggcc acacgcttgc attgctccat gcaaaacttc aatatcacca 180

aagcatattt cttttgtgaa atgaagatcc cgtcattaca ttgagaaatc tccattctaa 240

gaaaatactt aatttcaccc aagtcaacca tttcanattc gttgtccatg tcccttattt 300

cacctaagtc agtcattttc ccacttcttc acgtaccag 339

<210> 1275

<211> 283
<212> DNA
<213> Glycine max

<400> 1275

tttgcaaggt gaaatcattt atcctatctc cgacagccaa tgggtgagtc ccgtccaggt 60

agtcccgaag aagaccggcc tcacagtgat cagaaatgag aaggaggagt tgattcctac 120

tcgggtgcag aacagttgga gagtctgcat tgactatagg aggctgaacc aggttaccaa 180

aaaggaccat tttcccctgc cattcattga ccagatgctt gaacgcctgg caggtaaatc 240

ccactactat ttccttgatg gttttttgg ttatatgcaa att 283

<210> 1276
<211> 287
<212> DNA
<213> Glycine max

<400> 1276

ttgtgctaat atgttctatt gacactcttt gtttctgaac ttcttctttc acggcaaagt 60

acttcaattc catatgctta gcacccgtag agtacttgtc gttcttagaa aagaatattg 120

ttgcggagtt atcacaatac attttcagcg gcctagcaat actgtcgaca attccaagcc 180

ctgaaataaa gtttcgcagc caattagcct gaattgtagc ctcaaaacat gctacaaatt 240

catcttccat ggtggatgca gcaacaactg attgttttgc actcttc 287

<210> 1277
<211> 408
<212> DNA
<213> Glycine max

<400> 1277

agcttggtca taattataaa aagatagatg cttgtccaaa acactgcatg ttgtatttgg 60

gagatgatga aaaaagtttg gatgcttgta agcattgtgg tacatctaaa tggaaacccc 120

acaagaagaa gaaaatagct gcaaaggttt tacgctactt tccattgaaa ccaagattgc 180

aaagattgtt cacatgtcgt aagactacaa aagatatgag atggcatgtt ttggaagaca 240

ataaagatgg gttgttaaag catccaagag atggagagac atggaagaca tttgatttaa 300

tccatcctga gttttcttca aatcctcgaa atgttcgttt aagccttgct actgatggtt 360

ttaatcctgc taggaccttg agttctacct atagcatctg gccagttt 408

<210> 1278
<211> 594
<212> DNA
<213> Glycine max

<400> 1278

agcttaagcc ttttatacat gcttagtaag gatcaaagat gttaaaaaaa tggattgatc 60

tctaagtttc taaaaagcaa tgagttcaac acactataat tgattacaaa gttttgttat 120

caatcacaaa gtgttagaac aaacaacaaa tctctcttct acttgaaatt tttggcaagt 180

tttgacaaat taatcgatta cttgtttcaa taatcgatca tagaagtcag tttcaaaaga 240

agaaagactt tgtagcttaa gctaatcgat taccttttat tgtaatcgat taaattgtat 300

ctagaaataa tcaaagttag tttcaaaaga agaaagactt tgtagcttaa gaagttctct 360

acatgatgaa ataatcaatt accacacctg ataatcgatt attccagaaa atacagaagc 420

atgagaagct ctttatttga aacaagataa tagattatca tttcctataa tcgaatacaa 480

gatttatgaa aatgcataac aaaaaggatt ttgacgtatt aatcgattac cataatctat 540

aattagttaa aattggttta cccatcaaaa ttataaatac ccttttatct tatt 594

<210> 1279
<211> 507
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1279

agctagtaat acattaattg ataaaataaa actttggcat ttgagattag gtcatgttag 60

tgaacgggga ttacatgaaa ttgagaaata aaatctgtta ggtggcgata aactagataa 120

acttgaattt tgtgatcatt gtgtgcttgg taaatcacat agaataagct ttggcactgg 180

tattcatgtt ttatctaggc cttttgagta tgtgcatttt gatttatagg gaccatttag 240

agtgaaaatt catggtggaa gctcatactt tctcaccatc atagatgatt tctcaagaag 300

agtatgtctg tatgttttga aaaataaatc agaagctttt caaatattca gagagtggaa 360

aactcttatt ggaaatcaac ttggtacaaa actaaaaatt ttaaggactg acaatggcct 420

gtagtttgtt tcaaagcaat tcaatgagtt ttgcaggaaa gtaagtatca naaggcccaa 480

aacaatccct tacacaccac aacaaaa 507

<210> 1280
<211> 284
<212> DNA
<213> Glycine max

<400> 1280

tctgttatga atttcgagtg tctcgatata ctacgggaca caatcggaca tccgagtaaa 60

aagttattga catttgaatt tgctcatagc attcgttgtc aattacgagc gtctagatat 120

attaaaggat tcattcggac atccgagtaa aaagttatta tctttttatt ttgctcagag 180

cttctgtttt caatttcgag catctcgata tattacagga ctcaatcgga tatccgagtc 240

aaaagttatt gtcgtttgga tttgctacga gcttccggtt tcaa 284

<210> 1281
<211> 278
<212> DNA
<213> Glycine max

<400> 1281

tgtaatcgat tacagcattt gtgtaatcaa ttaccactaa ggaattttca aaaaataact 60

cccaagagtc acatctattc aaaagatttt tgaatggcca tcaaaggtct ataaataggt 120

gacttgggac acgaaatttc ttagagtttt cctgaacaaa ttgtcttatc ctctcaatac 180

caaattgtct tataactctc aaaaagaatt ccttggccaa aacacttgca aattcaataa 240

ggaatcttaa gtgatcttca attttaatat ctttctct 278

<210> 1282
<211> 493
<212> DNA
<213> Glycine max

<400> 1282

agcttggaag ccaaggcctt gaggtttgtt tttatgttgt tggattgatt ttatatcctt 60

cattcatatc atggctctga gttggtatct tccttgtctt gtgtgaatca tttttggctg 120

taaggtttcc aagttgggat tcgggtgtat gggcctgacc aaagtgtaca atgatcctgt 180

tcctaaagag gttggcatct ctttgatcaa atacacattc agtaaaggga tcactttctt 240

tgttactgta gatttttatc gaccccatgc caacaaagtt ttggtcgaaa aggttaatta 300

ccttaacact ttgtaacata tttgtttcac tttaacaata acaacccata atataatgta 360

acataacatt ttaattaact ctgaggtggt caggggcttg cctcaagatc aaattcagat 420

tcccccaaag tttggtattg tcaaaatgga taatggtaat gtgatagtga accggttccc 480

ctgaatatgt ctg 493

<210> 1283
<211> 434
<212> DNA
<213> Glycine max

<400> 1283

agcttcttgc aacattatgg tcaatgagct gcataatgag gggaaaaagc aattttcctg 60

ttataaaaaa tatattagcc aattttgatg atgctttctg agaattgaga agcttgcctc 120

ctaaaaggga ttgggatcat gctatcattt tgaagaaggc tcaaattcct aatatttgcc 180

cccacatgta tatgcattat caaaaaaatg agatagagaa gattgtgaag gatatgcttt 240

gtgctgtaag gcccaacact aacccttca gtagccctgt tatacttgtc aagaagtatt 300

gtgtgtggag attttgtata gactatcagg ccatagacaa gtaaacaccg gataaatttc 360

caattcccat aatagatgaa ctactagatg tattgggtga tgcagtgatt tttgtaagat 420

gaactactct tttg 434

<210> 1284
<211> 168
<212> DNA
<213> Glycine max

<400> 1284

tataatatat cgaggcgctc gaaattgaac aacggaagct cttgagaaat tcaaatggtc 60

ataacttta actcggagtt caattcatgc gcatcacata tagagacgct taaaaatgaa 120

caacggaagc tctccaaaag ttaaaatggt cataagtttt cacactga 168

<210> 1285
<211> 282
<212> DNA
<213> Glycine max

<400> 1285

tgaaattgaa catcagaagc tctcgacaaa ttccaatggt cataacttgt cacaaggaag 60

tccgattctg gcgcatcaca tatcgagacg ctctaaattg aaaaccggaa gctctcgaga 120

aagtcaaaag gtcataactt gtctcacgga agtcagattc gggcgcataa tatatcgaga 180

cgctcgaaat tgaacaacgt atggtctcga gaaattcaaa tgttcataac ttgtcacacg 240

aaagtccgat tcaggcgcat aatttattga gaagctggaa at 282

<210> 1286
<211> 195
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1286

tgaaggtagg agaagatgag tggagggaga gggagtgaag aggcacgaaa ttttatgcct 60

caaatgaggt ctgaactttg aagtgtaatt ctcaaatgat caaagttaca acaagtgtta 120

cacatgcttc catttatagc ctangtagct tccttgagaa gcttccttga gaaacttcct 180

tgagaagctt ttttg 195

<210> 1287
<211> 276
<212> DNA
<213> Glycine max

<400> 1287

tacatcgact gccagaaggt gcataacaaa ctcgttgaaa ttagttgcaa cttgtaactg 60

tttctcggag gaagaaagaa agaaaaaacg gttataacaa actttttttt ctgctacggc 120

tgctgctgtt gcaagttggg gcgcctccgg aaatagcgcg tttgttggag gaaatccggc 180

gagaaaacga cctatgcaag agcgacgtcg tttcttcttc cacgtgcttt ggagccgatc 240

ccgagcttga cgagttcatg gtccccccct ctttct 276

<210> 1288
<211> 419
<212> DNA
<213> Glycine max

<400> 1288

agctttacta gtgttccaag acatgatgtc tgctggagaa tgtccaaact atgtaacctt 60

cattggggta ctttctgctt gtgttcattt agctcttgta caagaaggat tctactattt 120

tgatcagata atgaagaaat ttgacgttga gcctggactg gagcactaca catgtatggt 180

tgcacttttg ggtagggctg gtttacttga tgaggctgaa aactttatga agacaacaac 240

acaggtcaaa tgggatgttg ttgcgtggcg tactttgctt aacgcgtgcc acattcatcg 300

aaattacaat ttagggaaac aaattacaga aactgtgata cagatggacc ctcatgatgt 360

gggaacatat acattgctat caaacatgca tgccaaggca aagaaatggg atggagtgg 419

<210> 1289
<211> 288
<212> DNA
<213> Glycine max

<400> 1289

tgtcgaaaag gcaaagccgt tttacaaact gctcaagaaa actgagccct tcctgtggga 60

cgagacatgt gaacgagcct tcctggcttt caagaaaacc ataactacac caccgatcct 120

gagtcggcct aggctaggag tacccatact cctatacctt tcaataacta acaaagctgt 180

taactcgacc cttctgcaag aggaagggaa gcattaactc cctatctatt tcaccaaccg 240

catacttcat gaggccgaga agtgctacca aatgatagaa aatatggt 288

<210> 1290
<211> 440
<212> DNA
<213> Glycine max

<400> 1290

agcttgcagt gattcactct gatgtgtgtg gcccatttga aatcaaatct catggaggta 60

acttgtattt tgtctctttt atagatgact ttacaaagaa aatgtgagtt tacctattac 120

aaagaaagag tgaagtattt gtaacattta aatcattcaa gttactagtt gaaaaagcaa 180

tctggttgtt caatcaagat gcttagaact gatggtggag gagagtacac ttcacttgaa 240

tttgagaatt tctacaagga agaaggaata attcatgaag taatggctcc atacactcct 300

caacacaatg gaactgctga gagaaagaat agaatagtgc aaaatatggt tagatgcatg 360

ctgagaaaga agcatcttcc atatgatttt tgggcaaagg cagtatccac aacttctcac 420

atcttgaata gatgtcctac 440

<210> 1291
<211> 441
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1291

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tgcaaattca gtagaacaga taaatatatg atgctctaat ttacaaaacg aaataaaaaa 120

aataaattgg ctttcatgtt gattgtaaac cttttgagtt tggacactta cacattctgg 180

tgaagctgac aaatgcagta tatgtagccg aagacaaggc aggcaaaaga aacattggca 240

aaactcggat tgccctcatt ttccaattca tatccattga tcttgttgtc ataatagcat 300

aacctacagc aatgacctga aagttgaaac cattttaagc aaaatccatt tataaaaaca 360

ccctcaataa tcaataagaa tatattaatt tgtcagagaa aaaatttaaa atttcagtta 420

accctccatt gtcactcaat a 441

<210> 1292
<211> 289
<212> DNA
<213> Glycine max

<400> 1292

tatcagaaca acatttttt tcaaaatgca acaatgagaa aagaaagcac aaagaggaaa 60

ttcacagaac caaatgagat taacatcaat tcacattttg tttctaaaga atataagaga 120

aaacacccga ttcactcagg cagaggaaaa cctctcaaag gtgcataatt ctcatgcagg 180

caattgttcc atcacaattc caatcactga tatgtcataa atcaattttt gcaagtcatt 240

tcccatcaaa tcaaagataa attgcataat catcatggat cattagggc 289

<210> 1293
<211> 407
<212> DNA
<213> Glycine max

<400> 1293

agctttctcc actaagttgc ctaatgcctg aaatgtcttt tctgatggta gtggtcctag 60

atgcaagaaa gaatttctcc aagaacaccc tcttaaggtc atccctgctg aaaatggact 120

tgggagcaag gtagtgtagc caatcttttg ccactccctc caaagaatga ggaaaagcct 180

ttagaaagat atgaccttct tggacattag ggggtttcat ggtggaacaa acaatatgga 240

actccttaag atgcttataa ggatcttcac ctgcaagacc atgaaacttg ggcagcaaat 300

gtattagtcc agtcttgaga acatatggaa caccctcatc aggatattga atgcacaagc 360

tctcataagt gaaatcaggt gcaaccatct ccctaagagt cctctca 407

<210> 1294
<211> 439
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1294

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tcttctattt tcagattggg aatgcctcta acagcacctt ggtcaatgat tttcttcatg 120

cctcttaagt gcagatgtcc aaatctttga tgccatattt tgacttcatc ttctttggag 180

gatagacatg tggaggagta actggtttct tgaggtgtcc ataggtaaca gttgtccttt 240

gatctgctgc ccttcattag aacttcactc ttctcatttg ttaccaagca ttctgacttt 300

gtgaagttta cattgaatcc ttcatcacaa caactgactg atgctgatca agtttgcagt 360

cagtcccttc accagcaata ctttgttcag actangaagt ccatcatgga ctagccttcc 420

catccaataa tcttttctt 439

<210> 1295
<211> 304
<212> DNA
<213> Glycine max

<400> 1295

attacgagtg cctgtatatt gatgcgcctg agtcagacat tcgagtgaaa agttatgacc 60

atttgaattt ctcgagagct tcctatggtt aattttgagc gtgtcgatat attatacgcc 120

tgaatcgaac ctcatggtga aaagttatga ccatttgaat ttcttgagag catccgttgc 180

tcattatcga gcgtctctat atgtgatgca cctgaatcgg acctccgagt gaaaagttat 240

gaccatttga atttctcgag agcttccgtt gttcaatttc gagcgtctcg acatattatg 300

cgcc 304

<210> 1296
<211> 402
<212> DNA
<213> Glycine max

<400> 1296

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ggtcataact tttttcacgg atgtccgatt caagcgtatc acatatacag acactcgaaa 120

ttgaacaacg gaacctctcg agaaattcaa atggttataa cttttcacac agatgtctaa 180

ttaaggtgca tcacatatag agacactcga aaatgaacaa cggaagcttt cgagaaattc 240

aaatggtcat aacttttcac actgaggtcc gattcacgct tataacatat cggggcgcct 300

aaaattgaac aacagaagct cttgtgaaat tcaaatggtc ataactttta actcggatgt 360

ccgattcagg cgccttacat atagagacgc tcaaaaatga ac 402

<210> 1297
<211> 276
<212> DNA
<213> Glycine max

<400> 1297

tagagccaat tcaaacgaca ataacttttt actcggatgt ctgattgagt cccgtcatat 60

atcgagacgc tcgaaattga atgttgaagc tcttagccaa ttcaaacgac aataactttt 120

tactcgaatg tctgattgag tcctgtaata taacgagacg ctcgaaattg aatgttgaag 180

ctctgagcca attcaaacga caataacttt ttactcggat gtctgattga gtcccgtcat 240

atatcgagac gctcgaaatt gaatggggaa tctctg 276

<210> 1298
<211> 418
<212> DNA
<213> Glycine max

<400> 1298

agcttaaaca ttcaacttcg agcgtcttga tatattacga gtctcaatca aacatccgag 60

aaaaaagtta ttgtcgtttg aatttgctca caagttcaac attcaatttt gagcgtctcg 120

atatatgacg ggactcaatc agacatccga gtaaaaagtt attgtcgttt gaattaactc 180

agagcttcaa cattcaattt cgagcgtctc gatatgtgac gggactgaat caaacatccc 240

agtacaaagt tattgtccgt tgaatttgct caaaggtttc acattcaatt tcgaacgtct 300

cgttttatta cgggactcaa tcagaccatc cgagtataaa gatattgccg tttgaatttg 360

ctcagaacct caacattcaa ttttgagcgt ctcgatatat gacggggact caatccta 418

<210> 1299
<211> 378
<212> DNA
<213> Glycine max

<400> 1299

agcttctggt gggacatctt gacttgcttt ccaatctgac attcaccaca gattctgcct 60

tcttctattt tcagattggg aatgcctcta atagcacctt tgtcaatgat attcttcatg 120

cctcttaagt gcagatatcc aaatctttga tgccatattc tgacttcatc ttctttggag 180

gatagacatg tggaggagta actggtttct tgaggtgtcc ataggtagca gttgtccttt 240

gatctgctgc ccttcattag aacttcacac ttctcatttg tcactaagca ttctgacttt 300

gtgaaagtta cattgaatcc ttcatcacac agctgactga tgctgatcaa gtttgcagtc 360

agtcccttca ccagcagt 378

<210> 1300
<211> 276
<212> DNA
<213> Glycine max

<400> 1300

ttgagcaaat tcaaacgaca ataacttatt agtcggatgt ctgattgaga cccgtcatat 60

atcgagacgc tcgaaattga atgttgatgc tccgagcaaa ttcaaacgac aataactttt 120

aactcggatg tttgattgag tcccgtaata tatcgagacg ctcggaattg aataccgaag 180

ctctaagcaa attcaaacaa caataactat ttactcggat gtccgattga gttccagaat 240

atatcgaaac actcgaaatt gaatgttgaa gctctc 276

<210> 1301
<211> 478
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1301

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aacataaaaa gggaaaaggt aatattgtag ccgatgctct ttctcggcgt catgcattac 120

tttctatgct tgaaacaaaa ttgattggtc ttgaatgttt gaaaagcatg tatgaaaatg 180

atgaaacttt tggagaaatt tttaaaaatt gtgaaaattt ttcagaaaat ggtttcttta 240

gacatgaagg ctttcttttc aaagaaaaca aattgtgtgt gcctaaatgt tctactaaaa 300

aattgcttgt ttgtgaagca catgaaggag gtttaatggg gcattttggg gtccaaaaga 360

ctctagaaac attacaagaa cattttttatt ggcctcatat gaaaaaagat gtgcagaaat 420

nttgtgaaca ttgcattgta tgtaaaaaag caaagtctaa tgtaaagcct catggatt 478

<210> 1302
<211> 290
<212> DNA
<213> Glycine max

<400> 1302

agcttatgag aattccaagc tttataagca aaaagtaaaa atctatcatg acaaaaagct 60

atcaaaaagg aatttttagt ctggtcaata ggtattgtta tttaattgtc aattaagatt 120

gtttctaggt aagcataaat ccaagtggtc tggaccattc atcatcaaag aagttatgcc 180

acatggagca atgatattgg aagacccaac caccaaaagg acatggaccg tgaatggtag 240

caagaggata atcactgttg tccagctgca agaggcttga accataaaaa 290

<210> 1303
<211> 500
<212> DNA
<213> Glycine max

<400> 1303

agcttttttat tgtaatcttg aaattcagga caacactctg atttctgaaa tttttgggat 60

atttatggtc attgaccagt ccctttttcca tgacttaacc aaattaccca gtgacggtgt 120

accatttgaa agcacactaa atgacgactg gaaatttgat ttctctgccc atgatgcccg 180

ccagttggtt tgcaccaaca atgcagatat gaccggacgt cttcttgtcg ggtcattggc 240

ttttgaaagc cgcatccttc actatttaat tgtgcgtatt ctgcttccac ggtcttccaa 300

ccttgcccag gtttctgagg aagatctaat tatcatgtgg gcccttcata cagggcgtca 360

acttgactgg gcacacttag tcagatatcc catgcataag gcattgcgaa taaatgctcc 420

actaccatat cccacacttg tcactctctt tttccgccat ttcaaaatcc ctcttgatct 480

gaacccttat gttccaatca 500

<210> 1304
<211> 276
<212> DNA
<213> Glycine max

<400> 1304

tccatcaagt tatgaccatt tgaatttctc gagatcttcc gtggttcaat ttcgggcgtc 60

tccatatgtc atgtgcctga atcggacctc cgtaagaaaa tttatgacca tttgaacttc 120

tctagagctt ccgttgttta atttcgagct tctcgatatc tgatgtgcct gaatcggaca 180

tccgagtgaa aagttgggac aatttcaatt tctccagagc ttccgttgtt caattttgag 240

cgtctcgata tgtgatgttc ctgaatcgga cctccg 276

<210> 1305
<211> 517
<212> DNA
<213> Glycine max

<400> 1305

agcttcttct tgtttcttcc cccattttaa aacaacattt ttcttaatta cctcattcaa 60

aggtgcttgc aaggtactaa aattcttcac aaatcgtcta tgaaaacttt tcacctcagt 120

cacacttcta ggtgcaggcc actcttggat agccttgacc ttttctttat caacttgaac 180

ccctttggaa cttactacaa aaccaagaaa cacaacatgg tctttgcaaa aaaatacatt 240

tttcaaggtt agcatacaat tgttccttcc taagcacaca caacaccgat tttaagtgtg 300

caacatgcaa atcaagggtt gtgctataaa caaggatatc atcaaagttc accaccacaa 360

atttaccaat gaattctctc aagacatggt tcattaatct catgaaaatg cttggagcat 420

tagtcaaact gaaaagcata accaaccatt catataatcc atatttagtt ttgaaagcgg 480

gttttcattt ctctccttct ttaatcctta tttgatt 517

<210> 1306
<211> 461
<212> DNA
<213> Glycine max

<400> 1306

gcttaaggac tatgattatt caacatcaca gaggtttgtg actactggtg gtgatttcgg 60

caacccctgt tcgcaaaccg tggcgaattg gtctccccat tgagaagtat gaggatgctt 120

acaagttggt ctactgtcca agtgtgtgca acgattgcag ttatccatgc ggtgatattg 180

gaatatacca agatgaatat ggcaagcgtc ttgctctaag ttctgaacca tacaaagtga 240

agttccagcg ggcttaatta ttgaattgat aacaaaacta attaaagaat aatgaataag 300

tgtaatgaac tactttatgc ttttgctgca tatatggtaa ttctcatgtt gagttccttg 360

ccacggactt gataataaat aaacaagtta ctttctattt ttagtctttc caaaatttct 420

tgtttctgtt cgtctttgtc attgtttgca tttgggatgc a 461

<210> 1307
<211> 271
<212> DNA
<213> Glycine max

<400> 1307

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gtccaagaaa agaacgtact tcctgcatgg aagcggggta aggaagagaa gtaataacat 120

atatcttggc cttattgacc tcaatacttc tactagagac caaatgccct aagactatac 180

cttcatggat cataaaatga catttttcaa agttaagaac aagattagtc tcaatgcatc 240

ggtcaagaac tctagagagg ctatccaaac a 271

<210> 1308
<211> 326
<212> DNA
<213> Glycine max

<400> 1308

agcttgtttc agaggcgtgg agtttactat cagataaggt caaaagacta gcatataacc 60

agaacaggag attggaagga tttcacgata atgctcccaa caagaatggt tatataaaac 120

ttaacaagaa tgcaacttcc agcatgagaa caggaaataa tgatgctcgg gcacatccac 180

atccgcatac accctccatt cctcctccac atacaaatgc tggtaccttt tggactatct 240

gtaataagtg caagacacat tatgaatatc tcaggacata tttgaatcaa acccttttat 300

gtcccaattg taaacaagct tttgtg 326

<210> 1309
<211> 280
<212> DNA
<213> Glycine max

<400> 1309

tcaaaaaatt tgaatggtca taacttttca cacgaatgtt ccattttggg acataagata 60

tcaagacgct tcaaattgaa caaccgaaac tcctgaaaaa ttccaatggt cataacattt 120

cacacgaatg ttccattggg ggacataact tatgtatacg ctcgaaattg aacaacctta 180

gttctccaga aattcgtaat gtcataacat tttactccga tgttccattc gtgggcctat 240

tatatggaga cgctcgaaat tgaacagcgt gatgttaatt 280

<210> 1310
<211> 716
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1310

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gttggatcaa atggagaata gagatcatcc tgaagaagaa aggaggaaaa gaaggaatga 120

tggtgttcct aaacaaaacc gaattgatgg tattaaactc aacattcctc catttaaagg 180

aaagaatgat ccggaagcct acttggagtg ggagatgaaa atagagcatg ttttctcatg 240

caacaactat gaggaggacc aaaaggtgaa gcttgccgcc acggagtttt ccgactatgc 300

tcttgtgtgg tggaagtgat tatgcaagtt gaagtggacg tttccattgg gaaatacaat 360

gataaggtac tttgtgatgt tgttcctatg gaggccagtc acttactttt ggggagacca 420

tggcaatttg ataaaagagc ccatcatgac ggttacacca accagatctc tttcattact 480

ttggtgttgc ataaaaaatg tacacatgta gtcggctagg ttttttgtcc caaccttacc 540

cacttttttgt ttctagccaa attggcttgt tccattattt tgcccggaaa aatttacccc 600

ctttgcaaaa aaatattgct ttcaacttat gccttttttt tagggatgaa ctgaaccttt 660

ttcccgcatt gtcggtaaat accccaatta atctttcgcc cccttgccaa tttttt 716

<210> 1311
<211> 444
<212> DNA
<213> Glycine max

<400> 1311

agcttataat atatcgatag gctcgaaatt aaacatcgga aactctcgcg aaattcaaat 60

gggcataaat tttcacacgg atgtccgacc cgggcgcata atatgtcaag agtctcgaaa 120

ttgaacaacg gaagctcttg agaaattcaa atggttataa aatttcacac ggatgaccga 180

ttcaggcaaa tcacatatcg agacgatcag aattgaacaa cggaagctct tgagaaattc 240

aaatggtcat aacatttatc tcgaatgtcc aatttaggcg catcacatat agtgatattc 300

gaaattgaac aacagaagct ctcgagaaat tcaaatggtc ataacttttc acactgaagt 360

ccgattcacg gttataatat atcgatacgc tcgaaattaa acatcggaaa ctctcgagaa 420

attcaaatgg tcatgaactt ttca 444

<210> 1312
<211> 417
<212> DNA
<213> Glycine max

<400> 1312

agcttggtta tctccttctt cactacatca ataatcaccg ggttgagtct tctctgttgc 60

tggcttactg gtttagctcc atcctctcca tttattcgat gcatacatgt ggatgggcta 120

ataccacgaa tgtccgccag ggtccagcct atagccttct tatgcttctt gagaactaac 180

aacaacttct cctcttgctc atcagcaagg gaggcagata taatcactgg aaaactcttg 240

ctatcatcca agtaagcgta ttttaaattt tatggcagag gcttcaattc tggtgtggtc 300

aactggacag tggtagaaag agatggtttc ttagccttta cctcataaag aaaagcagat 360

gtatgtgtac tttttgaaac tggttagtcc tatctgactc tataaaatca atctcaa 417

<210> 1313
<211> 462
<212> DNA
<213> Glycine max

<400> 1313

agcttgctaa cccatggaag cttgataacc cattcttctt tccttaagac atgatgcata 60

agcctcataa aggtgcttgg tgcattaatg agcccaaaaa gcatcactag ccattcatac 120

aaaccaaact tggtcttgaa agcggttttc cactcatcac ccttttttcat cctgatttgg 180

tgataaccac ttttaagatc aatttttgaa aaggtattgg caccatgcaa ctcatcaaga 240

aaatcatcaa gtctaggaat ggggtgccta tactttacag tgatgttgtt gatggccctg 300

caatctgtac acattctcca tgtaccatcc tttttgggca ccaacaacac tggcacaaca 360

catgggctta ggctctcttg gacccaaccc ttctccaaca attctttaac ctgagactct 420

atctctttag tctcccgagg gttagtccta ttggctggcc ta 462

<210> 1314
<211> 552
<212> DNA
<213> Glycine max

<400> 1314

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atgatttcaa gattcagtca acaagttcaa gatcaagatt aatttcatgt ttcatgagaa 120

gaaatcaaga agattcaagt ttcaagagaa gtttgatttc aagattcaag agaaggtgaa 180

ttcaagattc aagagaagaa atcaagaaga cttcacaagg gaagtattga aaagatgttt 240

caagaaacaa acatagcaca attttgtttt tcaaaagagt ttttctcaaa attttctaag 300

ttaccagagt gtttactctc tggtaatcga ttaccagttt cctgtaattg attaccagtg 360

acaaagtttg atttgaaaag cttttaactg aatttgcaac gttccaattg atttttaaat 420

ggtgtgatcg attacaatat attggtaatc aattaccagt gtatcattga aattcaaatt 480

atattgtgaa gagtcacatc ttttcataaa atgctttgtg taatcgatta catggttatg 540

gtaatcgatt at 552

<210> 1315
<211> 365
<212> DNA
<213> Glycine max

<400> 1315

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aaccaaacgc ggaaggtttt tttggtgagg tagccatgga aaagcagagc gtttggaatg 120

atttcgtaaa tctcacaatg ctattgggaa atgctggtaa aaacacgaat gccaagcaga 180

tataaatttg aatgaagaat gtataggggc gtgtgaggca acggtcgaat tcgttttggc 240

ttaatattga acgtgctatt aatgttaagt gattcgtttg ggcacgttca gattgctgta 300

gctgctataa ttcctctagc aaacaaatgc ccagcttgcc cctcagtttt tcaaactgat 360

ttgca 365

<210> 1316
<211> 501
<212> DNA
<213> Glycine max

<400> 1316

agcttctagt atacgattta tctgaagaaa ttcattttct atcgcacaac ttccaccacc 60

accaagagca gctaagtact gcaatgcaat tttagctgtt tctgttttcc cagatccact 120

ctcgccactg cgaacaaatt tctaacaatg attattaaca agcacaccag tgaatgtatc 180

ttattactac tatgaaaatc caatgatatt ggtttaggaa catatattaa gtgtcatgca 240

caaaatgtag cccataaatg cagtaaggag ctgaccttat gataatggac tgatttactt 300

catctgtaag atacaaaaag aaaaagaaaa cctttataaa tgtctcattc aagtagaatg 360

caaagattgc aaagaaggga agagaaaggg agaatttcat tcacctctta tcaccttgtt 420

ataaagccga tctgccacag cataaacatg aggactatca ataattctct gcctataagc 480

tgagacagaa tcatttccat a 501

<210> 1317
<211> 435
<212> DNA
<213> Glycine max

<400> 1317

tgcttctaca attgacatat actttgacaa tgttggggga gacatacttg aggcagccct 60

tcttaacatg agaaggcatg gacgaattgc agtggccaga atgatctcac agtaagatct 120

tgatgagcct caaggcataa agaacttagt gaatatcata tacaagcaga tcaaagtaga 180

agccttcaca gtttatgatt actatcacct ctatcctaaa ttcttggata ctgttttgcc 240

ttacattagg gaagggaaga taacatatgt tgaagacata actgagggtc ttgagaacgg 300

tccaattgca ctagaagcaa tgttccaagg tcgtagtgct ggtaaacaag tcattatact 360

tgctcgtgaa taatttagta caaccttact gtttgatctt tcaattcatt ttgggtgtgt 420

tgtaactctc atttg 435

<210> 1318
<211> 470
<212> DNA
<213> Glycine max

<400> 1318

ctgatggtgt cgagaagaaa tcacatgttt ggcatcatca aaaaggggga gaatgtgaat 60

gtatgtatac atgattttga tgatgccaaa gaaaaatcaa acaaggttgc ttcaaatgat 120

aagcatttgc ttcaagaata attcaagagt gcttcaacaa acaaagcctt gtttcaagat 180

tcactaaaga ccaagccttg ccttaaaaca aagtgctttc aagacatgca aagctctggt 240

aatcaattac cacgaagtgt aatcgattac cacaagacat ggttgagaaa tagctgttga 300

aaaaggtttt gaatttgaat tttcaacatg taatcgatta ccatatgtct gtaatcgatt 360

accagcaacg aaactttgga aattcaaatt ccaaagtcat aacccttcaa attataactg 420

tgtaatcgat tacacaaaca ttgtaattga ttaccagtgg aaagttttca 470

<210> 1319
<211> 391
<212> DNA
<213> Glycine max

<400> 1319

agctttcact cggaggtccg attcaggcgc ataatatatc gagacgctcg aaattgaaca 60

atggaagctc ttgagcaatt caaatggtca taacttttca ctctgaggtc ggattcaggc 120

gcattgtata ttgagaagct cgaaattgaa caatggaacc tcttgagcaa tttaaatggt 180

cataactttt cactaggagg tccgattcag gcgcataata tatcgagacg ctcgaaattg 240

aacaatggaa cctcttgagc aatttaaatg gtcataactt ttcactcgga ggtccgatcc 300

aggcgcataa tatatcgaga cactcgaaat tgacaatgga agctcttgac aattcaaatg 360

tcataacttt tcactctgag gtccgattta g 391

<210> 1320
<211> 389
<212> DNA
<213> Glycine max

<400> 1320

tcaacatcag accacttcca gggtgctgga actacttcac atggatttga tggggcctat 60

gcaagttgaa agccttggag gaaagaggta tgcctatgtt gttgtggatg atttctccag 120

atttacctgg gtaaacttta tcagagagaa atcagaaacc tttgaagtat tcaaagagtt 180

gagtctaaga cttcaaagag agaaagactg tgtcatcaag agaatcagga gtgaccatgg 240

cagagaattt gaaaacagca ggttcactga attctgcaca tctgaaggca tcactcatga 300

gttctctgca gccattacac cacaacagaa tgggatagtt gagaggaaaa acaggacctt 360

gcaagaggct gctcgggtca tgcttcatg 389

<210> 1321
<211> 513
<212> DNA
<213> Glycine max

<400> 1321

agcttgtgct aaaggaagta agacatgtgt ttgagatgcg tttaaacctt acctcaacat 60

gaaagctaga tgaagatggg atgataaacc agttcgatac agatagatgg aagcttacta 120

gaggaagcat ggttgttgct taaggtaaga aggaaggctc attatacatc atgcagggaa 180

agatatgcaa agggaagaca aatgttgctc aagatgcaac caaagaattg tggcacaaga 240

tattgggtca cttgagtgag aaaggtttga agtttctagc aaatgatcac tttccaaaca 300

taaagaggca accacttgaa tccttgaaga ttgtcttgca ggtaaataat gcagagtgtc 360

tttccaaaga ttgaatgaac tagaaggaga aagcaaatcc ttgatcttgt ccacttagat 420

atttgctcaa tgtctaaaaa gtcccttggt ggtgcccaat accttggtac cttctttaat 480

gattactcca acaagctgtg ggtggattcg ttg 513

<210> 1322
<211> 525
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1322

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tcttaagaca gcaatgtaaa gatgtagggt atgataatag caaggcaaat tgaaatagaa 120

tatgtatatt gttatttcat tgatcctttg catgatatat ataatacatg tacaagaatg 180

ttctatacca attctaaggc atgacagacg tgatccataa tcagtggcat ctgatttatt 240

ctatgcatta taaggtaaat aaatatagaa tcaaggtaac atangaaagt aaatatatac 300

acagcatatt tgcaatcatg tagaagatat ttcctaatac tccccctcaa gttggtgagt 360

gaatatcgtg aagtcccaac ttgttgcgca atgtcacaaa ttgatctttt tccaaagctt 420

ttgtaaacac atctgctagc tagaattttg ttggcacata agaaaagatt gatcatccca 480

gcttgtagtt ttttcccgac tatatgacaa tcatttccat atgtt 525

<210> 1323
<211> 385
<212> DNA
<213> Glycine max

<400> 1323

ttcctcgagc acgttcatca tccacactgc ttgacaagca ccaagtgatg ctgccacata 60

ctcaacttca gaggtagaca aggccaccac atcctgcttc cttgaactcc aagccactgg 120

tgcatcatag tacatgaaca aataccctcc agtactcttc ttctgttctg gatctctttt 180

ccaatcagaa tttgtgtaac caaacagatc tgattcatat gattcaactt caaaagggaa 240

caacacacca ttgtcaattg tccctttaac aaacctaagt attcttttgg ctgcttgcat 300

gtgtgaaagt ctaggttttt gcatgaacct gctaataaac ttacttgcaa gcagatatca 360

tgtatgctgc tgcataagta cctca 385

<210> 1324
<211> 376
<212> DNA
<213> Glycine max

<400> 1324

ttgcatcaga caaagatgat agcaaatcca ttttaggata tgtttacact ttaaatggtg 60

gtgcaataag ttggaaaagt tccaagcaag ctatggtagc agattcaact actgaagcag 120

aatatatagc gacaagtgaa cccgctaaag aagctgatag gataaaaatg ttcatagttg 180

aacttggtgt ggttacttca atagaagaga cgggcccatt aacgtgcgac aataatgggg 240

ctattgctca agcaaaggaa ccaagatcac accaaaagtt caaacatatt gtgcgaaggg 300

atcacttgat tagagagata atacaacgag gtgacgttaa gattgaaaat gtttatggaa 360

aggagaatgc aacaga 376

<210> 1325
<211> 464
<212> DNA
<213> Glycine max

<400> 1325

acactataca atacctcagc ttcactgaat agcttgtgtt attgaagaat attcttcttg 60

aatagaacac gttacccaaa aatcagtacg aggcaaataa gatattatgt cttgcacata 120

tggagtacca aaaaatacat gcatgcccta ataattacat tttgtataga aatcagtttg 180

tcgaaacaca caaatacccc acaagtgggt atcacagtac aaattgaagg ataacacatg 240

tggtgatgat gcaacgaaaa acaacaacta tttatcaaag gtgtgctaat atctttcaat 300

tattccaagg ttgcagtgat tgttttctaa tggacatgat accaaaaaac ttaacatggc 360

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agacaattga tcatttgtat cctaaaattg cataggacct atga 464

<210> 1326
<211> 550
<212> DNA
<213> Glycine max

<400> 1326

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ttagttggat ctatacaatt cacctagcag ttgtaaaaag tccaggggggc tgaaaaagga 120

tgattatata atgcacaata ttgaaaatat tgttgtatga ttgtgctaat cctaattgta 180

ttgagaatat tgctacatga ttgtgctgat cttaattgat tctatttgta ttaattctga 240

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tgggatcact tatttttagg atagatagtt gtatcagata tgtcaggaaa agctataaga 360

gaaatcttag ttaggtggtt ggatgacctt gtatatatat ctatcaattg tttttaatag 420

aggcagaaca acaaggagga ggtgaagcaa aagctaagga gaatgaaact cgagatgtca 480

ttgaagatca aggaggaggt gaaaaagcag ttcgacgtcg atttcttggc ggtggcttga 540

taccccgaat 550

<210> 1327
<211> 527
<212> DNA
<213> Glycine max

<400> 1327

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aaattctaac agtaagttaa caaggcttgc cagacttcca acaaaatttg tccatcctct 120

acaactttca agaacacatt ttctctcaaa atatcaagct gacacatgcc acattgttat 180

tcaaagtaga tttttcattc acaggaattt caggcacatt attgcataaa aagttataga 240

caccttgatc agttaataaa gacattagaa gctgctttac tgccaaaatt aaacgaaaga 300

ttttcttttt tattggtttg aattacagat agtttaacag cttgtggata atatcaacca 360

caggtttctt tttcctgtca tcatggcata gcaaaggcca agtatgagaa ctgaaatatg 420

gaaaacatgt tggtaatcaa taccttaata cattgatgta ttccgaagca attccttccc 480

acattatttg ttggaaaaag aggatcatct atgtgaattg gatcaat 527

<210> 1328
<211> 523
<212> DNA
<213> Glycine max

<400> 1328

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ggtttctaat gactcctctg cggcctccac ataaggcata gaagatgggc agctcaccaa 120

gatgtcttcc tcgcctgaca cgatgaccaa atgcccctcc actacgaatt tcaacttttg 180

gtggagtgta gagggcacaa ctcccattga gtggatccac ggacgcccca acagacagct 240

gtagggggg ttaatatcca ttatttggaa ggtgacttga caggtgtgag ggcctatttg 300

tactgggaga tcgatctctc ccctaacctc tcggcgagtg ccgtcgaagg cacgaaccac 360

cattgaactc ggctttaagt gggaagcatt gaatggtaat ttctccaaag tgctctttgg 420

catcacgttt aaactggaac cattatcgat gagcactttg gctacgatat ggtccataca 480

cttgactgat accgtgaaag cctttgtatt gccctctccc cct 523

<210> 1329
<211> 430
<212> DNA
<213> Glycine max

<400> 1329

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agtcccgaag aagactggcc tcacagtgat cagaaatgag aaggaggagt tgattcctac 120

tcgggtgcag aacagttgga gagtctgcat tgactatagg aggctgaacc atgttaccaa 180

aaaggaccat tttcccctgc cattcattga ccagatgctt gaacgcctgg caggtaaatc 240

ccactactgt ttccttgatg atttttctgg ttatatgcaa attactattg ctcctgagga 300

tcaggaaaag accacattca cctgcccctt cggcactttt gcttataaga agatgccttt 360

tggcctgtgc aatgcccctg gtaccttcta gcggtgcatg attaatattt tcagtgattt 420

tttagaaaat 430

<210> 1330
<211> 237
<212> DNA
<213> Glycine max

<400> 1330

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tcaatttcga acttctcgat atgtgatttg cctgaatcgg acatccgtgt gaaaagttat 120

accagttgaa tttctcaaga gcttccgttg ttcaattttg agcgtctcga tatgtgattt 180

gcctgaatcc gacatccgtg tgaaaaggta tgccccctga atttttcacg agctttc 237

<210> 1331
<211> 358
<212> DNA
<213> Glycine max

<400> 1331

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gtcataacta ttcacacgga tgtccgattc gggcgcataa tatgtcgaga ggctcgaaat 120

tgaacaacgg aagctgttga gaaattcaac tggtataact ttttacaccg atgtcccatt 180

cgggcgcata atatgtcgag aagctcgata ttgaacaacg aaagttcttt agaaattcaa 240

atggtcataa cttttcacac ggatgtccga ttcaggctta taatatatcg atacgctcca 300

aattaagcat ccgaaactct cgcgaaaatc aaatggtcat aacttttcac acggatgt 358

<210> 1332
<211> 286
<212> DNA
<213> Glycine max

<400> 1332

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tcaatttcca gcgtctcgat atgtgatttg cctgattcgg acctccttgt gaagagatct 120

gagcatttac atttgacgag agctttcgtt gttgaacttt cagcgtctcg atatgagatt 180

ggcttgaatc ggacatccgt ttgaaaactt acgaccattt gaatttctcc agaactatct 240

ggtgagaatt tccagcgtct ggacatatta tgtgcccgaa tcggat 286

<210> 1333
<211> 349
<212> DNA
<213> Glycine max

<400> 1333

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tgtcatcatt tttcacacgg atgtccgatt cgggcgcata atatgtcgag aggctctaaa 120

ttgaacaacg gaagctcttg agaaattcaa ctggtataac ttttcacacc gatgtccgaa 180

ttaggcaaat cacatatcga gacgctcaaa attgaacaac ggaagctcct aaaaaattga 240

aatggtcata acttttcact ctaaagtcca attcatgcgt atcacctata gggacactcg 300

gaattgaaca acggaagctc tcccgaaatt caaatggtca taacttttc 349

<210> 1334
<211> 345
<212> DNA
<213> Glycine max

<400> 1334

agcatctcaa tatgtgatgt gcctgaatcg gacctctgtg agaaaagata tgaccattag 60

aatatgtgga catcttctga agttcaagtg atagagtgtc tcaatatgag atgtgcctaa 120

atccgacctc cgagtgaaaa tctatgacaa tttgaatttc tcagaatctt acgctggtca 180

ataaagagcg tccccatatg tgatgtgcct gaatccgact accctgtgaa aacttatgac 240

cattttgaat ttctccaaaa gaatttgtcc ggccatatgg agcatccatg atatattagt 300

gcgactgatt cccacattcg atggaaaagt tatgaacttt taaat 345

<210> 1335
<211> 443
<212> DNA
<213> Glycine max

<400> 1335

agcttctggt gggacatctt gacttgcttt ccaatctgac attcaccaca gattctgcct 60

tcttctattt tcagattggg aatgcctcta atagcacctt tgtcaatgat tttcttcatg 120

cctcttaagt gcagatatcc aaatctttga tgccatattc tgacttcatc ttctttggag 180

gatagacatg tggaggagta actggtttct tgaggtgtcc ataggtagca gttgtccttt 240

gatctgctgc ccttcattag aacttcacac ttctcatttg tcactaagca ttctgacttt 300

gtgaagttta cattgaatcc ttcatcacac agctgactga tgctgatcaa agttgcagtc 360

agtcccttca ccaacaggac tttgtccaga ctaagaaagt catcatggac tatacttccc 420

attccagaga tcttttcttt aaa 443

<210> 1336
<211> 521

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1336

tcactgaata gcttgtgtta ttgaagaata ttcttcttga atagaacacg ttacccaaaa 60

atcagtacga ggcaaataag atattatgtc ttgcacatat ggagtaccaa aaaatacatg 120

catgccctaa taattacatt ttgtatagaa atcagtttgt cgaaacacac aaatacccca 180

caagtgggta tcacagtaca aattgaagga taacacatgt agtgatgatg caacgaaaaa 240

caacaactat ttagcaaagg tgtgctaata tctttcaatt attccaaggt tgcagtgatt 300

gttttctaat ggacatgata caaaaaaact taacatggca tgcagctggt agaaaaagtg 360

atggattgct ccaacatccc gttgattatc cctaatagaa gacaattgat catttgtatc 420

ctanatttgc ataggaccta tganacctaa ggcttggtct tgcttcagct ggaatgaatc 480

atgttggtaa cttaagcacc aaccataatt catggcatgt t 521

<210> 1337
<211> 451
<212> DNA
<213> Glycine max

<400> 1337

tggaacatat aaactgaatc ctaggccccc ttaaggactt aatcaaaata tttgctggct 60

gatcattaga attaatgaac tcagtgataa tttctttgga cagtagcttc cccgaataaa 120

gtgacagtca atctctatgt gcttgagcct ctcatggaag actgggtttg aagcaatgtg 180

aagagcagcc tgattatcgt agtataactt catttgcacc actctgcaga atttcaactc 240

ttcaagaatt tgtttaccca cataagttcg catgtaacca tacccataga tctgtattca 300

gcctttgcac tagatcgagc aacaacaatt cgcttcttgc ttttgcaaga aataatattt 360

cctcgaatgg agacagacac aatatcctga tgtggatctc ctatccatgg gatatccaac 420

ccagtgtgca tcacagtacc cacatatttg t 451

<210> 1338
<211> 483
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1338

tgcttctatg tccttttcat tgctttaatt gttgagtaat ccttgaaaaa ttgtcttgtt 60

aaaattccat tggtttagct ttcatttcat tttatttggt ctttggttat tacttgtctc 120

tttgtttcct tgtttgttgg ttgccatata gggaattgga aggaggattg gtgccatccc 180

ttgaagaatt tgagttaaga agaaaggggc caaccacctt aagagctatt ggactaagaa 240

gcactccaaa ttgagtgaat caccaaagag agaacaacca ccaaaattga ggactgttct 300

gtaattttgt aatttgcaat ttacttacct tcattgcttt caagttttgt aacaaaaagg 360

cgtttcattg gaagtgtgtt gggagcctcc aattggttac caaacttcca tttgtgtgta 420

ataattttag gcaatntttc cttangatag tgagtgtttt gttgggaacc ttgaatgtgg 480

tca 483

<210> 1339
<211> 521
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1339

agcttgccca gagaaggagt ccacggagga aatgcttacc acctcaaaag actggaaagc 60

ggtttctaat gactcctcta cggcttccac ataaggcata gaggatgggc agctcaccaa 120

gatgtcttcc tcgcctgata cgatgaccag atgcccttcc actacgaatt tcaacttttg 180

gtcgagtgtt gagggaacaa ctcctactga gtggatccac gggcgcccca acagacagct 240

gtagggggggg ttaatatcca ttatttggaa ggtaacttga caggtgtgag ggcctatctg 300

tactgggaga tcgatctctc ccctaacctc ttggcgggtg tcgtcgaagg cacgaaccac 360

cattgaactc ggctttaagt gggaagcatt gaatggtaat ttctccaaag tgctcttatg 420

catcacgttt aaactggaac cattatcgat gagcactttt gctacgatat ggtccataca 480

cttgatngat acgtgcaaag ctttattatg ccctctcccc t 521

<210> 1340
<211> 586
<212> DNA
<213> Glycine max

<400> 1340

agcttgcata agacccatat atagtttata atttgtccta ttgtcttatt gaacatgagc 60

aaaaattgca tcccattttg atacaattaa tctttcttta atcactttgg tttgttgttg 120

tagtctttca ttatgaaaaa aatctgaact acatagataa caattagaaa aagtggtgat 180

tgtggcaatg atcactttaa aatagtcaat aaaaaaaaat cccttaaact cccacatcta 240

attctcttgg accatgaaaa aacatgacag ttaaaaataa aacaatttga atatgtgatc 300

cctggactat attaatgatc taatgattaa attaatgtta tgattttctt ttatgtgtag 360

aaatcaaata taatattaaa aatttataat aactcacaca ctctactcaa tcaaactaat 420

aagatttttt aaaagattaa atattaatga tgataagaga aaattatgta tttcttttta 480

tttattctcc atgaagataa gggatttgat aacagacgaa atccccttaa tcatacataa 540

catcaacatt atatcaagga aaaaaaaact atatgaattt caataa 586

<210> 1341
<211> 478
<212> DNA
<213> Glycine max

<400> 1341

ctaagcttct atgaaggttc gttcctaatt tctctacaat tgcatcacct ctcaatgagc 60

tggtgaagaa aaatgtggca tttacctagg gtgaaaaaca agagcaagcc tttgcttttc 120

tcaaagaaaa gcttactaag gcacttgttc tagctctttc tgacttttct aaaacttttg 180

agctagaatg tgaagcctct ggagtgggag ttggagctgt attgttacaa ggtgggcacc 240

ctattgctta ttttagtgaa aaaattcata gtgccaccct caactacccc acctatgata 300

aagagcttta tgccttaata agagccctcc aaacttggga acattacctt tgttccaagg 360

aatacgtcat ccatagtgat catcaatcac ttaagtacat tagagggcca agcaagttaa 420

acaaaaggca tgcaaaatgg gtagagtacc tagagcaatt tccatatgtt atcaaata 478

<210> 1342
<211> 514
<212> DNA
<213> Glycine max

<400> 1342

ctcagcttgc attcctctct tcccttaaac ttcttttatt tattgctatt tatcttttgc 60

tttaaagaag tttattttga attgtctttt gagtaattca tgttaagggt gcattgttaa 120

tccaaaaaga aagagtgata gttcaattgg ggaatagtct ttgcatctta attcaacccc 180

ccttttttctt aaggtaactg aggccatttg tcccacatcc tattcttgat aactcacttc 240

tctctaaaaa gacaaaatga ggtcacatga acgtctatat ttttacttga aaacacagtc 300

aatcaaatgc ctttttattt ttttatttttg aaacttattt tgaaacttat ttgctttgaa 360

ctttactcgc tgttttacga caccccccacc aacgtgcaag acgagtaatc tctgattgaa 420

cagtcttaga agtcaacact caagaacgca agtcgcttga gccaacagaa ccatggcttt 480

gccccacatt ccagtgaaag ttgaataacc aaca 514

<210> 1343
<211> 372
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1343

gctttgaaan ataataactt gaattttaaa atacccattt tctctccccc tttggcaaca 60

tcaaaaaggc caaagtgcgt gaaacatgaa taatttaatc atacacaaag cataatttgt 120

aaaacaaaca tataagattc taaaaacata cataaagcat aattttaata aaaccaaatt 180

gagatgcaaa ccacttagtc atatatcaca aaataaccaa gtctaagtat aaaacataag 240

catctaagtg ccaaataaag acaccaagat cagtcataat taactaagta ccaaatacct 300

aaaacataac taatgttcac agaataaata aataacataa tggtgtaaat cattcacaaa 360

acataataaa ag 372

<210> 1344
<211> 505
<212> DNA
<213> Glycine max

<400> 1344

ttgcaatcac taagagactc ttttaacaac gatagactaa gacttagctt tcttattgat 60

ctttggtttc ttggtcttga tttggactta aaataaaact tgtgtttctt ttgtcttggc 120

atcatcaaga ccatcataca catacattca caaacatcgc tatattgtcg taacaaccca 180

ttgtcttttg aaccatggat ccctcccact caagttttgg tgttatgcat tgtaaatcgc 240

aacgtgtctc atcaatcgga tgccctctct cacactaaac gaaaagtctc cattagaagt 300

cttgtttcat cgtccatcaa attatagtaa actaaaagct tttggttatc tttgttttcc 360

ttggttcact ccatatacaa ctaacaaact tcagaccaag tccgtaccat gtgtttctta 420

ggttacaatc ttactcaaag tgcatatctt ttgttatgat ctttcagagt ctaagttgtc 480

acctcccgca tgttgaatca ttgaa 505

<210> 1345
<211> 481
<212> DNA
<213> Glycine max

<400> 1345

tgcttctaca tatgggttct atcgcacaga atggcatgat cactggctga catattctca 60

attagctctg ttgctttttt ggggtcttca gctttatttt tccccctgca gaagcatcta 120

gcaatttctt ggtttgtggt atcagcccat ctataaacat attcaattga attgtcttgg 180

aaaacctatg ggtgggagtt cttctcaata aacctctgaa cctctccaat gcttcactca 240

tagattcatc acggaactga tgaaatgaag agattacagc tttcccttcc gcagtcttgg 300

actctgggaa gtatttcttt agaaactttt caacaacttt ttcccaagtt ttcagactgt 360

taccttaaa taagtgaagc cacctcattt gctctcctgc caatgagaat gagaatatgc 420

tgagtctaat agccttatct ggcacaccgg caatcttaac actgttgcat attttaatga 480

a 481

<210> 1346
<211> 637
<212> DNA
<213> Glycine max

<400> 1346

gcttgtctta agttctgaga gacaaaagga gtcatgtact tatgaagatc tcttaccaag 60

tttatgtagt attttgctac cttttgtcct gtctcatacc tatctgcttt gtattggatc 120

atccacaggt tcccggctct atgagggaaa gcagtttctg ttgatggatt ctcagccatt 180

cttccaccat aagggttgaa atacattact gctttctcta attcaatcat cttcttccaa 240

atccctccca accctccttg ggtattggtc tcttcacata gtcagatttc cttttcaagt 300

acttgagaga ccaaggttgt ctctctagca aaatctcaac tggggttgca atgtccatgt 360

tgtaccaaaa cagcacggat tgaagccagc ttgtttcgat gcattcagat tgcttcaacc 420

ccaattaagg agacctctcc tccatgacag aaaacagagt tttggagtcg ctgaggaaga 480

gagctatgaa ggtagcccct cactgtcttt atgatcttct gttggagata attctgttcg 540

agacattgtt gatcaactaa tatggacact tcttcaaatt taagtcttga ttcatcacgt 600

tgctggagac tattaacccc ttttgttggt ctcaact 637

<210> 1347
<211> 585
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1347

tgaagtttgc atcttgcttg attctattat tgaagaagct aattaagaac tctattcaaa 60

atggcttttg ttactgtcaa ctatttgagg ttcaaatgaa tcaggttcca cagatctttt 120

gtcatttgtt tcaatagttc atttcatttg tatataactt ccgtgtgatt taatcatgat 180

gtgatacatg tgcatttgaa taaattctta taagcttgtt caactcattt gaagtttttg 240

tttgtttgaa gtccgtgaat cataaaattc atgtttataa tactattgtc tggctcaatg 300

cagtgcatac agaggactat acattctcaa ctggatctat cgctacttta ctgagcccca 360

ctttgtccat tggataagta tgattctctc ttattgtgtt ttatgggtac tatttttttt 420

gcttctacgc ttattataat tattaagtaa ctacactctg cattattcac tactatgtct 480

tgtggaacct tttcatcgca tatttttaag ttcatacttn taaaattctt catacctgag 540

atgcatttgt gacgttgttc aaaatgtttt tcccttatca tacaa 585

<210> 1348
<211> 464
<212> DNA
<213> Glycine max

<400> 1348

tctagccaaa tggacttacc ttgaattaat tcctttgata gccccctttga gcctattttc 60

ccctttcttt gttttgaagc tcattacaag ccttaagtga aaaaaccatg atatcacctt 120

acccttaagg aattatggag ctttggaatt gttttgggaa taagctggga ataagtgtgt 180

gtgggggggg gggggccat ggatccctcc cactcaagtt ttggtgttat gcattgtaaa 240

tcgcaacgtg tctcatcaat cggatgccct ctctcacact aaacgaaaag tcttcattag 300

aagtcttgtt tcatcgtcca tcaaattata ggtaactaaa agcctttggg tatctttgtt 360

ttccttgggt cactccatat acaactaaca aacttcagac caagtccgta ccatgtgttt 420

ttaagttaca tcttactcaa aggcatatct tttgttatga tctt 464

<210> 1349
<211> 457
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1349

agcttcacaa ggatgtgtta tggtacactt tttaagaaag agtatattag caagttatac 60

tttgagtatg tagcttttaa gataatcgga attataactt tctaacttat taaaaaatga 120

ggatacttta ataaatcttt gattagaatt tataataagc aaatattttt taatatacat 180

atatatatat atatatatat atatgaagaa ttttaattat gatataagat tctctaacta 240

ttgataattt gttttaaaga atattaagat gtaatctaca tataaagata aatatagaag 300

gtcgaaagag gtaaactatt aagtatatta aatatgtaaa taaagataaa aagagaatag 360

tttgaaatag ttgatagaaa aaatagttga ctagttttag aaataggctg tgaaatgtat 420

gtgtgaaatg cntctccnac gatgagaaga gagagag 457

<210> 1350
<211> 407
<212> DNA
<213> Glycine max

<400> 1350

ttgagccaat tcaaacgaca ataacttttt actcggatgt ctgattgagt cccgtaatat 60

aacgacacgc tcgaaattga atgttgaagc tctgagctaa ttcaaacgac aataacttttt 120

tactcggatg tctgattgag tcccgtcata tatcgagacg ctcgaaattg aatgttgaag 180

ctctgagcca attcaaacga caataacttt ttactcggat gtctgattga gtcccgtcat 240

atatcgagac gctcgaaatt gaatgttgaa gctctgagcc aattcaaacg acaataactt 300

tttactcgga tgtctgattg agtcccgtaa tatatcgaga cgctcgaaat tgaatgttga 360

agctctgagc caattcaaac gacaataact ttttactcgg atgtctg 407

<210> 1351
<211> 375
<212> DNA
<213> Glycine max

<400> 1351

catgcaagct tggttaagaa gattcctaaa aaagttagag cttaactaca cacacctctc 60

taatagctaa gctcaccttc ttgagatgag aagctagagc ttagctacac acccctataa 120

taactaagct caccctatg ccagaaaaaa catgaaaata caaaaaaagt ccttactaca 180

aagactactc aaaaggcccc gaaatacaag gctaaaacct tatactacta taatggccaa 240

aatacaaggc ctaaacgaag aaaaaaccta ttctaatatt tacaaagata agcgggctca 300

tacttagccc atgggctcga aatctaccct aaggctcatg ataaccctaa ggcctttcct 360

tggattatct ggccc 375

<210> 1352
<211> 383
<212> DNA
<213> Glycine max

<400> 1352

agcttgctta agaagattcc taaagaagct agagcttagc tacacatacc tctctaatag 60

ctaagctcac ctccttgaga tgagaagcta gagcttagct acacaccccc tataatagct 120

aagctcaccc ccatgacgaa aaacatgaaa ataacaaaga aaagtcctta ttacaaagac 180

aactcaaaat tccccgaaat acaaggctaa aaccctatac tactagaatg gccaaaatac 240

atggcctaga cgaaggaaaa acctattcta atatttacaa agataagcgg gctcatactt 300

agcccatggg ctcgaaatct accctaaggc tcatgagaac cctagggcct ttccttggat 360

ctctagccaa tctaattgga gtc 383

<210> 1353
<211> 510

<212> DNA
<213> Glycine max

<400> 1353

tgtgcggtga actaacctcc tttaacatgg aattgtggtg caattgtgat ttgatacaaa 60

ttgatttaac taagaagggc aggaaaaata agggaaagat catatttgat gtggacatcc 120

ccacagatag tgttttcaga ttatagctta cacagaatgt tagcataaat atagttcaaa 180

tggctgaaat attttacttc ttagaattca ttcattatat tattactaat ttaaggatcc 240

tggtgacaaa tatgattgtt ttaaatgaca tcaaaagtgg atgaatttga ggtgtaaatc 300

tatattgtat gtttgacttg aaattggtga gaacgacaag aggggtcatg tgataaatta 360

ttggcttttc aactattgat agattagttt tgcgaattcc tgcataagta gattattata 420

ttgacgtggt gatttgttta gcagacattt gtcatggaac ctgcatttct tccttcactt 480

attattgata tatttaaaag agtttggaaa 510

<210> 1354
<211> 582
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1354

cttggatctt cttcatcaat ggagtcctat gcttcttgaa ttttaatcac aggggaatgg 60

aaaagaagaa gagttgagag gagacaccac ttcaaggaga agatgagtca agaagaagct 120

caccaccata gaaagccatg gataagagct tgaaggtaga agaagatgaa tggagggaga 180

gggagagaag gagcacgaaa ttttatgcct caaaagaggt ctgaactttg aagtttaatt 240

ctcaaatgat caaagttgaa aaaattcaca cacatggcct ctatttatag cctaagtgtc 300

acacaaaatt ggagggaaat ttgaatttct attcaaattt cacttgaatt tgaaattgaa 360

tttgtgaagc caaattttgg agccaaaatt tcactaatta tgattagtga attttagcta 420

tggttcagcc cactaatcca agatcaagtc caagattctc cactaagtgt gcttaggtgt 480

catgaggcat gntaagcatg aaagacatgc acaaagtgtg actatatgat gtggcaatgg 540

ggtgtagcaa gcaaatgctc acctcccctc tcaaatttaa tt 582

<210> 1355

<211> 426
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1355

tgcaaaccaa atgctcacca ctattagagg agaaatcttt aagttgtttc atataaacct 60

cctcctctaa atcaccatta agaaaagttg ttttcacatc catctgttgc aactcaaggt 120

caaaatgaga aactaatgcc aagataatac gaagagaatc tttcttagat actggagaaa 180

atgtctttgt gtaatctatt ccttcctttt gagtaaatcc ctcaacaaca agtcttgcct 240

tgtatctctc aatgttgcct aatgaatccc ttttggtctt aaatacccat ttacatctaa 300

tggcctttgc cccattangc atctttacaa ggttccaaac tttgttactc tgcatggaat 360

tcatctcatc cttcatggca tcataccata aatttgactc tttacaactc gtggcttgat 420

ccaaag 426

<210> 1356
<211> 470
<212> DNA
<213> Glycine max

<400> 1356

agcttgggac attcttgcaa atacctatgc tagttctgat aagttgaaaa gagtcaagat 60

gcatactttg aagcagcaat tcgagctatt acagacgaat gagaaggaag gtatagccga 120

atacctaaat cgtgtgcaaa atctgtcgaa tcaagtgatg gcttgtggtg aaaccttgaa 180

cgatcaagat cttgtagaaa aggttttaag aaccttaagt tcaagatttg attatgtggt 240

tgctgcaata gaagaatcta aggattttgc ataaatgaaa ttggatgagc ttcaatgctc 300

tcttgaagca cacaagctaa gaataaaaga gagggaaaca gataggtcat ctgaacaggc 360

tttacttgct cagagtggaa aaatattcca caatggctca cgcagtagta aagggaaggc 420

taaacccaaa taccctaaat tgaaaaaaca agagatgatg gtactgttga 470

<210> 1357
<211> 418
<212> DNA
<213> Glycine max

<400> 1357

agcttttgat actaacaagt gtatgtatac cttaatttct cttaacaaca accatattgc 60

ttattgtagg catggactta aacaatatcg taatggttgg gcggatggac caacttatat 120

tacacagtgc ccaatacaga caggaggcag ttatacttat gatttcaatg ttactgagca 180

gagaagaaca ctatggtggc atgcacacat tctttggctg aaggccactg tgtatggtgc 240

aataataatt atgcctaaag ctggaacacc atttcctttc ccacagccag ctagagaatt 300

tgaaattctc ctacgtcaga ttgaatttca agcgtataat cttaatattg gaaggataaa 360

agggtaagaa atatgctata agtaattttt tgtgcatgca atacgtgaat ggtggaac 418

<210> 1358
<211> 490
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1358

agcttattta tttgattaat gaatcatatt gattattaat taatgcttta tttgtttttt 60

taataagcaa aagtgatgat atatattata cacaaagggt aagcaaccta tttacaagta 120

ttgaaaactg aaaatactat ctccatacct tggttacaaa atattaacat aacaacaata 180

taaatattaa gtaaccaagg aatccaaaaa gagaaagttc acctccctgc aagtcactgt 240

aatactacta gtgacaatcc tacccaatca ccaaaaaaac ataaataatg ccttaccctc 300

ccacatgttg ttcccaaaat attaatgctt tatttgttgt tgatgtatgc aatgcaaggc 360

aattgtgaat cccaatgaat gaatgatttc atgaatgaga gcaagctgaa tgatcctctg 420

aacagctctg attatgtccc aacctatgag gacaangatg gtgactggat gcttgccgcg 480

aatgcccatg 490

<210> 1359
<211> 417
<212> DNA
<213> Glycine max

<400> 1359

taagctcggc ccacaaggtg ttccaacatt tgatccatga aatgaaaacg aaaatgatct 60

ttacttgtgg cttgatttaa cttacaataa tcaatgcaca ttctccacct catcaaaatt 120

cttgtgggga tcaactcatt cttcacattc ttgatgactg tcataccccc tttctttagt 180

accacttgta agggactaac ctatgcacta ttagagataa ggtatatcat ataggcttca 240

agaagatcta gcatcttttt cctcaccacg tccttcataa catgactaag tctcttttca 300

agatgagcta ttggtttgaa gatttcctta tgcataatct tatgcataaa aaatgatgga 360

caaatacctt ttatattaga aatagtcaag ccaatggatt ccttattctc tttcaag 417

<210> 1360
<211> 363
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1360

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agacctccca tctttaatgg agtgggttac cactactgga aaacccgcat gcaaatcttt 120

atagaggcaa tagatttaaa tatctgggaa gccatagaac aaggacctta tgttccctct 180

atagtggccg gaagtgcaac aatagaaaaa cctagagcag attggactga tgaagaaaga 240

agattatttc aatataattt aaaggccaaa aatattatta catctgccct aggaatagat 300

gaatacttta aggtttcaaa tngtaaagtg ctaggatatg tgggatcact acagtaacac 360

atg 363

<210> 1361
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1361

agcttaagct ccttcaactg cacaaggctc ttaatatttg aagagtatcc ttgtggaacc 60

ttcacccgac gaagacactg acaaaaactt atattatcct tctttgacaa agtatggcag 120

gatagggaca agtaaatttt cttcccatca gaccttggat gcaactgtga tcgtataccc 180

atatcagcta gatcttgacg ggtattcaag ccatccttcg tcttgccttg aatgttaagg 240

agcgtcccaa tcacactgtc acaaacattt ttctccacat gcataacatc aatacaatgt 300

ctaacgtcaa gatcacacca gtacggaaga tcaaagaana tggacctctt cttccatatg 360

caactctgac tnttatcctt cttgtgggtc ttcccaaata cagtattc 408

<210> 1362
<211> 402
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1362

tccatcagtg cataacgtga cttcaaaagt atttgctntt ccctttntat attnttatan 60

ttttttgggt tcgacaaggg ttgatgcaat cctaccccgc aagggcattg gatagaagac 120

tccaagacaa ttgagccaga gatgcaagag aaggccctag agttctcatg agccttangg 180

tagatttcgg gctcatgggc taagtatgag cccacttatc ttagtacata ttagattaag 240

gtttcattat ttttgggcct tgtatttagg gctcaataat gtaggtaagg taccctagaa 300

atgtatgatt tttcagccct tgtattttag ggcacctaga ctagttnttg tattangggt 360

agttttgtaa tttcacatgc attaagtgaa tatttgatgt gt 402

<210> 1363
<211> 364
<212> DNA
<213> Glycine max

<400> 1363

agctagtgcg ctcttggcac tgtcatttag ttgagaaatt ctgaaggaga cctattccgg 60

agatggattt attgatgatg acatacctgt tagtaacagc atacttatag ctagctgtat 120

agaacaaaag ggatgataaa ggcttaaact atacataaga atgtataatt atattttata 180

tataacttac tgaaataatt tattttatat gcagatagaa cgtaattacg gtacaactta 240

taatattatt aaagagataa aatatatagt ccaaaaggtt ctgatatact tagacatctt 300

aataatatca ataccttaat gagatccttc atttctctct attatctgtt cttaacacat 360

cata 364

<210> 1364
<211> 422
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 1364

cacttctgta gggtttcagg gctttccatc agctctgttt aatctgccat atactcagcc 60

ggtattaggc ctcatgagct ttctcatatt cagcagctta ttggatttag cttgngtgac 120

ttccctttca gatacttggg tgttcccctt ttatcatcta gattaaatgt atgtcattat 180

gctcccttac tttccaagat tactggcctg attcagggat ggagcaaaaa gtatttatct 240

tatgcaggta agttagagtt gatcagagcg cgtattcaac gaattgtgac attttggatg 300

gggatttttc ctttgccgca atctgttctg gaccggatca acgctntgtg ccgtaattnt 360

ctgtggngca aagcggatat tggaaaaaca agcccttggt tgcttggtca gtagtttgtt 420

ct 422

<210> 1365
<211> 378
<212> DNA
<213> Glycine max

<400> 1365

accctgatga ggatgtccca tatgttctta taactggact gattcatttg cttccaaagt 60

ttcatggcct tgtaggtgaa gacccgcaca aacatttgaa agaatttcac attgtctgct 120

ccaccatgaa acccccagat gtccaagagg atcacatatt tctgaaggct tttcctcact 180

cattataggg agtggcaaac gactggctgt attaccttgc tccaaggtcc atcacgagct 240

gggatgacct taagagagta ttcttagaaa aatttttccc tgcttccagg accacagcca 300

tcaggaaaga tatctcaggt attagacaac tcagtggaga gagcctgtat gagtactggg 360

agagatttaa gacactat 378

<210> 1366
<211> 427
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1366

atgtgttaac tctcaagctn tntatgatta tatctgtgtg aaatataaaa aattcataaa 60

attactaata tttaaggtag tatatgctta tcatttaagg taaaatatgt tnttaatttt 120

tatacttttg atcaaattta attttagtcc tttgtaatat gttaaaaatt taaagggatg 180

tcgcgaaaag gatatataaa cgaaataata taaattttaa catttatagt catattaaaa 240

ttcacattta atgtcatcta ataaatatta ttaattttca atactattta gcaagccttc 300

ttctcaccac atttaattta atgtcatcta ataaatatta ttaattttca atactattta 360

gcaagccttc ttctcaccac atttaatgtc gatcaattaa cnaattaaaa taataaacaa 420

ttaataa 427

<210> 1367
<211> 330
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1367

cttctcgatc tattatgcgc ctgaatcgga cctncgagnt attagttatg actattaaga 60

tatctcaaga gcttccggtg gttaattgcg tgcgtctcga tatattatgt gcctgaatcg 120

gacctctgag ctaaaagnta tgaccatttg aatttctcga gagcttcctg tgttcaattt 180

catgcgtctc gatatattat ntgcctgaat cggacctccg agttaagagt tatgaccatt 240

tgaatttctt gagagcttcc gatgttcaat ttcgagcgtc tcgatatatt atgtgcctga 300

atcggacctg cgagtgacta tttatgacca 330

<210> 1368
<211> 403
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1368

agctttcaag aaattcanat ggtcctaact tttaactcgg aggtccgatt gaggcggata 60

atatatcgac acgctccaaa ttgaacaatg gaagctcttg agcaattcaa atggtcataa 120

atagtcactc ggaggtccga ttcaggcgca taatttatcg agacgctcga aattgaacaa 180

cggatgctct caagaaattc aaatggtcat aacttttaag tcggaggtcc gattcaggca 240

cataatatat cgagacgcac ganattgaac aacggaagct ctcgataaat tcaaatggtc 300

ataactttta actcggaagt ccgattcagg cgcataatat atcgagacgc tcaaattgac 360

atcggaagct ctcagaaatt aaatggcata acttgtactc gga 403

<210> 1369
<211> 360
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1369

tgccacaatn tccatgaaat gtaaggccat cgtatgagtt gtataatggg aagggagcat 60

tcccaagtga attcctttag aanagcaatc aacgatgact aanatagtag tatgtctgca 120

gtacactagt aaaccaacga tgaagtccaa agaaaggtcc tccacagccg ggacggcact 180

ggcaggggggc agagcaacct ggcgggcttt cgggcttcat atttagtgtg ctggcaattg 240

atacaagctg caacaaacgt ttgcacatcc tttcttaacc ctatccaagt gaaatttttg 300

cacacccgtg caagggtctt cataataccc atgtggccac ttgtgggcat tgaatgaaac 360

<210> 1370
<211> 274
<212> DNA
<213> Glycine max

<400> 1370

caaagaaatg aaaagccctc aattgtggtg gctattatct ctatagtgat tcactcaatt 60

tggagtgctt cttagtccaa tagcgtctta atgtggttgg cctcttgctt cttgactcga 120

cttcttcaag ggatggcacc aatccttctt tctaattgct tatatggcaa ctcacaaacc 180

aggaagcata gagacaagta ataacccaag acccaaaaga tgaaatgaaa gctaaaccaa 240

tagatcttta acaagagata ttatcaagga ttat 274

<210> 1371
<211> 382
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1371

actaagctgg tacaaacctt cactacatca accgtaataa tcatcctctg actgctatcc 60

tgaatcaaac atgaattagg aaagaaggtt aacttgcaat tcaatacaga aaccaatttt 120

gatatagaga ttaaattgaa attaaaagat ggcaagtata gcacatcttc taagtgtaaa 180

aactcagtaa atttgactgt tccaaagtgt gtgactatga cttgntgacc agtaggcagg 240

cgaactacta tgggatttat ttctctatat gtagaataac aagtcaatga ggatgcaaca 300

tgaattgtag caccaaagtc caaaatccat gctgcagctt canacttgtg aatattacaa 360

acaaaggata gtatattacc ta 382

<210> 1372
<211> 419
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1372

agcttgtgca tgagagcgag aatgctagtg gttttgatag ttcttggagg accctaaaat 60

gggagggtta gaaattaaga ttaaaaattg agaaagtgga aatagttaat ttaaggggtg 120

aaatgagaga actacagata aaatgagatt gtgcatgttg ttgttgcgag cgatgacttg 180

gagcctggag acggcgtcct cattgacgac agcgtcggcg accttgatgg gatgatactt 240

ttctacccat ggaacgttgt aggcattgct tgatgatgac aatgacatgc ttctgccaac 300

ggtgaacaaa gggtttcaag tttcagacca gagcggagaa taaacgttct aaagcccaaa 360

ccctattttg cctaaaccac ttcaaaggtt catcacttct tatttcanac ggcatgttc 419

<210> 1373
<211> 451
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1373

cattacatag tttatttgat cttctacaca taatatacat tgatgtctag cttactatcg 60

ccatatagtt tggcgaatta tatcaaattc aagttagaca acattatttt caatatttga 120

ctcattgtat taagttgaat atgacaattc tattattatt tgtatctaaa gataattatt 180

ataaaattca atacatttac attacattcc ctacaagaat tataatacat aatattctat 240

aatattttat aatttgatga ccataataat gataaaatgc attacgctag ttaactccac 300

tgaaaccttn tcaatgaaac ttatgtctct aacatataat atcatattaa atatgaataa 360

ttttagtctc atgtacgtat gatataatat ggacttaact cataaaatnt tgacttttac 420

attanctcac gcttataaaa atttcttgcc c 451

<210> 1374
<211> 416
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1374

ngaaggcatg taacccacca tcttctcata ttagaacact gttaacgtgt ccactatcan 60

ttttatcatc tcgctttcca tcattgnggg cactacttaa gctgccagat ccctccacct 120

ctgggcgtat tctttgaatg attcattatc tctcttgcac atgttctgta gctgcattct 180

atctgcggcc atattggaat tgtaccgata ctacctaatg aaggcaacca ttaggtcctt 240

ccaggaatgg atccaagaag gttctagatt agtataccag gtgacggctg ccccagtaag 300

aatttcttgg aataaatgca tcaacacatt ttaatctttc gtgtatgccc ccattntcct 360

acagtacatc ttcaggtgat tcttggggca agtagtcccc ttgtacttat cgaaat 416

<210> 1375
<211> 476
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1375

actcagctta acattcanat tcgagcgtgt cgttatatta taggactcag tcagacatcc 60

gagtaaaaag ttattgacgt ttgaatctgc tcagagcttc aacactcaat ttcgagcgtg 120

tcgctatatt acgggactat atcagacatc cgagtaaaaa gttattgtcg tttggaattg 180

ctcagagctt caacattcaa tttcgagcgt ctccatatat tacgggactc aatcagacat 240

ccgagtaaaa agttattgtc gtttgaattt gctcacagct tcaacattca aattcgagcg 300

tctcgttata ttatatgact cagtcagaca tccgagacaa aagtattgac gttgaatttg 360

ctagagctta acattcatnt cgagcgtgcg ctatatacgg gacatatata catccgagta 420

taagttattg tctttgaatt gctacagctc aacattaatt cagcgtgcga tatata 476

<210> 1376
<211> 431

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1376

taagaattgg aggtcctaat gattccttga ggaggtccaa acattaagcc tttgaattgc 60

cccaagtatt acgtgtaata tcgcttgacg atgtcaaaat tcacagacga aggtagctct 120

tcatcatcca tgttcataag aaacaacgct cctcctgaga aagtcttctt caccataaac 180

gatccttcat agtttggggc ccatttacct cggtgatcct tttggacatg cgacactntc 240

ttcagaacaa gatccccctc gctgaactta cacgggcgca ctcttcaatc aaaaacgttn 300

ttcactctgc actaatatag tctcccatgg cttatagtag ccaatctcat accctcgata 360

agaattaatt ggtcaaagca tgcctgggcc cactctgctt cttccaatcc taactctgct 420

aagaatctta a 431

<210> 1377
<211> 265
<212> DNA
<213> Glycine max

<400> 1377

agcttgagta taggatcttg cccgctgaat acctaggcgc gatgatgaac ataggtggag 60

cctgtgagaa cgggctataa ccttaccgat atcacccaca tacaagccgc agacactcct 120

cggctagcac tgtgtgccta aagagagatc tatctcacat tacttgcgat acactaactg 180

ctcgcgggcc agaaccctaa acctgtccag ttctccgcct atatgtataa aacaacgcga 240

gacgcttgcc acccacctcg cccag 265

<210> 1378
<211> 418
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1378

agcttgttta ccccatgttg agtttgctta catatagagt tgttcatagc gccactaatt 60

gttctccttt tgaagttgtt taaggtttta acccactaac tcctcttggt cttttgcata 120

tgcataatgt ttctattttt aagcataaag aaggtcaagc aaaggcgaac tatgtgaaga 180

agcttcatga gagagtcaaa aatcaaattg agaggagaaa taaaagctta aacaagccaa 240

caaagggaga aagaaggttg tcttcgaacc cgaagattgg gtttgggtgc acatgagaaa 300

aggaaggttt ccggaacaaa ggagatcaaa gcttcaacca aggggagatg gaccatttca 360

agtgcttgaa agaatcaatg acaatgctta canaagtgag ttgcccggtg agtataat 418

<210> 1379
<211> 424
<212> DNA
<213> Glycine max

<400> 1379

agcttcacaa aagtttatat gacttgaaac atgcaccgat gcagtggtac aagaagttta 60

atgagtttat gagcaactca ggattcaaaa gatgtgacat ggaccattga tgctatgtta 120

agaaatatac taatagttat gttattcttg tcatgtatat tgatgacatg ttgattgcag 180

gatctagtat gacagacatt aacaagttga agcagcagtt ggcagaaaac tttgaaatga 240

atgatcttgg tccagctaaa caaatccttg gtatgagaat tcttagaaac agatcagaag 300

gaatcttgaa gctgtcttat gagaaatata tacacaaatt gcttgacagg gtttaccttg 360

gagattctaa gaccaggaat actcctttag gatctcattt gatagtttca aagaagcaat 420

cttt 424

<210> 1380
<211> 415
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1380

agcttgtgtt ttcaggagac gtcttagtaa ctgcaaaatg agatttcagg ccaatccaac 60

actggtaata atcttggtcc aagaacggtg attctgaggc ccattgactg atacggngta 120

tcaaactcga ttcaaacata aaagccattg tgtcagtgat cttgcaaggt cctacatcat 180

ttcctcgtgc aatggtagcc tgtaaaccaa gtaccaacac atacattact agaagattga 240

atccatcaat tcatattttt tgcatcttta gtagttagta cttaaaccaa atcaacaaat 300

ggcacataac taggttttgc acttggagta aacctcatta tagtttccga tattgtaaga 360

atttgttact aacactgcta aaaaatgatt cattcctatc attntcatat ttatt 415

<210> 1381
<211> 356
<212> DNA
<213> Glycine max

<400> 1381

agcttataat atatcgaggc gctcgaaatt gaacaacgga aggtcttgag aaattcaaat 60

ggtcataact tttaactcgg atgtccaatt catgcgcatc acatatagag acgctaaaaa 120

atgaacaacg gaagctctcc acaagttaaa atggtcataa gatgtcacaa agatgtccga 180

ttcacgcttg tattatatcg agacgctcac aattaaacat cgaaagctct cgagaaattc 240

aaatggtcat aacttttcac tacgatgtcc gattcatgcg catcacaaat acagacgctt 300

cgagttgaac aacggaagct ctggagaaat tccaatggtc ataacttttt acactg 356

<210> 1382
<211> 342
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1382

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aatagagacc atatgaattg ctcaagagct tccattgttc aatttcgagc gtctagatat 120

ataatgcgcc tcaatcggac ctccgagtta aaagttatga ccatttgaaa tgctcaagag 180

cttccattgt tcaatttcga gcgtcacgat atattatgca cctgaatcgg acctgcgagt 240

gacaacttat gaccatttga attgctcaag agcttgcatt gttcaatttt gagcgtcacg 300

atatattatg cacctgaatc ggacctgcga gtgacaactt at 342

<210> 1383
<211> 223
<212> DNA
<213> Glycine max

<400> 1383

gagctctcac tcggaggccc gattcaggcg cataatatat ctagacgctc gaaattgaac 60

aacggaagct atcgacaaat gcacatggtc aatactgcca actgcgagga cctattaagg 120

cgcattatat atctacacgc tcaatattga acaaaggaag ctctttgaat attcaaatgg 180

ttctaacgtt ggactcaaat gtccgagcta tgcgcataat ata 223

<210> 1384
<211> 409
<212> DNA
<213> Glycine max

<400> 1384

agcttgcctc ctaccaaagt tcaagcccat gtgcaaaatg taaggctttg ggaacatgca 60

agcccaatgc ccgcaaacca tgattgtcga atgctttcac ggctcgggcc tttttgggcc 120

ttttcgagca ttttaaggat cctatcttgc gaagaaaatg ctgtgattgt tctgaggttg 180

gaaacagctt caacagctat cttgctacta tcatcttggg ccttgatggc cttactagac 240

atgctcttga gaaggacacg ccttgtgtag aaacatgcta tgataatggg ttgaactgct 300

atcataacaa tggccaacct ccatgcaatg attaagccca ttgtaaaagc tattaccact 360

gctgaaatgg attgtaccac tagagccatt ctatctccca ctaaagacc 409

<210> 1385
<211> 289
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1385

tctcgaatat tatgcacctc gaatggactt ccgtgtgact agttatgacc attntaattn 60

ttcgagagca ttcggtgttc aatttcgagc gtctcgatat attatccatc tgaatcggac 120

ttccgtgtga taagttatga ccatttgaat ttctcgagag cttccgttgt tcaatttcaa 180

gcttctcgat atattatgca cctgaatcag acttccgtgt gaaaagttat gaccatttga 240

atttctcgac agattccgct gttcaatttc gagcgtctcg gtatattat 289

<210> 1386
<211> 396
<212> DNA
<213> Glycine max

<400> 1386

agcttgccgc cacggagtta tccgactatg ctcttgtgtg gtggaacaag ctacaaaagg 60

agagagcaag aaatgaagag ccaatggttg atacatggac ggagatgaaa aagatcatga 120

ggaagcggta tgtgccggct agttactcaa gggacttgaa attcaagctc caaaaactaa 180

cccaaggcaa caaggggttt gaggagtatt tcaaggaaat ggatgtgctc atgattcaag 240

caaatattga agaagatgag gaggtaacta tggctcgatt tcttaatggt ttgactaatg 300

atatccgtga tattgttgag ttgcaggagt ttgttgaaat ggatgatttg ctctacaaag 360

caatccaagt ggagcaacaa ttaaaaagga acggag 396

<210> 1387
<211> 310
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1387

tactcaattg aatcaacaac agtcccagaa ttctgacaag ctgccttctc aagctgtcca 60

aaaccccaaa aatgtcagtg ccatttcatt gaggtcggga aagcagtgtc aaggacctca 120

acccgtagca ccttcctcat ctgcaaatga acctgccaaa cttcactcta ttccagaaaa 180

aggtgatgac aaanatctac ctaacaattt ctgtgcaggt gaatcttctt ccacaggtaa 240

ttctgatttg cagaagcagc acattccccc tcttccattc cctccaagag cagtttccaa 300

cnaaaaaatg 310

<210> 1388
<211> 387
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1388

agcttnctta agaagattcc taaagaagct agagcttagc tacgcatacc tctctaatag 60

ctaagctcac ctcctttaga tgagaagcta gagcttagct acccacccnc tataatagct 120

aagctcaccc ccatgacaaa taacatgaga atacaaaaaa aaagtgctta ctacagagac 180

tactcagaat gccccgaaat acaaggctaa aaccctatac tactagaatg gccaaaatac 240

aaggctcaga cgaaggagaa acctattcta atatttacaa agataagtgg gctaatactt 300

agcccatggg ctcgaaatct accctaaggc tcatgagaac cctagggcgt tcccttggat 360

ctctagccca atctacttgg agtcttc 387

<210> 1389
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1389

agctntgagc aaattcaaac gacaataacc tttntactcg gaagtcggat tgagtcccgt 60

tatatatcca gacgctcgaa attgaatgtt gaagctctga gcaaattcaa acgacaataa 120

ccttttttact cagatgtcgg atagagcccc gtaatatatt gagacgctcg aaatggaata 180

ccgaagctct gagcaaattc aaacgacaat aacttttttac tcggatgttc gattgagtcc 240

cgtaatatat cgaaacgctc gaaattgaat gttgaagctc tgagcaaatt caaacgacaa 300

taaattttta ctcggatgtc cgatggagtc tcgcaatata tcgagacgct cgaaatggat 360

aaccaaagct ctgagcaaat tcaaacgaca ataacttttt actcggat 408

<210> 1390
<211> 356
<212> DNA
<213> Glycine max

<400> 1390

actgtgataa taaatcagcc atagagattt ctaatcttcc tgttcaatgt gattgtacaa 60

aacatgagga aattgacagg catttcatct aagtgaatat tgaagatggt attattgtct 120

ttccttttggt taaattataa caacaacttg ttgatatgtt aaccaaggta tttgcattcc 180

aaggtccgct tatatacttt attcttagat tacgttggga aatataatga caattgattg 240

cactcaactt tgaaagcggg gatgttagca atccatttaa ttgttaggga tcagctatga 300

ctttgaattt aaattataaa tgattcacat cccctgatat ttattccttt ttattt 356

<210> 1391
<211> 438
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 1391

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tctcatagct gcggctntgt tttggctctt gagcccggga atgatctttc agttgccggg 120

gaagaatgca ccctttcagt ttatgaacat gaagaccact gttgcatcca tgtttgcgca 180

cactgttatt tatggtctgt ttctgatgtt gttcttcgtt ggtcttagta tccatcttta 240

tatttaagca gcagcaaagg gtatttaaag aaaacttatg tgttgcttta tcttttaaag 300

tagatcatgt aacaaccttc tcttgttgat caatatgtat gtgctctttt cgaatttcca 360

cttgatcagg cttctactaa tactttcacg agtgatatgc tcgtcgttca ttatttaaaa 420

gtgacgtgaa ttactatg 438

<210> 1392
<211> 437
<212> DNA
<213> Glycine max

<400> 1392

tgaagacaag actatacgag gtatctttct tgggtatagc aatatctcta agggctaccg 60

tgtctacaac ttgcaaacta aaaaactcgt catcagtcga gatgttgaag ttgatgagta 120

cgcttcttag aattgggatg aagaaaaaat ggagaagaac attcttatac ctcgtcaacc 180

tactctctaa gcaagaaagc ctgatggaag taagacctca gtgtgaacca ctcttcactc 240

tccaccacaa caacaagatc aagaactatc atcaccagag tatactccaa gaggagtaag 300

atctttggtg gacatatatg aaacctgtaa cttggccata cttaaacttg gaagctttga 360

agaagcgtca aagcaggaag tatgggtcaa ggcaatggaa gaagagatac agataatcga 420

gaaaaacaac acatggg 437

<210> 1393
<211> 402
<212> DNA
<213> Glycine max

<400> 1393

tgaatcggac atccgtgtga aaagttatga gcatttgaat tacttaatat cttccattgt 60

tcaatttcga gcatctcgat atattataag cctgaatcgg acattcgtgt gaaaagttat 120

gaccatttga atttctcaag agcttccgtt gtttaatttc gagcctctcg acatattatg 180

cgcgttgaat ccgtgctatc ctgtgtgaac aagttatgac cattttgaat atttcgacag 240

cttctgatgt gtaattctga gcgtattaat atattataag cctgaatcgg acctctgtgt 300

gaaaagttat gaccatttta atttccctag aactttcggt ttttatattc tagcgtgtct 360

atatgtgatg cttcttaata taacatcctt gtgaaaagtt tt 402

<210> 1394
<211> 380
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1394

agcttatata aatcgatacg ctcgaaattt tacatcgaaa actctcgaca aattcaaatg 60

gccatatctt ttcacacgga tgtctgattc gggcgcataa tatgtcgaga ggctcgaaat 120

tgaacaatcg aagctcttga gaaattccaa tggtcataag ttctcacacg gatgtccgat 180

tcaggcttat aatatatcga tacgcgcaaa attaaacatc ggaaactctc gagaaattca 240

aatggccata acttttcaca cggatgtccg attcgggcgc ataatatgtc gagaggctcg 300

taattgaaca acggaagctc ttgagaaatt canatggtca taacttttca cacggatgtt 360

cgattaaggc gcatcacata 380

<210> 1395
<211> 448
<212> DNA
<213> Glycine max

<400> 1395

agcttggatt tcctttgctc cggaaacctc ttctttctca tttgaaccca aacccaatct 60

ccgggttgga aaacaacctt tttgcgcccc ttgtttgctt gtctagcata gctctcattt 120

ctcttttcaa tttgggcctt gactctttca tggagctttt tcccatagtc cactttggct 180

tgtccttcct tatgcttaaa aactgaaata ttaggcattg gcaacaaatc aagaagagtt 240

agtggattga aaccataaac aacctcaaaa ggagaacaac tagcggtgtc atgcacaacc 300

ctattataag aaaattcaat atgaggtaag caaacttccc aatttttaag attttttttа 360

aatggtcctt agcaaggtac ccaaagtcct attcacaacc tctgtttgtc catcccattg 420

agggtgacaa gcagtagaaa atagtaac 448

<210> 1396
<211> 369
<212> DNA
<213> Glycine max

<400> 1396

cctgctgcat gcaagctttg agcaaataca attacttaac tttttactcg gatgtctgag 60

tgagtgctgg aatatatcca aaagctcgac attgaatgtc taagctctga gcaaattcaa 120

acgacaataa ctttttactc ggatgtctga ttgagtcccg taatacatcg agacgctcga 180

aatggaatac cgaagccctg agcaaattca aacgacaata acttttttact cggatgtctg 240

attgaggccg gtaatatatc gaaaagctcg aaattgaatg tagaagctct gagcaaattc 300

acacgaccat aactatttac tcggatgtct gactgagtcc cgaatatatc ggaacgctcg 360

aattgaatg 369

<210> 1397
<211> 451
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1397

agcttcaaga aaaagatggc ctcatcatat ttcttatttc cagaagggaa ttctatcaat 60

agacctccaa tctttaatgg agagggttac cactactgga aaacccgaat gcaaattttt 120

atcgaggcaa ttgatctaaa tatctgggaa gccattgaaa tagggcctta tatacccacc 180

acagtagaaa gagtttcaat agatggtagt tcatcaagtg aaagcataac catagaaaaa 240

cctagagata gatggtctga agaggataga aaacgagtac aatacaacct aaaagccaaa 300

aacataataa catctgccct acgaatggat gaatatttca gagtttcaaa ttgcaagagt 360

gctaacgaaa tgtgggacac tcttctatta acacatgaag gaactacaga tgttaaaaga 420

tctangataa atgcactaac tcatgagtat g 451

<210> 1398
<211> 379
<212> DNA

<213> Glycine max

<400> 1398

agcttcaaga aagtcctctc caagagtgac taatgaggct gttcataagg ctgtgagtgc 60

ttatttttctg tagttttctg ttcaactgct taattcagtt gagcaagatt tgttaggaaa 120

tttattgtct tgttcactgt tattgatgac atcttttatt ctcttctcag gctgctgcat 180

tgaagggttc tgatcatcgt cgcgccacaa atgtcagtgc tagattggat gctcaacaaa 240

agaagttcaa ccttccaatc ctcccaacca ccacaattgg atccttccct cagactgttg 300

aactgaggag ggtgcgtcgc gcatacaagg ctcacaagta agatatgcct tgagttgata 360

ggttggcttg tctcttgac 379

<210> 1399
<211> 401
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1399

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tgggctgtaa taatatattt tcttgatatg ataattaatt ctacgtgcat atcagcgtgt 120

atgccaaatt ttattaattt tttttactta aaatcccatt tacactaata accgcaataa 180

cacatactaa ttatgtaatg agtacttcaa ttagcctttt tgctttctta atcaattcaa 240

actattatcc tttatcccta tttctaaaag aaattctgat agtttttaaa gaaaaactta 300

atttaaaata atcttttgtt ttataaactt gaaatacaat gcatatttta aaaaatattt 360

atgtgtatta tgaactttaa ttttaatata tgttatatat t 401

<210> 1400
<211> 378
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1400

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aacggaagct ctcgagaaat tcaaatggtc ataactttta actcggaggt ccgattcagg 120

cgcataatat atcgagacgc tcgaaattga acaacggaag ctctcgagaa attcaaatga 180

tcataacttt tcacacggag gtccgattca tgcgcataat atatcgagac cctcgaaatt 240

taacaacgga agctctcgag aaataccaag ggtcataact tttcactggg atgtccgatt 300

caggcgcata atacattgag acgctccaaa ttgaacaacg gaagctctcc aaaaattcaa 360

atggtcataa cttttcac 378

<210> 1401
<211> 395
<212> DNA
<213> Glycine max

<400> 1401

cggttcttct atttgctatt gccgctgcag cattttacac aggctcgttg attaaaagat 60

gtatggacaa gaattcgaac attaaaacct acccagatat aggtgagctt gcatttggaa 120

agatggaagc tatatatcag gtcatgtaca cggagcttat tgtttaatag ggttcttgat 180

tctggaaggc gataacttga ataacttgtg ccccattgaa gaggttcaga tagctggctt 240

cgtaattggt gggaagcaac tgtttgtgat attggttgcc cttatcatct tgcccacagt 300

ttggttggac aacttgagta tgctttctta tgtatctgca agtggagtgt ttgcttctgc 360

tggaatcatc ctatcaatat catggactgg aacat 395

<210> 1402
<211> 383
<212> DNA
<213> Glycine max

<400> 1402

agtgcactgc caaagctttt attccatcat gtgtttgtgc attgaagaac tccaattgag 60

gcacatacat gaaaacctct gatgctcctg tgagcacata ttgtggcact tgccagaaaa 120

tggaaagtga acttgaccca tcacaattgc tacaatcttt tattgcaaac ttcaacctga 180

atttctctac caaccctgct gagaccatgg ccatgattgc aaggactaga ccaattccca 240

tcctttgaag ctctgtgagt ttggatttca ttactttggc cacaaaaggg tcgagggcgt 300

gcctatagat gaagatgaag aatgccacgc ccaaaatgtc gaagctggac atgcttgctg 360

gagggatttt gaaacttgaa att 383

<210> 1403
<211> 286
<212> DNA
<213> Glycine max

<400> 1403

ggctcctcca cctgctctaa tagcccaaaa gagaccttct ccctttgctt ttctatcaag 60

gatttggcca tttgcatcaa ctattcttgc atctaagaca ttgtcagctc caaggacata 120

ctttcatatt atggattcat atgcacctac cgtgaaggct cttcacacct taacttgtgc 180

aaaggtcttg ctggaaacca tgaaccgaac ttttctcata tattttgtaa tagaccttcc 240

ccatagtggc acccgcttga atccaagccg tgctggcttc tatatt 286

<210> 1404
<211> 274
<212> DNA
<213> Glycine max

<400> 1404

agctttatag gaagcactat ggttaagagg tttggtttca aaactacttc aagtgaaaga 60

gccaaaaatc actgtagtac actatgacag tcaaagtgca atgagtttga acaaaaacca 120

agtgtatcat aacaaaacaa agcatgtgaa tgtcaagtat cacttcattc aagatatgat 180

caatagtaaa gctattgcta ttaagaagat atctacaagg gagaatgttg cacacatgct 240

cacaaaagtt ttaccctatg agaaggtcaa ctat 274

<210> 1405
<211> 332
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1405

ntaactcgga tgtccgattc aggcgcataa tatatcgaga cttttgatat tgaataacag 60

aagctctcga gaaattcgaa tggtcataac ttttcacacg gatgtccgat tcgggcgcat 120

aatatgtcga gacgctcgat agtgaacaac ggaagctttc gagatattct aagtggtcat 180

aacttttca ctcggaggac cgattcaggc gcataatata tcgagacgct cgaaattgat 240

aaacggaagc tcccgagaaa ttcaaatgcg cataacttct aactcagagg tccgattcag 300

gcgcataata tatagagacg ctcgaaattg aa 332

<210> 1406
<211> 338
<212> DNA
<213> Glycine max

<400> 1406

agcttgtagc atatgcaaac ggcaataacg ttttactcgg atgttcgatt gagtcacgta 60

atacatcgaa acgctcgaaa ttgaaaacag aagctctgtg caaattcaaa cgacaataca 120

ttttaactcg gatgtccgat tgagctccgt aatatatcaa gacactcgaa attgagaata 180

aaagctctga acaaattcaa acgacaataa ctttttactc ggatgtccga atgagtccag 240

taatatatct agacactccg aattgagaat agaagagctg agctaatcca acgactttaa 300

cttttactcg aatgccgatg gcgcccgacg tgtttaca 338

<210> 1407
<211> 417
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1407

agcttaagct ccttcaacta cacaaggctc ttaatatttg aagagtatcc tagtggaacc 60

ttcacccgac gaagacactg acaaaaactt atcttctcct tcttggacaa agtatggcag 120

gctgggggca tataggttca ttccatcact gtctagtcca agtctaagat ttcttggctc 180

attcccgaaa tccggataca aaccatcaat cttcttccac tgggagcaat cagccggatg 240

acagaccatt ccatcagaaa tccttccatt tgcatgtcat gtaaggtctt ttgcgtcatc 300

ctcgttagca aagagacgct tannaccttg gaataattga agataccaca naaccttcgc 360

tggnggaccc ttgttggagt tntcatcaga aatgctntcc tcttaatcct tgacttt 417

<210> 1408
<211> 428
<212> DNA
<213> Glycine max

<400> 1408

tgtcacttga ggacaaccag acagacactc gccctctcga catctgtcca tgacattaac 60

caatgaggaa gtttattgct ttgacaccaa gagaggggtc atagtaaagt aattaacatc 120

gacgatcaaa ctttatggat agcagaaaca cgatattctg aacaacagta ggtggtggca 180

tttgggttca tgctatctga tagaacaagg actttgaaga catgttctaa taatatattt 240

cataatcttg aaactgttgt atttaagcta cagcaattgg agcttgctag tactcatgct 300

atgttggtta ctctctagtc tactgactac taaggatgga gctacatgca atctatgcta 360

tctatatgca gtatatgaag ttaacagctc ttcataggca atactataca catgacttct 420

atgaagca 428

<210> 1409
<211> 355
<212> DNA
<213> Glycine max

<400> 1409

gaaaattaac catattgtat tttatatttg atgttttata actcttttat taccttctac 60

tatatataga gagagagtga attatactat aatgagagtt gaataatatg cactcaggat 120

aaatcttttc gaatgaaaga tttttattaa ataaacaagt ttatttaaaa acttttgtct 180

agtgactaag ataagtattc ttaagtacac gtgaattgtt gtccaatgat atataacatt 240

tatttttcaa tgaatatctt gtgtctagaa tgtattaata gaaagctttg aaatatttta 300

ataagctaaa gaacaatggt caaaatacct cattttatac tgattcagtc aatct 355

<210> 1410
<211> 440
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1410

agcttaagct ccttcaactg cacaaggctc ttaatatttg aagagtatcc ttgtagaacc 60

ttcacccgac gaagacactg acaaaaactt atcttctcct tcttggacaa agtatggcag 120

gctgggggca agtaaatttt cttcccatca gaccttggat gcaactatga tctgataccc 180

atatcagtta gatcttgacg ggtattcaag ccatccttcg tcttgccttg aatgttaagg 240

agcgtcccaa tcacactgtc acaaacattt ttctccacat gcataacatc aatacaatgt 300

ctaacgtcaa gatcacacca gtacgaaaga tcaaagaaaa tggacctctt cttccatatg 360

caactctgac ttttatcctc tctttgggtc ttcccacata cagngntcag gtgttgaacc 420

cgctgatata cctgctcacc 440

<210> 1411
<211> 410
<212> DNA
<213> Glycine max

<400> 1411

ttaagaaatg tgaactccct tgcattgatt tcaaatattg aggtcaatcc gcgccctgat 60

gagactaatg aaggaggtat aattgctgaa attaagctaa aggagttaga acagaagtcg 120

gctgaagtca gtactgagtg gagtattgtc cctggacggg aggatccact ctggtattta 180

tttctgtcaa attgaatatc aattctcttt aacaaccgag gaatttttgg cccacccaat 240

taatttgttt actttctatt tgactttgtg taggcttcgc tccagcctgg tggcactgtt 300

agttttgaac atcggaatct gcaagggctg aatagatcta ttaatggttc tattacaact 360

agcaacttct tgaatcctca agtaggtacc cttgagctag atcctggagt 410

<210> 1412
<211> 443
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1412

gaaactcagc tttcacgact ctgactgggc aggctatcgt gattctagac gttccatcat 60

aggtttttcc atctaccttg gacactctct tatctcttgg cggtcgaaga aacaatctac 120

tatgtctcgc agctcctccg aagctgaata tagagcttca gcttcaacaa catgcgagct 180

tcaatggctc acctnnntac cttcttcaag aaatcttcat atctcgtttg gcccaactca 240

gccatctctt tattgcgata accaatcaac aatccagata gcctctaatc aggtgtttca 300

tgaacgcacc aagcatattg acatagattg tcatatcgtt cgagagaaag taaacaatgg 360

tcttatcaag cttcttcctg tctcgtcttc catgcaactc gccgacattt ttaccaaagc 420

tntatctcca tccatctttc aag 443

<210> 1413
<211> 454
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1413

gctttggagt ttccaagagc caattcgtct tcttcttttg ttcagacttc ttctggcttc 60

aattcatcag tgggctttcc ttctgtgtcc agcatcttgg gatgttccca gcctttgatg 120

acagctttcc aggttctgct atccagtgat ttgaggaagg ccaccatcct tgctttccag 180

tattcatagt tggttccatc taggattggc ggtctgttca ctggtcctcc ttctttctcc 240

atgttcatca gaatttatct ccctagatct cactctgtga tttcgagtgt ttgctctgat 300

accaattgaa attctgatac tgnggacaga tgtcgtaccg gatgtcacga catctcactt 360

cagaacatgc agattagatg cgttcgtctg aacagattac acatgtaaat aacacaagag 420

gattgttacc cagttcggcg caacttccct acat 454

<210> 1414
<211> 427
<212> DNA
<213> Glycine max

<400> 1414

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atacacctgt cgcaagggtt tgtggtttgt gctcctctgc tgaccaccat acagaccttt 120

gcccttccat gcagcaacct agagcaattg agcagcctga agcttatgct gcaaaattac 180

aatagacctc ctcaacctca gcagcaaaat caaccacagc agaacaatta tgacctttcc 240

agcaacagat accaccctgg atggaggaat caccctaacc tcagatggtc cagccctcag 300

caacaatagc agcctgcttc ttccttccaa aatgctgctg gcccaagcag accatacatt 360

cctccaccaa tccaacaaca gcaacaaccc cagaaacagc caacaattga ggccccctcca 420

caacctt 427

<210> 1415
<211> 280
<212> DNA
<213> Glycine max

<400> 1415

cttagaaatt ctgtcatgct gagatacttt cagttggacc agccttagag gagaaaaaag 60

agaaaccaaa gaaagaggat aagaagccag aagccaataa aaatccaaag gaggaatatg 120

ctcaacttct gaaggtatat gaagcctatt ataatcaaat aattgaacct gttctataaa 180

cttgaaaaat caactggctg gtattgtata tgagttgagg atataatgaa tcaagagaaa 240

tgtgacattt atgaatgact tatatgtaaa aaaggccgct 280

<210> 1416
<211> 448
<212> DNA
<213> Glycine max

<400> 1416

agcttaataa atctatatat ggtttaaaat atgcctccca tatttggtac cttaagtttc 60

atgggattat ttcttcattt ggttttgatg aaaaccccat ggatcaatgc atataccaca 120

aggttagtgg gagtaaaata tgttttcttg ctttatatgt agatgatatt ttacttgcac 180

ccaatgatcg gggtttgcta catgaggtaa aacaatttct ctctaagaat tttgacataa 240

aggatatggg tgatgcatct tatgtcattg gcattaagat tcatagagat agacctcaag 300

atattttagg tctatcacag gaaacctata ttaacaaaat tttagataca tttcgtatga 360

aagattgttc accagttgtt gatcctattg tgaaaggtga tagggttaat ttgaaccaat 420

gcccaaagaa tgactttgag agggaaca 448

<210> 1417
<211> 442
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1417

agcttcaaca tcagaccact tccagggtgc tggaactact tcacatggat ttgatggggc 60

ctatgcaggt tgaaagcctt ggaggaaaga ggtatgccta tgttgttgtg gatgatttct 120

ccagatttac ctgngtcacc tttatcagag agaaatcaga aacctttgaa gtattcaaag 180

agttgagtct aagacttcaa agagaaaaag actgtgtcat caagagaatc aggagtgacc 240

atggcagaga atttgaaaac agcagattca ctgaactctg cacatctgaa ggcatcactc 300

atgagttctc tgcagccatt acaccacaac agaatgggat agttgagagg aaaaacagga 360

ccttgcaaga ggctgctcgg gtcatgcttc atgccaaaga ancttcctat aatctctggg 420

ctgaagccat gaacacagca tg 442

<210> 1418
<211> 428
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1418

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tctcgagagc ttccgttgtt caatttctag cgcttcgata tattatgcgc ctgaatcgga 120

ctttcgtgtg aaaacttatg accatttgaa tatctcaaca gcttttgtag tttagtttca 180

aagctgtctc gattatatta atgcacgctt aatctggact ctccgttgtg aaaagttatg 240

aaccatttga aattctcgag agcgttcgtt gttcaatttc gatcgtctcc atatattatg 300

cgcctgaatc ggacttccgt gtgaatagtt atgaccattt gaatttctcg ggagctctcg 360

ttgttcaact ntgaccgtgt ccatatatta tgctcctgaa tcggacttcc gtgtgacaag 420

tgatgacc 428

<210> 1419
<211> 433
<212> DNA
<213> Glycine max

<400> 1419

agcttctcca tatattattc ccctgaatcg tgacttccgt ttgaaaagtt atgaccattt 60

gaatttctcg agagcattcg ttgttcaatt tcgagggtgt cgatgtatta tgcgcctgaa 120

ccggacttcc gtgtaacaag ttatgaccat atgaatttct caagagcttt cgttgttcaa 180

tttcaagcgt ctagatatag tatgcgcctg aatcggactt ccgtgtgaca agttttgacc 240

atttgaattt ttcgcgagca gtcgtggttc aatttcaacc ttctcgatat attatgcgcc 300

taaatcggac ttccgtctga aaaagtatga ccatttgaat ttctcgagag cattcgtttg 360

ttcaattcaa gcgtctcgat gtattttgcg cccgaatcgg acttccgttg acaatttatg 420

accatctgaa ttt 433

<210> 1420
<211> 424
<212> DNA
<213> Glycine max

<400> 1420

cgaaggcaaa ctggatgcgt tggtcaactt ggtaacccag ctgttcttga atagaaaaat 60

atacacctgt cgcaagggtt tgtggtttgt gctcctctgc tgaccaccat acagaccttt 120

gcccttccat gcagcaacct agagcaattg agcagcctga agcttatgct gataattaca 180

atagacctcc tcaacctcag cagcaaaatc aaccacagca gaacaattat gacctttcca 240

gcaacagata ccaccctgga tggaggaatc accctaacct cagatggtcc agccctcagc 300

aacaatagca gcctgctttt tccttccaaa atgctgctgg cccaagcaga ccatacattc 360

ctccaccaat ccaacaacag caacaacccc agaaacagcc aacaattgag gcccctccac 420

aacc 424

<210> 1421
<211> 418
<212> DNA
<213> Glycine max

<400> 1421

acttgatgat aaccattctg ctacttgtcc tcttgcgatc tcccattaga tttagcacac 60

cggaactgat tgttttcaca ccaagcgatg tctcatagtt tcattatcaa catctacgag 120

ccaactttat cgttagcgtg agctggtacg ctgaaaaaca gaggtgtagg ctttgggttc 180

atgctttctg atagaacaag tactttgaag acatgttgta ataatattct gcataatctt 240

gaaactgcat tatttaagct tcagcatatg ctgcttgcta gtactcatgc tatgattggg 300

actccttagt ctacttacta ctaatgctgg agctatttcc catctatgct ctcgatatcc 360

aatattggaa gtcaggagct tttcacaggc tatcctatac acattacttc tatgaagc 418

<210> 1422
<211> 363
<212> DNA
<213> Glycine max

<400> 1422

agcttagagc taattcaaac gacaataact ttttactcgg atgtttgatt gagccccgta 60

atacatcgag acgctcaaaa ttgaatgttg aagctcgcag caaattcaaa cgacaataac 120

tctttactcg gatggctgat tgagtcccgt aatatatcga gacgctcgaa attgaatgtt 180

gaagctctca gccaattcaa acaacaataa ctttttactc ggatgtgtga ttaagtcccg 240

taatacattg agacgctcaa aattgagatg ttgaagctct cagcgaattc aaacgacaat 300

aactcttttc ctcagatgtc tgattgagac ccgtaatata ttcgagacga tcgaaattag 360

att 363

<210> 1423
<211> 436
<212> DNA
<213> Glycine max

<400> 1423

agcttgtgta ttagggagag tattttagca tggaaggcta attaaggtga agtggatcag 60

agagagagat gaaaattcat gtttttttca tttctctctt cgagatcgcc agagaagaaa 120

tcaactaatg gcccattaga gtggagatat gtggttaatt agaaggaggg gaacaaatca 180

aggatgaggt gacaaggcaa ttccagcaag tgttttcaga atcaaagttc acacgacctt 240

gtttaccagg tgttgagttt aaacaaatta gccaggtaga tagctctttt cttattactc 300

cttctttgga gctggagatc aaggcagcgg tttggagttg tgatggtgat acaagtcttg 360

gccctgatgg gttcaatttt caattctcac ggcgtgttgt gaattttaag gcccaagatt 420

tgttgtatgg tgcatg 436

<210> 1424
<211> 229
<212> DNA
<213> Glycine max

<400> 1424

agcttataat atatcgatac gctcgaaatt aaacatcgga gactctcgga aaattcaaat 60

agtcataact attcacacgg atgtccgatt catgcttata atatatcgat acgctcgaaa 120

ttaaacatcg gaaactctcg cgaaattcaa atggtcataa cttttcacac ggagatccga 180

ttcgccacat aatatgtcga gaagctcgat attgaacaac gaaagctct 229

<210> 1425
<211> 324
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1425

agctttgatg tttgtgttga atgcattata tgtaaataga ccaaaagtaa gaaattaggt 60

gcatatagag ctacagacat cttggaattg atacatacgg acatttgtgg gccatttcat 120

gcaccttcac gaaatggtca acaatattnt atatcattca tagacgatta ctccatatat 180

gcatacttgt ttcttataca tganatgtca cagtctctgg atgtgttcaa aaaatttaaa 240

agtgaagttg ataatcaact caacaaaaaa atcaagagtg tcagatctaa ctatggtggt 300

gaatactaag gcaaatataa cggt 324

<210> 1426
<211> 433
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1426

cgacactatg atactcagct taacattcaa tntctagcgt ctctatatat tacgggactc 60

aatcagacat ccgtgcttaa agttattgtc gtttgaactt gctcagatct tcggtattca 120

atttcgagca tctcgatata ttacatgact caatccgaca ttcgagtaaa ttgttattgt 180

ggtttgactt tgctcagaac tttaacattc aatttcgagc gtctatatat attacgggac 240

tcaatcagac atccgtgtaa aaagttattg tcgtttggaa ttgctctaag catcaacatt 300

caatttcgag cgtcccgata tatgacggga ctcaatcaga catccgagta aaaagatatt 360

gtcgtttgga tttgctcaga gcatcagcat tcaattccga gcgtctggat atattacggg 420

actcaatcag aca 433

<210> 1427
<211> 390
<212> DNA
<213> Glycine max

<400> 1427

agctttgagc aaattcaaac gacaatacct tttgactcgg atgtcggatt gagtcacgta 60

atatctcgag acactcggaa ttgaataccg aagttatgag caaattcaat cgacaataaa 120

tttttactcg gatgtcggat tgagtcacgt aatatatcga gacgctcgaa attgaatacc 180

gaagctctga gcaaattcaa acgacaataa ctttttactc ggatgtgcga ttgagtcccg 240

taatatatcg agacgctcga aattgaatac cgaagctctg agcaaattga aacgacaata 300

actttttact cggatgtccg attgagtcac gtaatatgtc gagacgctcg acattgaata 360

tcgaagctct gagcaaattc atacgacaat 390

<210> 1428
<211> 412
<212> DNA
<213> Glycine max

<400> 1428

agcttcagaa ttggttaagc atggcagata atgtgatcga tcatctttgt aatgagtttg 60

agggcacgta caggttcacc gattgggaca ccattctttt ctccactttt cttgtatgaa 120

ccctctgttc tggagatccc gggtcctggt ttacaagcgg agtacatgca atcttggaca 180

tagaaagccg tgtagtaatt gacgccaatg aaatccaatc ctctcttgag tttctctttt 240

tcgtagctgg aaaatttggg caagaggctt ccaagaacgt tctccatctc tgtagggtac 300

tttccgaata tgattgggtc caagaacctg cattataata aagtgttact ctgggggagt 360

tgagtgaaca atagaaaatg ctattattaa gggagaacta gtattaacta ta 412

<210> 1429
<211> 428
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1429

cctgcatctg gacaagcaaa tgaagaagtt gcccatgatt attgttcagg ctagacacat 60

ggaaaggagg acaattaaac ctcataaaag atatggtcat gcatatctga tctcctatgc 120

tttaatagtt ggaaagaaga ttgaagttca agaggaacct cactcttatg atgaggtcat 180

aagcaacaag gacaattcaa aatggattga agctatggaa gaagaaatgt cttttctaga 240

aaagaattgt cctanagggc agtaaattgt tggatgcaga tggctattca agaggaaaga 300

aggttttgaa ggagttcana gtgtaaggtt canagctagg ctagtagcct gtgggttact 360

cacaaggaag gagtcagatt tgtagaaatc ttctcaccta tggtanaaca tagttcaata 420

agaagtcc 428

<210> 1430
<211> 315
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1430

ggctggtcca atagatttta tataacaact tgaatagtgg ctatatctag aagttggcac 60

caaattaact ggatttttgt tcagataggc tatatgttgt tgaagtgcca ttntcattta 120

ttcttgtaaa ttgcaggtga tagcagcaac aaaccgtgca gatattcttg accctgccct 180

tatgcgttct ggtcgattag atcgtaaaat tgagtttcca cacccaagtg aagaagcaag 240

agctcgaatt ctacacgttt ggtgtcttta aacttcatct gctgacttgt ttatcataca 300

gaacatctac tgact 315

<210> 1431
<211> 405
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1431

tcgtggatgc ttactccaga tacaactaga ttaggatgca atctccaaag gaggcgaaga 60

tgacatttat cactaaagat accaacttat gctaaagggc tatgcccttt cagcctaaca 120

aatgtagacg ctacatacca atgactgatg gaccgagtct ttaaacaaca aataagacaa 180

aacatcaagg tatatgtgga caacgttggc ggtaagtctc gaagcatagt ccaacatgtg 240

gcagatctgc aagaagtctt caaggaactt tacaagtatg acatgcgcct caaccctgaa 300

naatgtactt tcggtgtagg cagaggcaag ttcctcgact tcatgatcac tcaccaaggg 360

attgaagcca accctaacaa atgccctacc atactataga tgcac 405

<210> 1432
<211> 327
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1432

agcttatcct cacttgcana tttgataact attataatct cagcgtttca acatcaaaat 60

gatatgtaaa tggtttagac tcatcttcca tgtgatcaga gagatatgaa aggcatttaa 120

naacaagctc tagatgcaag tgtgaattgt cttctacaaa gaaaggaagg atcttctggc 180

taatctcaat ccaactacac cctggattct tctttaatcc aagctctttc atctttgatc 240

tcaccacacg tacttcatcc cacttatgtg cagaagcata catatttgac aagagaatat 300

atggtgatga atcatcacga tccttat 327

<210> 1433
<211> 466
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1433

ctggaactac ttcacatgga ctngatgggg cctatgcaag ttgaaagcct tggaggaaag 60

aggtatgcct atgtttgtgt ggatgatttc tccagattta cctgggtcaa ctttatcaga 120

gagaaatcag acacctttga agtattcaag gagttgagtc taagacttca aagagaaaaa 180

gactgtgtca tcaagagaat caggagtgac catggcagag agtttgaaaa caacaagttt 240

actgaattct gcacatctga aggcatcact catgagttct ctgcaaccat tacaccacaa 300

canaatgaca tagttgaaag gaaaaacagg actttgcaag aagctgctag ggtcatgctt 360

catgccaaag aacttcccta taatctctgg gctgaagcca tgaacacagc atgctacatc 420

cacaacagag tcacacttag aagagggact ccaaccacac tgtatg 466

<210> 1434
<211> 428
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1434

atcttgtcat gaatcctcgc cataaaatta catagacctg ccaattctaa atgaaaaatg 60

taataaatcc aatgctaaca aaaaatagaa tagcaacaca cactcaaatg acacatgcaa 120

taacatttca atgaataaca aaataacata aaaacaatga tactattcgt tgaactacta 180

agccaataca tgcaacaacc tgaaccaaaa aagaaaagcc aaattagcaa atagcagaga 240

agcagaaaca aaaattatat ctctgaacaa ataatattgc aaccatcaac aaacaaatag 300

aaaggccgaa aacaaacaca aaaaagttca gctgttggaa aacagaatac caacccatcc 360

ttataccaca catgcaataa gatntncatc aatgccaaca taccacanaa agtattacac 420

tatcaatc 428

<210> 1435
<211> 434
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1435

gcttatagtt attggaggga gaataaaata tattcattat caattgtacc tttcaagtaa 60

cgaagaattc tttntgcggc ttttagatga ggagaggtaa gagcctccgt aaagcgacac 120

acaactccca ccgtatatag aatatcgggc cttgtattgg ttagatacct taaactgccc 180

acaagactct tgaaaaccgt ggagtctacc ttctgtcctt catcaaactt tgatgacttc 240

aagccacctt ccataggtgt gttcacggga ttgcaatcaa gcatattaaa tttcttcaac 300

acttcttttg tgtagctttc ttgtgagaca aagataccat tctccatttg cttcacttcc 360

attcccaagg aatatgacat gagtcccata tctgtcatat caaattcacg agacatagac 420

tccttgaagt cttc 434

<210> 1436
<211> 284
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1436

ttcatcttac agacagcaca agaaagttta tacggataac cactctggta tttccacccg 60

tcaacgtgac tcaaatgtca gtatgacaga tcttgtgaag ggtggccgac aaaagcgagg 120

ctctngctcc tacgtatcct ccaatgagga actcagacct acgtagntct tgataacttg 180

tgagacttga aaagtctcca cccgaagatg ctgacatctt cggaaagggc gcagatgacc 240

acacttggcc tcatgctcgt caatcacact tggggtcact gaat 284

<210> 1437
<211> 437
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1437

acattntcgt gaatgtgaca atctattcct tagtggattg attcacctta acagcccana 60

aaatcatata agcataatta gatgcaacaa ctcactcatc tccaatcttc atatgattgc 120

accaaatgaa agcccaaaca ctgatgagaa tgttatctca cattcatcca acatttccat 180

aaagaactcc aagatggaaa ttggtaaatc atatataagt tacaatcttt aattgcataa 240

ttattatatc ttgtccttaa atcattcaat gagattgcat agccctttaa ttcctagttt 300

tttttataag gctactcaag tggtagatcc tctcttaatt ntttttattt aaaaattatg 360

tgatgcgtaa atattcatgt ttctcattta agttgacaat cttatgtaat aaaaagaaga 420

cacaaattct cttcata 437

<210> 1438
<211> 411
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1438

ctcagcttca catcagacca cttccagggt gctggatcta cttcacatgg acttgatggg 60

gccgatgcaa gttgaaagcc ttggaggaaa gatgtatgcc tatgttgttg aggatgattt 120

ctccagatat acctgcgtca actatatcag agaaaaatca gacaccttcg aagtattcaa 180

agagctgagt ctaagacttc aaagagaata agactatgtc atcaagagaa tcaggagtga 240

ccatggcgca gagtttgaaa acagcacgtt tactgaattc tgacatctga aggcacactc 300

atgagttctc tgagccatta cccacaacag aatggatatt tgataggaaa aacatgactn 360

tgcaagagac tgctanggtc atgcttcatg ccacagaact tctctataat c 411

<210> 1439
<211> 425
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1439

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tcaacaatct cttaccaaga tgttgtccaa ctatgggaaa atctcaagtt caatcttgtc 120

tcagtgactc tatgttctag ccttatagtg ttccttgtca ccttttactt catgagccgt 180

ccaaggggtg tttacttggt ggattttgcg tgctacaagc cagagccaga ttgcacttgc 240

acaagggaga ttttcatgca caggtctgtg gaaactggtg tgttttcgga ggagaacttg 300

gcctttcaga agaagatact tgagaggtct ggtttgggac aaaagactta cttgccccca 360

gcaatcttga gtatccctcc aaacccttgt atggctgaag caaggaaaga agctgagcaa 420

gtgat 425

<210> 1440
<211> 319
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1440

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tgatgaggtt atgcccgtgg tgtatgattt tacctacttg ttgcagctgt cgggggagaa 120

tttggacctc aggaggggga gggagattca tgggatggtg ataactaatg ggtttcagtc 180

caatttgttt gccatgactg ctgttgtgaa tttgtatgcc aagtgtatgc agatcgagga 240

tgcatacaag atgttcgaga gaatgccgca gagggacttg gtttcctgga acactgtggt 300

tgcgggttat gcacagaac 319

<210> 1441
<211> 465
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 1441

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ctttttaact caaatcaaat acaaaatcat gtaatgaata ataagttatg ttgctttaca 120

ctgggtgtca ataacattaa caattggtcc atcctttata atagttcttt gcaattcaca 180

aacacgtgtt acaccagagg agcttgnact tcgattgaag gctctccttc caagaacact 240

atttcctact gcactcttgc cattgccagt acgtccgact aaaactagtg tcctaacttc 300

attagacgag gatgtttttg ccattgatag taacaaattt atgttacagc tgcaaggaaa 360

atatatcata aataanaatt tagcaataga ataaattata cacacacaca catatatata 420

tgaacatata atgtaattac aactaataaa catttaanaa acaaa 465

<210> 1442
<211> 470
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1442

agctaccatg ttcacctcat gctcaactgc ctctatctta aaacaggccc tgtggtcatt 60

tggatgctta attgtgtaaa atagattgaa ggtaaccttt tgatcatcta cactcattta 120

taggttacca tttccaatgt ccactacata cttagcctca acgtgaaagg atggcctaag 180

atcaatggaa tttcagcatc ttcctctata tccatgatca caaaatccac aaggaatgtg 240

aattgacgaa ccttgaccaa cacatcctcc accacatcgt aagatcttgt aattgaatga 300

ttagcaagct gcaatgtcat tctggttggt gcaatctcta agttcctgat ccttctacac 360

ataaataggg gcattagatn gatgctagcc ctcaaatcga ttagttcttt tccaactgat 420

acaacaccta ttgagcacgg gatactcata ctccctggat ctttgtcctt 470

<210> 1443
<211> 419
<212> DNA
<213> Glycine max

<400> 1443

actaagcgtg gaaaattaac atatcatacc attcttcgac ttttattgat tatttgcata 60

attactttcg atgagttttg acaatctatt gtagaatatt tttataggac ctagattctt 120

gctgtaatat ttcaacataa acatcaattt atatatgtac ataataatac ttgaacaata 180

attttaactc ctcaacagaa ttgtacatta aagtgtttca agattttgca ccactacacc 240

taatttaaat tatatttaat ttcattattg ttgtgataat ctctttcatt tttaaaccat 300

gatattgata cgaaattgta ttcgtccaaa acaataacaa atctctatta aagaccataa 360

acacatgtaa tataaatata tgtcttcaac ataatttatt tcatgtgcaa taatgaatc 419

<210> 1444
<211> 453
<212> DNA
<213> Glycine max

<400> 1444

tttagatgat gcagatgggt ttgtatctac ctcatgcact cctctaatga ctatggcatc 60

atttctggcg ctaaactgct gggagttgga ggccatcttc tcaattaaat ttctggcttc 120

agcaagagtc atgtctccaa gggctccacc actggcagca tctatcatac ttctctccat 180

attactgagt ccttcataaa aatattggag aagaagttgt tctgaaattt gatggtgagg 240

gcaactggca catagtttct tgaatctctc ccagtactca tacaggctct ctccactgag 300

ttgtctaata cctgagatat ccttcctgat ggctgtggtc ctggaagcag ggaaaaatta 360

ttctaagaat actctcttaa ggtcatccca gctcgtgatg gaccttggag caaggtaata 420

cagccagtcc tttgccactc cctctaatga atg 453

<210> 1445
<211> 472
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1445

atccttagag tcacctgcgg ctgcagcttg cgtgatcctt gaagttnttc tatcatcata 60

gtttctaaat ctttggtttc cttgattgtc acaacaatgt gcacaaattt gggatctaac 120

gagcatagta tcttctccat aattcttaca tcttttaact tctcaccatt tctttctagt 180

tgatttgaaa ctacgggaat tcttgaaaaa taatcagaaa tggactccga ctctttcata 240

tgtaaggatt caaactcacc tcttaagagt ttggagacac accttattta ctttgtcttc 300

tcctttgtga gaggtttgaa gcttatctca tgcctcctta gcgaatgttg catcagaaat 360

cttctcgagc gcatcatcat ctaatgcttg aaagatgaag aagagagctt tcttgtctct 420

ctttcttgaa tcctttaaag tccctttttgt gcttgggata atgaagtctc at 472

<210> 1446
<211> 420
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1446

ggtctgccaa ttaggtgtca attcatctat atgatcacta acagaaagaa accactctat 60

ctctcgtcgc cacattgctt tcttctctga acgcaggggc tctaatctcc aaagttggcc 120

aaagagggta gctgcaaatt cagcaaagaa atgaacaaca acaatcaaag tcaagaatag 180

caaatgaata aaattcacca caccaattaa taaaaaataa aaacacagta actgcttcaa 240

gtgtgcattt tgcataccac atagattggt tatggcattt gagatagcca aggctgtagc 300

gaccccattt ccacaacctg acatatcttc tccaagtaac aattttgcaa acctctcctt 360

catcatctca atctctacaa gtgagaatga anatcanatc tcatcatact gatatcatca 420

<210> 1447
<211> 461
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1447

gcgcaacaaa tattatattg ttgcgtgatc agtgtaaatc actatctttg atcccaccaa 60

ataagatcga aatttctcaa gtgcaaacac aattgccagc aattctttct cagtggtggc 120

atagataatc tgggcatcat tccaaacttt gctagcataa tagatggtat gaaacattct 180

gcccttccgc tgccctgccc tagcatagca cctactgcat aatcacttgc atcacacatc 240

aattcaaact cttgtcccca gtctggtgct ataatcacat aagcagaaac caatttggct 300

ttgagagtgt taaaggcttc taagcattct tcattgaata caaacacaac ctccttgttc 360

aacagattgc ttacgggttt agaaantttg gagaagtttt taatgaatcg ccaataatat 420

ccagcatgac ccataaagct gcgtatgccc tttacattaa c 461

<210> 1448
<211> 377
<212> DNA
<213> Glycine max

<400> 1448

aacttctcct tcctcaggtg tacccaaacc caatcacctg gttcaagcat gactatcttt 60

ctgcttttgg tggcttgcct tgcataactc gcatttttct tttcaatttg agccatcact 120

tgctcatgca gcttcttcac attctcagct ttagcttgtg cgtccttatg cttaaacata 180

gcaatgttag gcatatgcaa caaatcaaga ggagtcaaag gactaaatcc atacactatc 240

tcaaatggtg aacaattaag tgtgctatgg acagcccgat tataagcaaa ctcaacatga 300

ggcagacatg cttcccaaga tttaagaatt ttctttaaaa cagtcctaag tagtgtgcct 360

aaagtcctat tgactac 377

<210> 1449
<211> 392
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1449

actggatgcg ttggtcaact gggtaaccca gctggccttg aatcatatat ctgtacctgt 60

cgcaagggtt tgtggtttgt gctcctctgc tgaccaccat acagaccttn gcccttccat 120

gcagcaacct ggagcaattg agcagcctaa agcttatgca gcaaatatat acaatagacc 180

tcctcaacct cagcagcaaa atcaaccaca gcagagcaat tatgaccttt ccagcaacag 240

atacaaccct ggatggagga atcaccctaa cctcagatgg tccagccctc agcaacaaca 300

acagcagcct gctccttcct tccaaaatgc tgctggccca agcagaccat acattcctcc 360

accaatccaa caatagcaac aaccccagaa ac 392

<210> 1450
<211> 311
<212> DNA
<213> Glycine max

<400> 1450

aatcatccgg atctgagatg ggcaagtcct ctacaacaac aatagactgt cccttatttc 60

caaaatgttg ctggtccaag caagccatat gttcctcctc caatgcatca gtggtagtaa 120

caacaacaac aaagacaaca agcaactgag gccccttctt aaccttcctt agaggagtta 180

gtgaggcaaa tgaccatcta gaatatgcaa tttcagcaag aaacaagagc ctccattcaa 240

ggtctgacaa atcagatggg tcagatggct actcaattga accaagctta gttccaaaat 300

tctgacaaat t 311

<210> 1451
<211> 352
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1451

acatgctttt ttgggtgtca tgctacaaag gagagagcaa gaaatgaaga gtcaatggtt 60

gatacatggg cggaaatgaa aaagatcatg aggaagtggt atgtgctggc tagttactca 120

agggacttga aattaaaagc tccagaacta accctatgaa acaaacgggt tgaggagtat 180

ttcaaggaaa tggatgtgct tatgattcaa gcaaagattg aagaagatga ggaggtaact 240

atggctcgat ttcttaatgg tttgactaat gatatccgcg atattgttga gttgcacgag 300

tttgttgaaa tggatgattn gcttcacaaa gcaatccaag tagagcaaca at 352

<210> 1452
<211> 359
<212> DNA
<213> Glycine max

<400> 1452

agcttcttag tttcagatga tgcagatggg tttgtagcta cctcatgcac tcctctaatg 60

actatggcat catttctggc gctaaattgc tgggagttgg aagccatctt ctcaattaaa 120

tttctggctt cagcaggagt catgtctcca agggctccac cactggcagc atctatcata 180

cttctctcca tattactgag tccttcataa aaatattgga gaagaagctg ctctgaaatc 240

tgatggtggg ggcaactggc acatagtttc ttaaatctct cccagtactc atacaggctc 300

tctccactga gttgtctaat acctgagata tccttcctga tggctgtggt cctggaagc 359

<210> 1453

<211> 363
<212> DNA
<213> Glycine max

<400> 1453

ctcacactga tgtccgattc ggggacatat tatatcgaga ctctctatat tgaacaacgg 60

aagctctcgg gagaatcgaa tggtcataac ttttcacacg aatgttcgat tctgggacat 120

aactcatcta gacgctcgaa attgaacaac ggaagctctc gagaaattcc aatggtcata 180

agttttcaca cggatgttcg attcgggaac ataatatatc tagacgctcg aaattgaaca 240

acggaagctc tcgagagatt cgagtggtca taacttttca cacgaatgtt cgattccggg 300

acataatata tcgagacgct cgaaatggaa caacggaagc tgtcgagaaa ttcgtatggt 360

cat 363

<210> 1454
<211> 311
<212> DNA
<213> Glycine max

<400> 1454

agctttttta tctagttaga tctaaattat caggtacatg agcataagag acacaaccaa 60

aaactctaaa atgttgaact gatggcttga ttcttctcca ggcttctttg ggtgttatgt 120

ccttcaccgc tagcgtggaa ctggggttta atacatgcac aacccaatat actgtttctg 180

gccaaaaagt gttaggcact ttcttttcaa tgctgcgaac caaattcatg actgtgcgat 240

tctttcattc tgcaacacca ttttgatgcg gcgaatatgt agctattaat cggctgtgcg 300

ctccatgcac a 311

<210> 1455
<211> 349
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1455

agcttttacc aaagagttnt actctctggt aaacgattac cagtttactg taatcgatta 60

ccagtagcaa aatttgtttt caaaagcttt caaattgaat ttacaacgtt ccaattaatt 120

tcaaaatggt gtaatcgatt acaagatttt ggtaatcgat taccagtgtg tttgaacgtt 180

gaaattcaaa ttcaattgtg aagagtcaca tcctttcaca aaaatgcttt gtgtaatcga 240

ttacaatgat ttggtaatcg attaccagtg ataagttttg aataaaaatc aaaagatgta 300

actcttccaa tggttntcaa gtttttctaa aggttataac tcttctaat 349

<210> 1456
<211> 484
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1456

tgtaccctac acagaatata aggataattg tgtattttaa aatgagaaaa aatacttttt 60

tttgtatttt atatattttt ctttaattaa aatttcaatt ttaattaatt catgtaataa 120

atgctagtat gatatataaa tattgcttat attaaatatt agtatgatat ataacttaat 180

ttagtaaatt tcaattntga tttgacaata acaccaaaga ttttttttgta aagaattaca 240

tataaatttt atcttttaaa aatggctaat taccattttt ttttgtgttt cttcgtgcaa 300

gtatttttt tgtaatacca aacatgtttc atatgtaaaa atttgtgaag taaatnttac 360

atttacttat ntatatatgt cttctgagaa taaaacatac aattaagaaa tttaattaat 420

attctgcatt atacactgaa aatattttta atttcttatt acattcttng nctnttatat 480

attc 484

<210> 1457
<211> 463
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1457

agcttgtcac ttgatgtcaa ccagtctgct atttgttctc ttgtcatctt ccattatatt 60

tagcaatttg gaaatttatt gcttttacac caagtgatgt ttcatagttt agttattaac 120

atctacgatc aaactttatg gttagcataa actggaacgc tgaacaacag taggtgttgg 180

ctttgggttc atgctttctg atagaacaag tactttgaag acatgtttta ataatatttt 240

tcataatttt gaaactgttt tatttaagct tcagcagttg ttgcttgcta gtactcatgc 300

tatgttggtt actctctagt ctacttacta ctaatgttgg agctntttcc catctatgct 360

ctctatatcc agtatttgaa gttaagagct cttcanaggc aatcctatac acattacttc 420

tatgaagcaa ctgtcggagc tggtcttcca atttgtagca ctt 463

<210> 1458
<211> 483
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1458

cactcaagct ntacacgaat gtccgattcg ggcgcataac aaattgaaca atgaaagctc 60

tcttgaattt cagatggtca tagactttaa cacataagtc tgattctggc acatcacata 120

tagagaagct caaagttgaa caatagaaac tctcaagaaa taaaaatagt cataactttt 180

aactcggacg tctaattcag gcgcataata catcgagacg ctcgaaattg aacaacgaaa 240

gctctcgaga aattcaaatg gtcataactt ttcacacgga attccgattc atgcggatag 300

tatatcgaga cgctcgaaat taaacgtcgg aagctgtcga aaaattcaaa tggtcatacc 360

ttttcacatg gatgtccaat tcggatgcat catatatcga acaacggaag ctctcgacaa 420

attcaaatgg tcataactnt taccacggag gtcagaatca cgcgcataat atattgagac 480

gct 483

<210> 1459
<211> 352
<212> DNA
<213> Glycine max

<400> 1459

tgacaactta tgactatttg aatttcacga gagcttccgt tgttcaattt cgagtttcac 60

tatatgtgat gcgccaaaat tggacattcg aattaaatgt tatgaccatt tgaatttctc 120

aagagcttcc ggtgttcaat tctgagcgtc tcgatatgtg atttgcctga atcggacatc 180

cgtgtgaaaa gttatgacca tttgaatttc tcaagagcta tcgttgttca atgtcgagcc 240

tctcgacata ttatgcgcct caatcggaca tccgcgtgaa aagttatgac catttgaatt 300

tctcgagagt ttccgatggt gaatttcgag cgtgtcaata tattataagc ct 352

<210> 1460

<211> 343
<212> DNA
<213> Glycine max

<400> 1460

tatgattcca tgtgctgcga attcttggat tggatgttta tgtccattgg cttccccagc 60

ccagttctgt acttggatca tggagtgtgt ttcttccact tcctttagtg tggcagacaa 120

tggatccatt tatggtcact tcacaggaca gcggggtctt agacaagagg atcctctctc 180

cccttatctg tttgtgctct gtttggagta cttttccaga gatatgagca gcctcaatga 240

tgatgccaat tttaaatttc atcccaacta tgcaggtatt cagctatctc atttggcttt 300

tgcagatgat attatgcttc tatctagatg agatatccat tct 343

<210> 1461
<211> 469
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1461

tatatccatg gcctcctatg gtggtgagtt tcttctaaac tcatcttctc cttgaagtgg 60

ngtctcctct ctctctcttc cttctccatt ccgctgccat tcatcttcca agaagcaaag 120

gaatccattg atgaagaaga tcctaggcct acaagctcca atggagctta catcatgtgg 180

tatcaagagc atctccatct aggtgatgtt cttttgcttc ctctatcttt ttgttcggtg 240

aattctctnt aattccttgt tcttcatctt attctccatg tatatcctcc attgtcttgt 300

ggtttggtgc tgttaagagt agattcaaaa aaaataaacc aattaaatct tagatctaca 360

cttgttcttg catttctatg gttcanattn tgtagatcta ctcttgaatc angtttttgt 420

gtngattnta ggatctatnc attttcattc ataatattct tgtgctgat 469

<210> 1462
<211> 292
<212> DNA
<213> Glycine max

<400> 1462

agctctacat gtctcatgac acctaagcac acttagtgga taatcttgga cttgatcttg 60

ttttagtgag ttgaaccata gctgatattc actaatcata atgagtgaaa tatttggctc 120

caaagatggc tccacaaatt aaaattcaag ttcaagtgaa gattgaatac aaaatcttac 180

ttgctatcta tattgcggga cacttacgct atatataaaa gctctgcgtg tgcatgttct 240

caactcttga cattcgagaa attacacttc caggcttaga ccttatttga gg 292

<210> 1463
<211> 277
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1463

gatcttccgt tgttcaattt cgaccttctc gacatattat gcgcccgaat tggacattcg 60

tgtgaaaagt tatgactatt tgaatttcct gagagtttcc gatgtttaat ttcgagcgta 120

tcgatatatt ataagcttga atcggacatc cgcgtgaaaa gctatgacca cttgaatttc 180

tccagagctt tcgntggtga atttcgagcg tctccatatg tgattcgccc gaatcggaca 240

tccgtgtgaa aagttattcc cgtttaattt ttcacaa 277

<210> 1464
<211> 217
<212> DNA
<213> Glycine max

<400> 1464

attcaaatag tcataactat tcatacggat gtcccattcc ggcgcataat atgtcgagag 60

gctcgtaaat gaacaacgga agctcttgag ataatcaact ggtattacct ttcacaccga 120

tggtccattt acgccgaaca catattatga agctccaaaa tgcaccaccg gagcttctcc 180

gaaatttcaa agggcataaa ttttttcacc gatggcc 217

<210> 1465
<211> 365
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1465

gtactatctt catgcgattc ctttntctcc ctcctctaat attatctcac aaatcccaac 60

ggttaaggga tgctcaattg aatttcgaac aacatatcca aattttacta caatccaatg 120

gttaacgaat ccaagatcgt atttttacca agacagtttt gggtttctgc gggaaaataa 180

aatgctacaa tgcgaagggt tttatactaa gctcagacat gattttgaaa ttcccaacgg 240

tgagaatggt cggaattggg ttttgaaccg ggtgcttaaa tttcacgatg atccaacggt 300

gaatgagtcc gagatcatca ttcttctgag acatgtttag tggtctacgg gaaaagagag 360

gttga 365

<210> 1466
<211> 387
<212> DNA
<213> Glycine max

<400> 1466

agcttattca tggatattgt aggacgttta cttggtatgc cacgaagcat tgtctcggat 60

cgtgatccct tattcgtgag taaattctgg aaggagctct tttctctcag tgggacaaag 120

ctctgcctca gctccgcttg tcacccacaa ttcgatgagc aaaccgaggt tgcaaaccgc 180

atcatcgaac aatatttgag agcatttgtt catcaaaacc cttcgcaatg ggggcactat 240

ttgctgtggg ccgaatggtc ctacaataca tcttgccact cagccaccgg cgtcacgccg 300

tttgaagtaa ccttcagcag gaaaccaccc aatttccctc attatgtcac aggaactgcc 360

aaggtcgacg ctgttgacga tatgctc 387

<210> 1467
<211> 374
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1467

agcttctggt gggacatctt gacttgctgt ttaatctgac attcattaca cattctgcct 60

tcttctatta tcagattggg aatgcctcta acagcacctt tgtcaatgat tatattcatg 120

cctcttgagt gcagatgtac aaatgtttga tgccataatc agacttcatc ttctttggag 180

gatagacatg tggaggagta actgggttct tgagatgtcc atangtagca gatgtgcttt 240

gatctgctgc ccttcattag aactatactc ttgtcatttg tcaccaagca ttctgacttt 300

gtgaagtgta cattgaattc ttcatcacac agctgactga tgctgataaa gtatgcagac 360

actcccttca ccaa 374

<210> 1468
<211> 396
<212> DNA
<213> Glycine max

<400> 1468

agcttaacaa ggctctctgt ggcttataaa acatgcccca agacagtggt ttgacaggtt 60

gaaatctact tttcttcagt ttggctttgt gggaagcaaa tgtgattctt atctgttcat 120

ctacacacat cagaagcata ctgtccatct tttagtctct gtgaatgata tcatcatcac 180

aagcaattct atctctctta ttcaacagct aacttccaaa ctaaacactg ccttctctct 240

taagcagcta ggtcatttgg attatttttt gggactagag atcaaatacc ttgctaataa 300

ttctatacta gggactcaaa gcaaatatat ttgtgattta cttcacaaac tcaaatggct 360

gaagcacatt ctatttcctc tcccatggtt tctaac 396

<210> 1469
<211> 388
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1469

agcttcttgt gattcacaaa gctactccac cctgtagtta acaagtgccg gcgcggcgtg 60

cccctataaa tgtgcctaaa tttccatgtc tcaccatgaa catccttggc aaggatgttc 120

tgaacgggag ggtccgcgga atattccaac cgaggaaaaa ttgtctcagc acaatatctg 180

ggaacagaaa agcccccacc attgttggca tcaaactgtg tcaaggtttt ggcaaaagaa 240

ggggatttat ctttattttc agatccattg atgcctacaa cagcatcatc ctcaaaatca 300

ccctcgtttc tggtcaaatg aacaagccta agctntacat aaacctcatc agtttcaaga 360

tcagccatgt attagatagc tccaactt 388

<210> 1470
<211> 438
<212> DNA
<213> Glycine max

<400> 1470

tctcatttat ctccaccatc cggtccaact tccgcttgaa ctctgggttt tcaacatcaa 60

gaacggctgg gataatccga tcagtcgtgc ggtttgtctg cataaataat ccagacattg 120

aagcttgagt aactggttgt aatatacgag ttcatcatta gatgcttgtt gatcgacttt 180

attagtgata gtttctaatg ctaactcgag gctccattac tttcattata tcatgttctg 240

ttactaaatt gactatgtaa ttgagaatgg ataaaaacaa atattgatta tacaaaataa 300

caatggagga atggtgatta tagaaaaatg caaacacaaa ctaacctcga taatgacatg 360

catgtcaaat tcttttgtgt taagtccaat gccttcgtag aaagctgtac gttggcaatc 420

atcgagatac attgtgac 438

<210> 1471
<211> 434
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1471

tcatgagaga gtcaaagatc aaattgagag gaaaaataat agctatgcta aacaagccaa 60

caaagggaga aagaagttgt cttcaaaccc ggagattggg tttgggtgca catgagaaaa 120

gaaaggtttc cggaacaaag gaaatcaaaa cttcaaccaa ggggagatgg accatttcaa 180

gtgcttgaaa gaatcaatga caatgcttac aaagttgagc tgcccggtga gtataatgtt 240

agttccacct tcaatgtctc tgacttatct ctttttgatg cagatggaga atccgatttg 300

aggataaatc cttctcaaga gggagagaat gatgaggaca tgaccaaaag caagggccag 360

gatccacttg aaggacttgg aggacctatg ancagggcta gagcaaggaa agccaatgaa 420

gctcttcaac aagt 434

<210> 1472
<211> 444
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1472

ctcaagcttg gcgagagtta aacaagaaca ctntntggcc aatatggaac tccttcctaa 60

gaatcctaga gtcatgaatc ctcttcactt tctctttgta gatcttggat ttctcatagg 120

cttctaagcg aatctcttca agttcttgca attgaagctt cctttccata cccgcttcat 180

caaatgccat gttacaaccc ttcaccgccc aataagtgca gtactcaatc tccaccggaa 240

gatggcatgc cttaccaaaa accaccatat agggagacat ccccaaaggt gttaggtaag 300

ctatcttgtg ggcccataaa gcatccaaaa gtagcttgct ccaatccttc ctattaggat 360

gcactacctt ctacaacact tgcttgatct ctctattaaa aacctccact tgcccattag 420

tttggggatg ataagctata gcaa 444

<210> 1473
<211> 436
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1473

agtaagatac tattgctgtg gagttgacgt acaggttctc actgctgttn tgtgtctgga 60

tatgtgttta ggtgtgaaat atggaggtaa agctgcagac acgtgggcag taggagttac 120

tttatactgt atgatattgg gtgaataccc ttttcttgga gacacacttc aagatacata 180

tgacaaagta agaaatacac actcagacat atatgacaaa gtaagaaaaa catgcatgtt 240

tttattataa ttacaacaaa aatgtcattc tgttttcaaa agttctcact ttactaagtt 300

tcgtaacttt ttcacccgga tattatactc tgattggcat tcatattttc tggtgcctat 360

atcacaatct tagcttgcta ttttcttcct gatccagata gtcaataatc ctttagtact 420

ccccaacgat atgaat 436

<210> 1474
<211> 442
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1474

tgagggaana cttgatgcct tggtgaacct agtaactcag cttgccataa atcagaaatc 60

tgcatctgca cctgttattg ttgcaagagt ttgtggtcta tgttcttttg ctgatcacca 120

tacagatctc tatcattctt tgtagcaatc tggagtcaat gagcaacctg aagcctatgc 180

tgcaaacatt tataatggac cccctcagca gcaaaaccaa caacaacaga ataattatga 240

tctttcaagc aacagataca atccaagttg gaggaatcat ccaaatctga gatgggcaaa 300

tcctccacaa caacagcaac aacagcctgt ccctcccttc cagaatgctg ctggtccaag 360

caggccatat gttcctcctc caatgtagca acagcagcaa caacaacaac aaagacaaca 420

agcaattgag gccccttctc aa 442

<210> 1475
<211> 433
<212> DNA
<213> Glycine max

<400> 1475

tccttaagaa gattcctaaa gaagcttgag cttagctaca catacctctc taatagctaa 60

gctcacctcc ttgagatgag aagctagagc ttagctacac ccccccctata atagctaagc 120

tcacccccat gacaaaaaac atgaaaatac aaaaaaaagt ccttactaca aagactactc 180

aaaatgcccc aaaatacaag gctaaaaccc tatactacta gaatggccaa aatacaaggc 240

ccagacgaag gaaacaccta ttctaatatt tacaaagata agcgggctca tacttagccc 300

atgggctcga aatctaccct aaggctcatg agaaccctag ggccttccct tggatctcta 360

gccaatctac ttggagtctt ctacccaatg cccttgcagg taggattgca tcattccctc 420

caccttggaa aga 433

<210> 1476
<211> 443
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1476

ntaagagana ttcccttctt cttcttatca ttctcctcat gttgattcaa tctcttcaat 60

tccattcatg ttcctgtaac tttccaaaca aggtagcaag agacatgtta gtaagatttc 120

ttgattcaat aatggtcatt acctttggtt gccattccct acttatgcat cttaacactt 180

tattgacaag atcttcattt ggaaatattt ttcctaaaga tgcaagatga tttattatgt 240

aggtaaatct cttttgcatg tcttgtatag tttcatttgg attcattcta aataactcat 300

attcatgagt taaagtattt atcctagatc tttttacatt tgttgtccct tcatgggtta 360

cttgtaaggt atcccacata tctttctcat gtttgcaatt tgacacccta nagtattcat 420

ctattcctaa tgcagatgta atg 443

<210> 1477
<211> 450
<212> DNA
<213> Glycine max

<400> 1477

tccaatgaga gaaatgggtc taatttatca agctcctatg ggccatcaac ttttggaaca 60

agtgtagtaa aggaggggtt ggccgccttt gggattacac catgttcata aaagtcagca 120

aaaaccttca acacatcatc ctttagtctt ggccaatttt ttttaaagaa cttaagttaa 180

agccattcga agccagactt ttgttactat cacaatctca tattgcttct ctaatctcac 240

tctcctcaaa ccttcaaaca agcatatcac tctccacatc agttttatgt ttgaacgact 300

ctttaactct ccaaccttgg tctaatcctc cttcatcttg aaatctcctt ttaaagaaac 360

acttcacatt ctctttaacc actcttggat ccttctccca cttaccattt accaataaac 420

cacttattgg aattttcatc cttctccatt 450

<210> 1478
<211> 442
<212> DNA
<213> Glycine max

<400> 1478

tactgcgacg agtgcgcttc ttgtaaagaa tacggtatcc gcactcacgg cactgtataa 60

cgtcaccggg cttcagcgta ttctccattc cacaatctgc aacagataca aacacaaaat 120

cacatttcac tcttaaaacc ctaaacccta aacacacact tttaacattg gcaaaaaagg 180

taaacgaaaa acgcaattag gtcaaaaaga gctgtgatta gataagaaac ctccgcatat 240

gtagctgact ggctcaggct gaggatccat cgctggttcc agcgaggtgt aaaggaagaa 300

ggttctaggc tttagccttt agctttctgc tcaacgaaga aaatgtaaag tggctcagaa 360

tcagaggctc taaaacgaag gattgggctt catcttcagc ttttatgggc ccaaattcgc 420

aacttacatg tccaaaaccg ag 442

<210> 1479

<211> 441
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1479

tccatcactt ttgacgactg ttaagtgaga ttccttagca ttggcctgat accttgcaca 60

taagtaagca cttagcatga catatggtct atttttaatt aagtagagga gtgatccaat 120

catacctcta tatcttaact catccactga tttacctttc tcatctaagt caaggtaagt 180

taaagttgcc attggagtag atgcttcttt gcattnttcc atgccaaatt tcttaattag 240

ttttgtacaa tatttcgttt gatttaggaa ggttccatgt ttcatttgct tgacttggag 300

tccaagaaag aagttcaact ctcccgtcat agacatctca aattccttct gcatacaact 360

agaaatttcc ttacacaaaa tntcattagt agcaccaaat ataatatcat taacatatat 420

tttaacaatt agcaactcac t 441

<210> 1480
<211> 455
<212> DNA
<213> Glycine max

<400> 1480

actaagcttc tatccaaggt tcgttcctaa tttctctaca attgcatcac ctctcaatga 60

gctagtgaag aagaatgtgg catttaactg gggtgaaaaa caagagcaag cctttgcttt 120

gcttaaagaa aagcttacta aggcacctgt tctagctctt cctaactttt ctaaaacttt 180

tgagctagaa tgtgatgcct ctggagtggg agttggagct gttttgttgc aaggtgggca 240

ccctattgct tattttagtg aaaaacttca tggtgcgacc cttaactacc ccacctatga 300

taaagagctt tatgccttaa taagagcact ccgaacttgg gaacattacc ttgtttccaa 360

ggaatttgtc attcatagtg atcaacaatc acttaagttc attagagggc aaagcaagtt 420

aaacaaaagg catgcaaaat gggtagagta cctag 455

<210> 1481
<211> 442
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 1481

ttaaatcaat aaatcaatat caatatatta tataaaacaa agttattgat tgtgtctgtt 60

acttaagaca catgacaaac gctgatgcag ttaggcctcg cgtaattaaa tattatttcc 120

cattgaagaa acaaaataaa attcaaaata agaaatcaat caaacaccaa gtaattctat 180

cacacaataa ctctaaattt atttgttata ttcataataa catgctattg tttaattatg 240

taaactgaaa ctgattgacg ggaaaagaag aatgatagtt tagataactc agaaccaact 300

taaataaaca attttaatga ccaagggctt aaaggatgaa aatatccaac atcttttaat 360

attgtatgta cctttcagta gaatttttat attgatgaat gctaacaaaa ctcattnttt 420

aacttgatgg aatccttact at 442

<210> 1482
<211> 442
<212> DNA
<213> Glycine max

<400> 1482

tcgtggcact ttgccaagac cttttaaagg actgtcggct cataactctg gatctcaatg 60

gcaaccaatt attagaaggt tttttgccag aatctttgtc caattgcatt gatctggagg 120

ttttagatct tggaaacaat caaataaagg atgtgtttcc ccattggctt caaactctac 180

cagaattgaa agtattggtt gtgcgagcca acaagttgta cggtcccatt gccggtttaa 240

agatcaagca tggatttccc tgtttagtca tctttgatgt ctcttccaac aacttcagcg 300

gcccaatacc aaaagcctac atacaaaaat ttgaagcgat gaagaacgtt gttatagata 360

ccgatcagca gtacatggaa atttctattt ttgaatataa taacatgtac agtgattctg 420

tgattataac aacaaaagca at 442

<210> 1483
<211> 444
<212> DNA
<213> Glycine max

<400> 1483

actcagctaa taattatttg gtaaaaaaaa catctacaat cagtcaagga gataagaaaa 60

acatcatcct aaaaagtatt atatcctaat atgtcccttc caacccttca atccttgttt 120

gatggaccat caacggtatt ccaagtagct gattcataaa aaaagaaagc ataatgaata 180

ccatttttat cttaaattga aaaggctaag agattagtta aaaagataat atattttatt 240

gttgaacctg tgatgggggc ggaagtggct ataagaccct agacaatccc aaatcgatca 300

ttgataacca ctgcaaaatt aagattaatt attacaaaaa cagaggcaaa tttaaagtat 360

agataaaaga ccaacaaata tgtcataagg gttatcaaac aaaaaacttg aataggctat 420

cgtattggag aaatagttag catt 444

<210> 1484
<211> 338
<212> DNA
<213> Glycine max

<400> 1484

actcagctta acatcagacc acttgcgggt gcaggaacta cttcacatgg acttgatggg 60

gcctatgcaa gttgaaagcc tttgaggaaa gaagtatgcc tatggtgatg tggatgattg 120

ctccaaattt acctgggtca actttatcat agagaaatca cacacctttg aagtattcaa 180

ggaggtgagt ctaagacttc gaagagaaaa agactgtgtc gtcaagagaa tcaagagtga 240

ccatggctga gagtttgaaa acagcaagtc tactgaattc tgcacatctt aaggcatcac 300

tcatgagttc tctgcagaca ttacaccaca acagaatg 338

<210> 1485
<211> 399
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1485

actatagaaa ctcagcttaa cattcaattn tgagggtctc gatagattac gggactcaat 60

cagacatccg agaaaaaagt tattgtcgtt tgaatttgct cagagcatca acattcaatt 120

tcgagcgtgt cgatatatta cgggactcag tcagacatcc gagttaaaag ttattgtcgg 180

tcgaatttgc tccgacgatc aacattcaat ttcgagcgta ctgatataat acgggactca 240

atcagacatc ctagtaaaaa gtggttgtcg tttgaatttg ctcagagctt caccattcaa 300

ttttgagcgt ctagatgtat tacgggactc aatcagacat ccgagtaaaa agttattgtc 360

cggtgaatta gctcagagct ttcacattca gtttcgagc 399

<210> 1486
<211> 434
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1486

tgtcaaagag ggaagcaagt tagaaactct nttcaaagca agaacattgt ttctacttcg 60

aaaccccttg aactacttca cactgattta tttggtccct ctagaactat gagtttgggt 120

tgtaattact atggcttagt tatagtagat gattactcaa cgttcacatg gactttgttt 180

ttgaaaacaa aaaatgaagc ttttgatgct tttcgcanac ttgccaaggt gattcaaaat 240

gaaataggtc ttaacattgt ttcacttaga agtgatcatg aaggtgaatt tcaaaatgag 300

tcttttgaaa tattttgtga agaaaatgga atttaccaca atttttctgc cccaagaaca 360

ccccaacaaa atggtgttgt ggagaggaga aatagatccc ttgaagaagg tgcaagaacc 420

cttctaaatg aaac 434

<210> 1487
<211> 425
<212> DNA
<213> Glycine max

<400> 1487

tgtgttctcc cttgtagaac tactaactgc agtaacagtt gcggcccaac tatccggtgg 60

tgatgactat agaatcaatg ccttcacctc atcctcaaat ttaatctgca cagattccaa 120

ttgggcaaga atagtattaa actcattaat atgatcagtg acagagatac cttgtcccat 180

cttgaggatg aaaacccggc gcgtcaagta tactttgttg gctgctgacg gcttctcgta 240

cgtatctgat aatgccttca ttaagcctgc agtagtcttc tcgttcacga tgttgaacgc 300

gaggtgcttg gctaatgtcg atctgatcac gccaagagct tgtcgatcta gcaagatcca 360

ttcttatggc ttcatgtcct ctggcttaac ccctgataag ggctgataca gcttcttgtg 420

atata 425

<210> 1488
<211> 417
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 1488

tagcttcacc ataaaaaatg gtgtcatccg ctttctgttc gatgctgatc ggcacataat 60

tagcaccaac cagatagcct ttgaatagat tattctcctc agccctgctc ataacccaat 120

caaaccttct gcgagagata aacaagaggc gactaaggat ccccttggcg aatgcccttt 180

tgagggataa aatcagaatt cggacttcat tcccaaaaca gaaatagagg cggatatgac 240

acatcctttc atccacttaa cccagtgcgg actataacct gttctcccca gcatataaaa 300

canaatagct ccagataccg aatcatatgc cttttcaaag tcaaccttga acactangca 360

tgatcgattg cttctcttat cggcatcaat aaccctattt gctatgacta cactatg 417

<210> 1489
<211> 438
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1489

ntgcacgaag ttacttggta aaactatggc acatgttttc gggtagaatt gagacttgtg 60

aatgtaatgc aatttctgta atgatattga taagtagggc ctattagagt aggaaggcca 120

ttatagcatg tttgcccgag taccagtata ttgagttatt ttctctaacc aacatgtatt 180

atgcattttg ttaggatgga cccaaagagg tccaaaagaa ggatgtttaa gtggctcaaa 240

gattataaaa gataatgttt tttatttata aattatagtt ctttatttaa tttatattaa 300

aataacatga tgttgagact tggataatta ttatccattg attaaatgtc ccttagatta 360

tatatgtata ttcatcttta cctattatca tttattaatg aaatatcaag tttatcttat 420

tctctgtata gctgtatg 438

<210> 1490
<211> 436
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1490

agctattgtt gaataaatcg actcccatat tgatccgcac taccaatgat aataaaataa 60

tcaaatttaa ttcttcaggg tgacagcata taatgaccaa tagcaaacaa tatacctgaa 120

ttcaacaaca tgacccgcaa tttcagagag ctcaaaacac tttgttttat tggttttaaa 180

ctcttccaac agagaagaag caaaactttc atcaatgttc ccagtatctg catgccaagg 240

tcccatgacc ccggccaaat tcctcattcc agaagcaaaa cgcatattca gttcattgtg 300

cctaacagga cttgcagatc caactggnga agtggataca acagagtttg ccattggact 360

tcctgggtaa gacatcccga caccatatgc aggatttcca taataaccat gaggagtgga 420

gctgcctgat taccac 436

<210> 1491
<211> 417
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1491

agcttatgct gcanatattt acaatagacc tcctcaacct cagcagcaaa atcaaccaca 60

gcagagcaat tatgaccttt ccagcaacag atacaaccct ggatggagga atcaccctaa 120

cctcagatgg tccagccctc tgcaacaaca acaaaagcct gctccttcct tccaaaatgc 180

tgctggccca agcagaccat acattcctcc accaatccaa caacagcaac aaccccagaa 240

acagccaaca gttgaggccc ctccacaacc ttccctcgaa gaacttgtga ggcaaatgac 300

tatgcagaac atgcagtttc agcaagagac cagagcctcc attcagagct taaccaatca 360

gatgggacaa ttagctaccc aattgaatca acaacagtcc cagaattctg acaagct 417

<210> 1492
<211> 461
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1492

tgttgatttc ttcaggatga tcaacacaat attgcatttg ctgcttcaat tttggcctgc 60

agatttcaca aataatacat ttactatgct tatttggtag gtttaaattt tcatttttt 120

aagggaggta taatttttta ttaaaagtca ttgtattttt ttagaatttt attttatgtg 180

aggtcaactt aagtttttta ttttacacaa atgtaattta ttttattgcc atattatcca 240

attcattaat ttgatttagc aacacactga atttctataa gtgttaatat ttagcaacat 300

attctctagc acatctttta tatcacacat tctattatag attaaaattt attacaaact 360

aaaaaattaa cagagaaata actcattaaa taagaagtga gactaacaaa aattgtgatt 420

nntaataaat tctaatcaat ctttaataat atatttaaat g 461

<210> 1493
<211> 400
<212> DNA
<213> Glycine max

<400> 1493

tgaatcggac atccgtgtga aaagttatga ccatttgaat ttctcaagag cttccgtagt 60

tcaatttcga gcttctcgac atattatgcg cccgaatcgg acatacgtgt gaaaagttat 120

gaccatttga atatctcgag agcttccgat gatgaatttc gagcgtatcg atatattata 180

cgcctgaatc ggacatccgt gtgaaaagtt atgaccattt gaatgtctca agagcttcca 240

ttgatcaatt tctagactct cgacatatta tgcgcccgaa tcggacattc gtgtgaaaag 300

ttatgaccat gtgaatttct cgagagcttt cgttgtgcat tatgagcggt tctatatttt 360

atacgccaca atctgacatt ccagtgaaaa ggtattaaca 400

<210> 1494
<211> 380
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1494

agcttgccgc cacggagttt ttcgactatg ctcttgtgtg gnggaacaag ctacaaaagg 60

agagagcaag aaatgaagag ccaatggttg atacatggac ggagatgana aagatcatga 120

ggaagcggta tgtgccggct agttactcaa gggacttgaa attcaagctc caaaaactaa 180

cccaaggcaa caaggggttt gaggagtatt tcaaggaaat ggatgtgctc atgattcaag 240

caaatattga agaagatgag gaggtaacta tggctcgatt tcttaatggt ttgactaatg 300

atatccgtga tattgttgag ctgcangagt ttgttgaaat ggatgatttg cttcacaaag 360

caatccaagt ggagcaacaa 380

<210> 1495
<211> 458
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1495

ngagaagttg catcaacaag ctgaccagat aatgcataac attatcaatg agcatagaga 60

ggctaagtca agtgccacag gagaccaggg agaggaggaa gttcttttag atgtgctctt 120

gaagaaggag tttggcttaa gtgatgaaag tatcaaggct gtgatctggg taaggataga 180

cattttccac caattttatt gcatgataga aaaatggaga aaagtatgct ttactgcctt 240

cacactttag tttcaaaaac tattttgtat tttctaaaat gattagtaat cattttgtca 300

ttcaaaattt aataggtttt gcaaattgct ttgaatataa gtgtttaaaa agaaaagaaa 360

aatataaaca gttaaggaca tattttctca tcctctttct gtaagtgctt tattcaagta 420

tctagaaggc aaacttttaa aaattagaaa tgtgatat 458

<210> 1496
<211> 354
<212> DNA
<213> Glycine max

<400> 1496

agcttgaaat tgaacaacgg aagctctcga tttaatcgag tggtcataaa ttttcacaca 60

gatgtccgat tcggggaaat aatatatcga gacgcacgat attgaacaac ggaagctctc 120

gagaaatttg aatggtcatt acatttcact cggatgttcg atccggcgac ataatttatc 180

gagacgctcg aaattgaaca accgaagctc ttgacaaatt ataatggtcg taacttttca 240

cgcgaatgtt cgaattcggg acataactca tctagacgct cgaaattgaa caacggaagc 300

tctcgacaaa tttgaatggt cataatgttt cacacggatg tccgatctcg gaac 354

<210> 1497
<211> 451
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1497

agcttcgaca ccctaatgtt gttcaatttc ttggagctgt tactgacaga aagcctctta 60

tgttaattac tgagtatctg agaggagtat gtgaatgcat ataactagac acctaggttc 120

tgatgctctg aacttatgca atcttatgct ntaagattaa actctactaa atctctattt 180

catgcccatt tttagggtga tcttcataag tacctcaagg acaaaggtgc acttagntcc 240

ttcaacagcc atcaatttgg cttggatatt gctaggtatg gtgtgtcata ccttaagttt 300

cctttatntt tctttntaaa atttttataa agagaacaaa cagaaaacca canaacanga 360

gaatcattaa cccatagatc tcttcaacct ctccatanat ctggtatata natataaacc 420

actcctaaat aattctcaca cgtcagttac t 451

<210> 1498
<211> 448
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1498

agctngaagg ggtgtaaccc atcattctct atagtagaac agccggaacg ngtctactat 60

cattattatc atctccctct ccatcattgg agatgctact tgagctgcta ggtcccttca 120

cctctgggca tattccttga acaactcatg ctccttcttg cacatgtttt gcaattgcac 180

tctatctaga gccatgtccg agttgtattg atactgcctg atgaaggcag ccattaagtc 240

ttgttaagaa tggactcggg aaggttccag aatagtatac caggtgacga ctgccccaat 300

aagagtttcc tggaagaaat gcatcaacaa tttttcattt ttcgagtatg cccccattnt 360

ccctactgta catttcaggt gattcttggg gcatgtagtc cccttgactt atcaanatct 420

gcaccttgaa cttcggaggg ataacgat 448

<210> 1499
<211> 394
<212> DNA
<213> Glycine max

<400> 1499

tgcgggagtt tgtgatagcg attatgacgt tgatgttgat gatagaaaag cactaccgga 60

tttgtattgt ttatgggcga atgagttatt acatggagat ctaagaagca aggcattgtg 120

acactttcta cttgtgaagc caagaatgta gctgcaactt cttgcacatg tcatgccatt 180

tggctaataa gaatgttgga ggaacttcag ttgttgcata aggaaagcac aaagatctat 240

gttgataata gatctgcata agagcttgcc aagaatccgg tgttccatga acgaagtaag 300

catatagata caaggcgatc attcattaga gagtgcaata ccacgacaga acgagaactg 360

acttatgtga aaactcacga tcaagttgcg gata 394

<210> 1500
<211> 366
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1500

agcttgtgcc tcttcacatc tgaaatatga atgtagcata tagatccaaa gacccttagg 60

tgttntgctg atggcttctt ccccgtccaa gcttcaattg gagtcttgtc ttttacagac 120

ttagttggac atctgttgag tatgtaaaca gcagtgtaga ctgcttcagc ccagaatgtc 180

ttaggtagtc ccttctcctt gagcatcgat ctagccattt ccataatttt gaaattcttt 240

ctctcggaca ctccattntg ttgaggagaa tatgcgactg taagttgtcg ctcaatgcct 300

tcatcctcac aaaatctttc aaactcgcga gaggtgtact ctntgccgcg atcacttctt 360

agtact 366

<210> 1501
<211> 461
<212> DNA
<213> Glycine max

<400> 1501

tgtaatcgat tacacacata ctgtaatcga ttaccagagg atgtttttat aagacattct 60

caacagtcac atctttgtat ctggttctta agtggccatc ataggcttat atatatgtga 120

ctagagacac gaatttgaaa aaagtttttc agaacaaaaa aggtcttatc ctcttaaaaa 180

gcaaaatcgt tttatcctct tacaaattcc ttgtccaaaa cacttgtgat tcaataagga 240

attatttgag tgctcaaatt gttcaattta tctctttcaa gagagatgtc ttcttctctt 300

cttcttcatt ctgaaaaggg attaagagac cgatggtctc ttgttgtgaa aggattctaa 360

acacaaagga aggattgtcc ttgcgtgttt agaatttgta aaaggacttt acaagataat 420

ggaactctca agcgggtgct tgtggactgg acgtacgcac a 461

<210> 1502
<211> 468
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1502

ntaggcaaat tcaaacgaca ataacttttt actcggatgt ctaattgagt cccgtaatat 60

atcgagacgc tcgaaattga atgttgaacc tatgagccaa ttcaaacgac aataacttt 120

tactcggatg tctgattgag tcccataata tatcgagacg ctcgaaattg aatgttgaac 180

ctctgagcca attcaaacga caataacttt ttactcggat gtccgattca gtggtgtaat 240

atatcgggac gctcgaaatt gaatgttgaa cttctgagcc aattcaaacg acaataactt 300

tttactcgga tgtatgattg agtcccgaaa tatatcgaga cgctcgaaat tgaatgttga 360

acctctgagc caattcaaac gacaataact ctttactcgg atgtccgatt cattgacgta 420

atatatcgcg acgctcgaag atgaatgtcg aacctatgag ccaattca 468

<210> 1503
<211> 395
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1503

atcctcagag acacctgagg catgcaagct tcaacattca aattcgagcg tctcgttata 60

ttatattatc tagtcagaca tccgagaaaa aagttattga cgtttgaatt tgctcagagc 120

ttcaacattc aatttcgagc gtgtcgctat attacgggac tatatcagac atccgagtaa 180

aaagatattg tcgtttgaat ttgctcagag cttcaacatt caatttcgag cgtgtcgata 240

tattacggga ctcaatcaga catccgagta aaatgttatt gtcgnttgaa cttgctcaga 300

gcttcaacat tcaagttcga gcgtctcgta tattatacga ctcaatcaca catccgagta 360

aaaagttatt gtcatttgaa tttgctctga gcttc 395

<210> 1504
<211> 439
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 1504

acccgggatt cttagagtca cctgccgcat gcaagcttat ggtaatcang agttagttcc 60

tctctcttaa ggaaaaactc aacattattn tcattggatt tacataatga anaattgtcc 120

taatgataag gttgatcact tcaaggctca tctagttact aatggtttca ctcacgttta 180

tggtgatagc ttttcacttg tcaccaagat gccatttgtt tgtctcttcc ttgccatgac 240

tcccatgtgt tattgggctc tatttaaact agacgttaan aatgtctttc tacacaacga 300

acatggagag aaaatttata tggaacacct cattgttttt aggaggagtc taatttgggt 360

tataaacttc attgctctct ttatgggtta aagcagtctt cctgtgcttg gttccaaggg 420

ttagtattgg tattcaact 439

<210> 1505
<211> 300
<212> DNA
<213> Glycine max

<400> 1505

cacatactgt gatccatcac cataggattc tatcaggaaa cattctccac agtcagatcg 60

atatatctgg ctgttatgtg gccatcaaag gcttatatat atgtgactag agacacgagc 120

ttgcaataag ctatacagaa cagaataggt cttatcctgt taaaaagcga tgtcgttcta 180

ttctcttacg aattccttgc ccaaaacact tgagattcag taaggagtta tatgagcgct 240

caccattgac atggtatctc tttcaagaga gaagtcgtca tctcttcttc ttcactctga 300

<210> 1506
<211> 363
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1506

agctntggcc aaaccccagc agcagttgtt ttcttagaga cttgtcttag caccttgtct 60

ttgagactga ggataattac actgtgtgcc ttttgcagta gtgctttctt atccccatca 120

gccatcatct tttcaagttt ggcttctcca tcaagtgctt ccaccaggcc ctgctgaaca 180

agaagagctc tcatcttcaa tcgccataac ccanaatcat tntgccctgt gaatttttca 240

acctcatact tggccgagtc catttcttga atcgaactca aaaatcgctc cacgctcacc 300

gcaccaattt ggtgtgccaa gatcagaatt tagttcacaa aagagtgagt ttcttgtatg 360

aac 363

<210> 1507
<211> 492
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1507

gcattacgga cctatgaaac tcagcttagc agcttattgc cataattcac aaacctagat 60

tccaaataac agcaactcan agtagttatt agatagcatg gaatatattt catttttata 120

aaaaataaat actatttaag agaaagttaa ggatacaaat ataagaggat aagatatcac 180

ccctaacaga gcaaaacaaa tgtagttatt tgatttagta cataattaca tcactgtaag 240

tgatgtatat tcacttacgt tttagcagcc tgcctgccct taccaattgc agcaccgaaa 300

tatctctaga acaattacca aatgaacaaa tcattacaaa aataccacat ggaacttcca 360

aaaaggaata tcaattgcat gtgtaattat aaagaagtct ggaagttgct atcaaatgac 420

aaaaagtagc tcacatagga nacaccggaa ggttcaacca tgtacaactg tggtccatcc 480

ctgtcataac ct 492

<210> 1508
<211> 358
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1508

agccttctac ttattaatta tcataattta gtttanaaat aaccaagtag agaataatat 60

ataaattata tatttttatg gaattatttn tgtgaaataa atttataagt tatagattca 120

aatgtatgtc tcttttcgta tattaaaaaa ataatatcta tctatactat tataattcan 180

aattaatttg attattcaat atacaaattc aataagtatt ntatcaatta tttgaactat 240

caattaagta aactaacaca tantttgaaa ttactaatat tattattttt ctattntact 300

cctannattt aaactcantt tttttatggt cttcgtatta atcctataat atagaatc 358

<210> 1509
<211> 455
<212> DNA
<213> Glycine max

<400> 1509

gagtttctga tgaattcttt taccactgat tgatgtctat gggatctaag tttcagaaag 60

acccattctc caacttcaaa acacaagtcc ctcctcttct tgttagcata ccttgtcatt 120

tgttcctgag ctatgagcaa gacgtgagtt gagttgaatc aaagcctcat ctctttcact 180

cgactccaat gccgcagcag caaccttagt ctcattatac agaaatctca acaatgcaag 240

aggttgcctc ccatatacca cctccaacgg agtcatccca atagacacat gataggaagt 300

gttgtgccaa actcaggcca agggacccac aatgaccaag tctatggatg atcataagca 360

gagcaccgta gataactatc cagacacctg gctaccacct gcgtttgacc atctgtgtcc 420

ggatgatatg ctgaactcat tgtcagctta ttacc 455

<210> 1510
<211> 465
<212> DNA
<213> Glycine max

<400> 1510

cctgagattg agagaaaatg attattaaac acaaaatgga agtactaagt atttattacc 60

tatacttaat agaaaatact tataacacta caaaataacc ataaattgga agagtttgat 120

acaatttaca caagttttat acacaaaagt tagtcgtatt catcgactaa caggtggaag 180

aatgcgttga ataatagcac tatagttacc ttccacaaca attatgtcac tatggatgta 240

caagttcttc ttggttaaca tatccttcaa aaatttggca tagaagggca tttgctgaag 300

tgcttctcca aaaggcaagg taatttccag tttcttgaag ataccaagaa atctagccaa 360

atgtcactct ttatcttttc atgagggtac caattgataa ggtacctcct tgcattcaat 420

aggaggagcc tctttcttct tttctatgtt agcctcactc ttacc 465

<210> 1511
<211> 460
<212> DNA

<213> Glycine max

<400> 1511

gcttaatggc tcaatgagca aggggaaatg atagtcaatc aacatgtaaa catacccttt 60

tctataggag actactatga tgacgtttta tatgatataa tccttatgga tgcagggaac 120

attttgttgg gtagaccatg gcaatttaac aagaaagaca tccacaatgg tctcaccaat 180

gaaataaccc tcacccatgt aagcaaaaag ctcaaacttg ttcccttgac accttcacaa 240

gtggttgggg atcaagtaca aataaaactc aaatgggatg aggaaaataa taaaataaag 300

actagaagaa caacctttaa tggttaagga ggagtgtaag gaggtaggtg tctcctccaa 360

taggttagct aagaagaaaa gtcattctgc aataaagaca aacattaaag acactttcct 420

tcttagacaa cctccacata ttctcctttg taaaggacac 460

<210> 1512
<211> 379
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1512

agcttctggt gggacatctt gacttgctnt ccaatctgac attcaccaca gattctgcct 60

tcttctattn tcagattgng aatgcctcta acagcacctt tgtcaatgat tntcttcatg 120

cctcttaagt gcagatgtcc aaatctttga tgccatattc tgacttcatc ttctttggag 180

gatagacatg tggaggagta actggtttct tgaggtgtcc ataggtaaca gttgtccttt 240

gatctgctgc ccttcattag aacttcactc ttctcatttg tcaccaagca ttctgacttt 300

gtgaagttta cattgaatcc ttcatcacac agctgactga tgttgatcaa agttgcagtc 360

agtcccttca ccagcagta 379

<210> 1513
<211> 393
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1513

agctaagtct atgatgtact tcccttcggt ctgtatgact atagatatga actgcgacgc 60

tgtcaacttn ttagaatgac aaatcaaggg atacaaatca cttttgcccg tggttattga 120

atatttatct gattttcagt gtccatgccc cctacatctc attttacaga tagtatataa 180

ccttttttttt ttctttttat cacattctgc atatgtacca tagaagatga tttcctgtgt 240

atgatcaacg accctgcaac aatttaaaaa ccccttactg tacttgtttt taaataggag 300

catttaatga ttgctacttt tctactaaca cacttattta aatcagtttt tacaacatga 360

ttaattttaa ataaacttac tgcttcatat cat 393

<210> 1514
<211> 406
<212> DNA
<213> Glycine max

<400> 1514

cgcgactatg aattggaagg ctcttgaggc aattcaccat tgttaactgc ctcacaatag 60

atctgctggc atgaaaaaaa atagagtacg catttcacta ggaaaacttc agcatgcact 120

gcagcattct atagacaaat ctcgtacaaa cgtaagttat taagcttata tatctcacat 180

tgagcattcc ttgactatat gaatgtccaa agagaaaaac atatgccaaa gggtgtatat 240

cattttactc acttcatgtt tgcctgtgtc aatgccattg caagatgcta gaaagaagta 300

cgagttaggg tcccttgcta atgaactctg tattctggat acaggctcag caacagttct 360

gaattccagt gttccaacac cagttgaagc tattaaagga gtaaag 406

<210> 1515
<211> 431
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1515

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tcttctattn tcagattggg aatgcctcta acagcacctt tgtcaatgat tntcttcatg 120

cctcttaagt gcagatgtcc aaatctttga tgccatattc tgacttcatc ttctttggag 180

gatagacatg tggaggagta actggtttct tgaggtgtcc ataggtaaca gntgtccttt 240

gatctgctgc ccttcattag aacttcactc ttctcatttg tcaccaagca ttctgacttt 300

gtgaagttta cattgaatcc ttcatcacac agctgactga tgctgatcaa gtttgcagtc 360

agtcccttca ccagcagtac tttgttcaga ctangaangt catcatgaac tagctttcca 420

tgccaatgat c 431

<210> 1516
<211> 260
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1516

agctnttcaa tcaatctttg gctagctaca ttagtgcaac tacccncatc aataatcaaa 60

gagcatattt tccccatgat catgcaccta gtatgaaaag agttcttcct ttgagtttca 120

tctctatcct ttcatgcact ccccattaac ctcctaacca tcanaagatt accttccagg 180

ggttgtgcat cacattcact ttcactctca ctagaagaac tagaagagct agaagaagat 240

gcactagtga tatccccatt 260

<210> 1517
<211> 346
<212> DNA
<213> Glycine max

<400> 1517

agcttctatg ttcaatatcg agcgtttcaa ttaattatgt gcctgaatcg gacatccgag 60

tgaaaagtta cgaccatctg aatttcttga gaacttctat ttttcaagct caagcgcctt 120

tatatatcat gggcctcaat cgtatatcca tctcaaaagt tatggtcgtc tgaattggac 180

aagagctttc gtgttgaatt tcgagcgtct cgatatattg tggacctgaa tcggacatcc 240

gagtaatatt ttatgaccat atgaatttcc ctacaactta cagtattata taaggagcgt 300

ctctgtatat catgggactc aatgcgacat tcatgttaaa agttat 346

<210> 1518
<211> 259
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1518

cccttcaagt aacgaagaat tctttttgca gcttttatat gagaagaggt aggagcctcc 60

gtanagcgac acacaactcc caccgcatat agaatatcgg gccttgtatt ggttagatac 120

cttanactcc ccacaagact cttgaagacc gtggagtcta ccttctctcc ttcatcanac 180

tttgataact tcaagccacc ttccatatgt gtgttcacgg gattgcaatc aagcatatta 240

aatttcttca acacttctt 259

<210> 1519
<211> 459
<212> DNA
<213> Glycine max

<400> 1519

tgcttctaca acctaagcac acttagtgga gaatcctgga cttgatcttg gattagtggg 60

ctaaaccata gctaaatttc actaatcata attagtgaaa ttttggctcc aaatttggct 120

ccacaaattc aaattcaagt gaaatttgaa tagaaattca aatttccctc caattttgtg 180

tgacacttaa gctataaatg gaggccttgt gtgtgcagtt tttcaacttg atcatttgag 240

aattacactt caaagttcat acctcatttg aggcttgaaa tttcgtgctc cttctctcct 300

tctccctcca ctcatcttct cctaccttca agctcttatc catggcttcc tatggtggtg 360

agcttgttct tgactcatct tctcctttaa agtgacattt ccaatcatct ttcttacttc 420

tccattctgc tgccattgat cttcaagaag taaaggact 459

<210> 1520
<211> 462
<212> DNA
<213> Glycine max

<400> 1520

tacttatctt atagtttagg tgctttatct gttattggtt ctattgcttg atgctttgtc 60

tggtttaata ataccgctta tcctagtgag ttttacgggc ccactgggcc agaagcttct 120

caagctcaag catttacttt tctagttaga gaccaacgtc ttggggctaa tgtaggatct 180

gctcaaggac ctacaggttt aggtaaatat ctaatgcgtt ccccgacagg agaagttatt 240

tttgggggag aaactatgcg cttttgggat ttgcgtgctc cttggttaga acctctaagg 300

ggtccgaatg gtttagactt gagtagactg aaaaaagata tacaatcttg gcaagaacgc 360

cgttctgcgg aatatatgac tcatgctcct ttatgttcct taaattccgt gggtggcgta 420

gctacagaga ttaatgcagg caattatgtt tctactagaa ga 462

<210> 1521
<211> 407
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1521

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aaaaggggggg ttatttagag cacgttcaat ggacaatgga gatggaatag ccgtcggttg 120

gttaggacat cctgtcttta gagataaaga ggggcatgaa ctttntgtac gtcgtatgcc 180

tactttnttt gaaacatttc cggttgtttt ggtagatggg gatggaattg ttagggccga 240

tgttcctttt cgaagggcag aatctaaata tagtgtggaa caagtaggtg taattggtga 300

gttctatggt ggcgagctta atggagtcag ttatagcgat cccgctactg tgaaaaatat 360

gctagacgtg ctcaattggg tgaaattttt gaataaaatc gtgctac 407

<210> 1522
<211> 399
<212> DNA
<213> Glycine max

<400> 1522

agcttgttca tatagtttca acctgaggtt ctttaaagac ttagtaaaaa tatcagccaa 60

gtgctacgag atctatcttt atgtgtttag tatgttcatg gaagactaaa ttagatgcaa 120

tgtgaagaga gcaacttgat tttcacaaat aagcttagtg tcttgagtgt ctccaaactt 180

taattgttgg agaagttgcc taagccatgt aatttcgcat gcaacttctg tcatggtata 240

gtattcaact tcagcgctgg atctcgcaac tatatttttg cttttgcttc tccatgagat 300

caaattccct ccaagcagaa cacaatagcc tgaggtagaa ctcctgtcca atcagcacta 360

gagtaacaaa caattttgac attgtcttcg tcttcatat 399

<210> 1523
<211> 471
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1523

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ctccaatctt taatggagag ggttaccact actggaaaac ccgaatgcaa atttttatcg 120

aggcaataga tctaaatatc tgggaagcca ttgaaatagg gccttatata cccaccacag 180

tagaaagagt ttcaatagat ggtagttcat caagtgaaag cataaccata gaaaaaccta 240

gagatagatg gtctgaagag gatagaaaac gagtacaata caacctaaaa gccaaaaaca 300

taataacatc tgccctagga atggatgaat atttcagagt ttcaaattgc aagagtgcta 360

aggaaatgtg ggacactctt cgattaacac atgaaggaac tacagatgtt aaaagatcta 420

ngataaatgc actaactcat gagtatngaa tatttagaat gaatacaaat g 471

<210> 1524
<211> 459
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1524

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ctattttcag attgggaatg cctctaacag cacctttgtc aatgattttc ttcatgcctc 120

ttaagtgcag atgtccaaat ctttgatgcc atattctgac ttcatcttct ttggaggata 180

gacatgtgga ggagtagctg gtttcttgag gtgtccatag gtagcagttg tcctttgatc 240

tgctgccctt cattagaact tcactcttct catttgtcac caagcattct gactttgtga 300

ggtttacatt gaatccttca tcacacagct gactgatgct gatcaagttt gcagtcagtc 360

ccttcaccac cagtactttg tccagactat gaagttcatc atgaactagc tttcccattc 420

caatgatctn tcctttatag ccatctccaa atgtcacat 459

<210> 1525
<211> 373
<212> DNA
<213> Glycine max

<400> 1525

agcttgtaag gcttggatct tcttcatcaa tagagtcatt tgcttcttga agatcaatgg 60

cagtagaatg gagaaggagg aacggtgatt ggagatgcca ctttgttagt catcttatac 120

gactaacttt tgtatagaaa acttttacaa aatgtatata ttttccccaa tttatggtta 180

tttttgtagg attctaaata aattttgctt tgtttttatc tgtgctcagt agaagccttg 240

tgtatggaat taatgtcaat ttctcttcaa tttcaggcaa aaaggagtta ttttgaagaa 300

gtgctaaagt taatgtctcg ctaagcgagc tcaatgcgct tagcgagtgt catcctctaa 360

ccaagtcatc aat 373

<210> 1526
<211> 418
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1526

agctttgaga aaattgaatt gacaataact ttatacacgg atgtccggtt gagtattgta 60

atatatcgag acgctccaaa ttgaaaacgg aagctcgtaa gaaattcaaa cgacaataac 120

tttttactcc gatgtccgat tgaatcgggt aatatatcga gacgctcaaa attgagacta 180

gaagctctga gcaaattgaa atgacaataa ctttatacac ggatgttcgg ttgagtcccg 240

taatatatcg agacgctcca aattganaac ggaaactctt agaaaattca aacgacaata 300

actttttact cggatgcccg acatagtgtc ataatttatc aagagatgct ccatattgaa 360

tacggaagct cgtatcanat tcaaaccgac aataactctt gactcggatg tatgattg 418

<210> 1527
<211> 394
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1527

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gagaaggagg aaaggtgatt ggagatgcca cttcaaggag aagatgagtc gagaacaagt 120

ttatcaccat atgaagccat agataagagc ttgaagattg gagaaggtga gtggacggag 180

atggagagaa ggggcaaaac atttatgcca aatgaggtct gaactttgaa gtgtaatttc 240

tcaaatgatc aaagttgaaa aaatacacac ataaggcctc tatttataac ctaagtatca 300

cacaaaattg gagggcaatt tgactttcta ttcaaatntc acttgaattt gtggaaccca 360

aattggagcc aaaatttcac taattatgat tagt 394

<210> 1528
<211> 436
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1528

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aactgcttca tatgctaatg taactaggaa tgtggtggtt agattcataa aaaatgagat 120

aatttgcata tatgggttgc ccagcaaaat catcgctaac aatgccatca acctaaataa 180

cacgatgatg aaggagttgt gtgaggattt taagattcaa caccataatt cgacacctta 240

ccaacccaag attatcaatg tagttgaggc caccaataag aatatcaaga agatcattca 300

aaagatgata gtgatgtaca aggactatca taagatgttg tcgttctcat tgcatggnta 360

tcaaacttct gtgtgcactt ttactggggc aaacccaatt tcgttggtgt atgggatgga 420

agctctccac cctttc 436

<210> 1529
<211> 442
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1529

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gagccccatg aattgattgc ctagcgctgt tcgtgcatcc tccatcatca aatcttattc 120

ggaacctgat gagttgattg ccattcatgc atcctccacc attgagtccg gagccttacg 180

aattgactgc caagctctgt ttataaatca tctatcatca aatcttattc gaagccccat 240

gaattgattg ccattcatgc atcctccacc attgagtccg gagcgccccg aattgactgc 300

ctagcgctgt tcgtgcatcc tccagcatct tattcggagc cccaggaatt gattgtcgtt 360

tatgcatcct acaccattga gtccagagcc nncacaattg attgcctagc tatattcgtg 420

catcccacat catcaaatct ta 442

<210> 1530
<211> 445
<212> DNA
<213> Glycine max

<400> 1530

agcttgcaca caagattctc cttggctggc acttcaaaac cttctggttg ggtcttatag 60

atgtcttcct ctaaatcccc atgcaagaat gcagttttaa catctagctg ctccaagtaa 120

agattctctg cagcaacaat actcaaaata actctgatgg tagtcatctt tacaactgga 180

aaggagtctc tgtgatatca attccctgtt tctactgaaa ccctttcacc acaagtctcg 240

ccttgtatct tcttctaccg tcagattctt cctttagcct acagacccac ctattttgta 300

acgctttctt tccttctggc aatttagtta aagaccacgt cttattcttc tgaagggatg 360

tcatcttatc tttcatcgct agcttccact caatagtgtc attcccctgc atagcctcac 420

tgaaacattc tggctcacca acatc 445

<210> 1531
<211> 406
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1531

tccagatata gcatacatag ttagggtatt atgcagatat ttaagcaatc caagaatgga 60

tcattggaaa gaaaccaaaa gagttatgag gtatttgaag agaacaaagt attatatgct 120

cacatacaaa aggtcaggtc agttggagat cactgggtat tctgacttag attntgcaga 180

atacctagat agtttgagat ccacttcagg ttacattttc atgttagtcg gtggtgcggt 240

ttcttggcgc agtgccaggc aaacccttac tacttcatcc actatggcga caaaatatgt 300

ggcatgctat gaggcatcaa atcatggaat atgattgaga aattttgtca caggttntca 360

aattgtggaa tgaattgaaa gaccacttaa gttatattgc gacaat 406

<210> 1532
<211> 383
<212> DNA
<213> Glycine max

<400> 1532

agcttgttgg tgagagcaat gtcaagaatg tcaccaactt cagccctaat agttgggcct 60

ggaaactgac cgttgattcc catcagaacg tgttccaagc aatctggttt tctgatcatg 120

tactccacat caaacttgta gggtctcact attcctccga ttgacaattc taccaaaccc 180

aaccatatta tgcacccaac aaaaagagct ttcaagctca ttcttaatta attttgatca 240

gagaaagcct aattagcaat ataacaggaa ggtatcaagt agtaaaacga agctattgat 300

gaacaaattg aaagaatatg tatagaggat cgaggatttg gattggtggt accattgcct 360

tatatatata agagagagag aga 383

<210> 1533
<211> 345
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1533

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tctgacataa gcttcaacca attaacattg tttgtatgac aactgttgta gttggacagc 120

aatcacacag tttgtccacc atggtatgct ttatgttcct attggttata gttttagtat 180

gctttatgtt cctattggtt atagctttgg tgctggaatg ttcaatttgg agtccacaaa 240

aggaggaact ccatatggtg ttggagttnt tgctggagat ggtacaagac aagcaagtga 300

aatggagctg gagcttgcac agtatcatgg caagtatata tgaaa 345

<210> 1534
<211> 424
<212> DNA
<213> Glycine max

<400> 1534

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ccgtgtctac aacttgcaaa ctaagaaact cgtcatcagt cgagatgttg aagttgatga 120

gtatgcttct tggaattggg atgaagaaaa agtgaagaag aacgttctta tacccgctca 180

actacctcaa gaagaagctg aggaagaaga cccaggtgaa ccaccttcac ctgcaccata 240

acaacaagat caaaaactat catcaccaga gtctactcca agactagtaa gatctttggt 300

ggacatatat gagatcagta acttggccat acttgaactt ggaagctttg aagaagcgtc 360

gaagcatgaa gtatgggtca cggcaatgga agaagagata cagatgatcg atacaacaac 420

acat 424

<210> 1535
<211> 439
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1535

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tgaagtttgt cagaaaggga aacaagtaaa aagttctttt aaagaaaata aatgttattt 120

ccacttcgag gccattaaag cttctacacc ttgacttgct tgaaccaacc aggattgcat 180

ccctttttgg atgcaaatat ggtctggtca taatggaata ttacactaga tggacttggg 240

ttaggttcct aacccacaag aatgagtcct ttgatacctt ntataaatnt tgtaaaaaga 300

ttcaaaataa aaaaggcatt ngtatctctn taatcataag tgatcacagg gaagagtttg 360

aaaatgatat ntttgaatga aaagaatggt attcaccata tattttccac tganagaata 420

ccaaactaga atggagtta 439

<210> 1536
<211> 331
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1536

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cgctcaatac catcaaaatc agcatgttca atagccaata ttcccgcatc agctaagagc 120

tcctctggaa aattgcaaat caactgtctg ttaacaaaac agctgatacc atgacctatt 180

atcttctgca ccttttctct cattatctct ttctctgctg tttcaatttg agcaactcta 240

gccatagaat caacacgaac acgtgcacca tatatcttca ctttgtctgt gtccatggca 300

atgtttgcca ccagtatctt tgcattctct a 331

<210> 1537

<211> 338
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1537

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atatatcgag acgcttgaat ttgaatgccg aagctctgag caaattcaaa cgacaataac 120

tttttagtcg gatgtctgat cgagctccgt actatatcga gacgctcgaa atggaatacc 180

gaagctctga gcaaattcaa acgacaataa ccttttactc ggatgtctga ttgagacccg 240

taatatatcg agacgctcga aatggaattc tgaagctctg agcaaattca aacgacaata 300

acatttacct cagatgtttg attgagctct gaatatat 338

<210> 1538
<211> 432
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1538

ctgtgtatca ttatgggttt agagggccac aaaaagccac caatgaagga agaaatagat 60

actttgattc gaagcatatt tatttattga agataatccg gacaaaacct ttgcactttt 120

cctcaccttt ttaaattaat tactattaga attactattt tttattatct aatattatac 180

gagattacga gcttataatt actattggct caaactattg tcaagttatt tttttaatcc 240

acatttgata ttatcttata tatatggntc aactcttaaa aaanaaattg tgtgtactca 300

actcttgcat atagagattt agtatttcac agggaacaan aattctatat taatatagaa 360

atatataaca gaaataaaat atccaaatgt ataaagtagc aatttaatca aatattatca 420

tttcacaaag at 432

<210> 1539
<211> 285
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1539

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ggatccctgt cagatacaat actagaagga attccatgca accttattac ttccttgatg 120

tacaactcca ctagcttctc cattctatac ttcatattca ctgggataaa atgagcagat 180

ttggtgagtc gatctactat aacccacaca gcatcatgtc cacgactagt cttgggttaa 240

ctagatacaa aatccataga tatgctctcc catttccatt ctgga 285

<210> 1540
<211> 220
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1540

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tttctccacc atgtctgaca aaatggccag catgcacctc tgaaatgcgg ctggtgcatt 120

acataaccca aatggcatct gtctataggc aaagacacca aaagggcatg taaaggccat 180

cttctcccga tccttggggt ccaccgagat ctggttataa 220

<210> 1541
<211> 471
<212> DNA
<213> Glycine max

<400> 1541

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tccgattcag gcgcataaaa tatcgagacg ctcgaaattg aacaacgaat gctcttgaga 120

aattcaaatg gtcataactt gtcacacgga agtccgattc aggcgcataa tatatcgaga 180

agctcgaaat tgaacaacgg aagctcttga gaaactcaaa tggtcataac ttgtcacacg 240

gaagtccgat tcaggcgcat aatatattga gatgctcgaa attgaacaac aaatgctctc 300

gagaaattca aatggtcata acttgtcaca cggaagtccg attcaggcgc ataacatatc 360

gagacgctcg aatatgaaca accaaagctc tcgagaaatt caaatggtca taacttatca 420

cacggacgtc cgattcaggc gcataatata tcgagacgct cgaaattgaa c 471

<210> 1542
<211> 384
<212> DNA

<213> Glycine max

<400> 1542

agcttctcga tatattatgc gcctcaatcg taccttcgtg tgttaagtta tgaccatttg 60

agttctggcg tgcttccgtt tttcaatttc aagcttctcg atatattatg cgcctgaatc 120

ggacttccgt ttgaaaagtt aggaccattt gaatttctag agagcatttg ttgttcaatt 180

tcgagcgtgt cgatgtatta tgcgcctgaa tcggacttcc gtgtgacacg ttatgaccat 240

atgaatttct agagagcttt cgctgttcaa tttcgagcat ctagatatat tatacgcctg 300

aatcggactt ccgtgtgacg agttataacc atttgaatct ctcgagagca tccgtgtttc 360

atttcaacct tcttgatata ttat 384

<210> 1543
<211> 385
<212> DNA
<213> Glycine max

<400> 1543

aaattggtcc aaaacaaaac gtgagcccca tagacagcat ccaatagatg tcataccttt 60

tctgttacat atcgtggtag tgcaattgat gccagattgc acacagcagt ctcagttgga 120

cttgaatatt caattatctc agtacacaaa gctgacgatt taattggacc caaattctgg 180

tgattgcttt tcctattgca agtatgctag tagttgtaac aaaaatgctg gaattactca 240

tcgggtgaga acaataaata caaaatctca tgaggaaagt caaagacatc taagaacacc 300

accttataaa gcatgtacgg gggtgcggct tctatctgtg acttcagaat ttcgaaccag 360

aggctctgtg cctggacaac cttca 385

<210> 1544
<211> 465
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1544

ctaagctatg cacccctntn ttcaatatta atcaacctga aatcacacac aatcacaagc 60

aatcaactac actcaatgca aagaaaacaa aattaaaaat aaatgactgg gtttcctccc 120

agcaagcact tgtttaacgt cattagcttg acgcatcgct ctgttatcct agatcaatct 180

tggttctctc tttcagaacc ttctcatcca actccttcac ctgtaagcac acatcctggt 240

ccagcagttc tcttccttca ttaaatagat caaagctgat ttgttggttt tcaagactca 300

tttctaactt tttcttccct atgtccacca cacagcttgc aatagacata aatggacgtt 360

ccataatgac aggaatattt gcatcttcct caatgttcat tacaataaaa tcagtaggaa 420

aaataagatg ttntactcga accanaacgt cttcaatcac tccat 465

<210> 1545
<211> 441
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1545

agcttgctaa cccatggaag ctcctaatat ctcccacact tttttaggtg ggccattctt 60

ggatggcctt gattttctca gggtccactt ggaccccatt tctaccaact acaaacccta 120

agaaaactat attatctaca caaaaagtac acttctctat atttgcatag agggtgtttt 180

tcctaaggac tgaaagaact tgcctgagat gtcctaagtg atcatctagg ctcctactgt 240

atactaaaat atcatcaaaa taaacaacta caaatatacc tatgaaatcc cttaagacat 300

gatgcataag cctcataaag gtgcttggtg cattagtgag cccaaaaggc atcactagcc 360

attcatacaa accaaacttg gtcttgaaag cggttntcca ctcatcaccc tttttcatct 420

tgatgtggtg atacccactt t 441

<210> 1546
<211> 292
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1546

tctatagaaa ggtcattcct aatttctcta caattgcatc acctctcaat gagctagtga 60

agaagaatgt ggcatttacc tggggtgaaa aacaagagca agcctttgct ttgctcaaag 120

aaaagcttac taaggcacct gttctagctc ttcctgactt ttctaaaact tttgagctag 180

aatgtgatgc ctctggagtg ggagttggag ctgttttgtt gcaaggtggg caccctattg 240

cttattttag tgaanaactt catggtgcca cccttaacta ccccacctat ga 292

<210> 1547
<211> 452
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1547

tcaattataa gaacttgagg agatatgctt agaagcctat gagaactcca agatttacaa 60

ggagaaactg aagaggtttc atgactctaa gattcttaag aaggagatcc atattggcca 120

aaaagtgatc ttgtataact ctcgcttcaa gcttaatttt ggtaaacttc gatctatatg 180

ggatggacct ttttttatta ctaatgttnt ccccatggca caattgagat taaaaatgaa 240

gttattagca aagtcttcaa agtgaacggt caccaactca agctttttca tgagagcccc 300

aagtggtgga gcagtttgtg gcggacctct ctttgatctt gccaacttta tgtgatgatg 360

tcccttgaat ggaactngan gagtttccat ccccttcttt tgtatgttgt cacttttgtt 420

gcctttcatt gcatgctcac attgagaaca at 452

<210> 1548
<211> 455
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1548

ntgatgatgt tgagaagaaa tcacatgttt gtcatcatca ttaagggaga gaatgtgaat 60

gtatgtacac atgattttga tgatgtcaaa agaagaatca aacaaggctc atttgcatca 120

agattaatac aagattgttt caacaaacaa agccttgatt caagatttct tcaagatcaa 180

gccttgcctc aaaatgaaag atttcaagtc atccaaggca catgtaatcg attaccaaga 240

cacatgtagt cgattaccaa tggtttgaaa gtgtgtaatc gattacacat catatgtaat 300

cgattaccag agactttgaa cgttgggaat tcaaatatta aatgaagagt cacaattgtt 360

caagaaaaat aactgtgtaa tcgattacac taatgttgta atcaattacc agagagggat 420

ttcaaggaat atcgccaaca atcacatctt atcat 455

<210> 1549
<211> 450

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1549

agctntaaac ttcattgcat ccagccactt tctcttttct tcattatcca tggcctctct 60

aaatcactca ggttctccat catctgttag gatcacatac tcattaggag aatacctctt 120

agaaggttgt ctctccctgt tggactttct gagttgaact tgaggtggtt cggtggcatc 180

accaagattt tcatcttgtg acatgtcatg ctcctcttca tcatcatcat caacatgaac 240

atctacctca tctccaggtt gttggacact aacatcattc ttaactttag tattcagatt 300

ctgaataggc gattgaactg gttgaaaatc agccacacca ttgtcttcct tgggtgtaaa 360

cttatccacc ttatcaatgt cttcaatggt ttggtcttcc atgaatttca catcatggct 420

tctaacaagc ttcttctcaa taggatcata 450

<210> 1550
<211> 362
<212> DNA
<213> Glycine max

<400> 1550

atgagccaat tcaaacgaca ataacttttt actcggatat ctgattgagt cccgtaatat 60

atcgagaccc tcgaaattga atgttgaagc tcttagcaaa ttcaaacgtc aataagtatt 120

tactcggatg tctgattgtg tcccgtcata tatcgagaca ctcgaaattg aatgttgaag 180

ctctgagcca attcagacga caataacttt ttactcggat gtctgattga gtcccgtaat 240

atatcgagac actcgaaatt gaatgttgaa cctctgagcc aattgaaacg acaataactt 300

tttactccga tgtctgattg agtcccgtca tatattgaga cgctcgaaat tgaatgttga 360

gc 362

<210> 1551
<211> 412
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1551

agcttanaca ttcaatttct aggctctcga tatattacgg gacttaatca agcatccaag 60

aaaaaattta ttgtcgtttg aatttgctca gagattcaac attcaatttc gagcgtctcg 120

atatattacg ggactcaatc agacatccga gtaaaaagtt attgtcgttt gaattggctc 180

cgagcttcaa cattcaattt cgagcgtctc gatatgttac gagactcaat cagacatccg 240

agtaaaaagc tattgtcgtt tgaatttgct cagagattca acattgaatt tcgagggtct 300

cgatatctta cgggactcaa tcagacatcc gagtgaatag ttattgtcgt ttgaattggc 360

tcagagcttc aacattcaag ttcgagggtc tcgatatatt acgggactca at 412

<210> 1552
<211> 429
<212> DNA
<213> Glycine max

<400> 1552

tgagattgaa caacagaagc tctcgatata ttcaaatggt cataacttgt cacacgaagt 60

ccgattcagg cgcataatat atcgagaagc ttgaaattga acaacagaag ctctcgagaa 120

attcaaatgg tcataacttg tcacacggaa gtccgattca ggcgcataat atatcgagac 180

gctcgaaatt gaacaacgga tgcactcaag aaattcaaat ggtcataact tatcacacgg 240

aagttcgatt cagacgcata atatatcgag aagctcgaaa ttgaacaacg gaagctgtcg 300

ataaattcaa atggtcataa cttatcacac ggaagtccga ttcaggtgca taatatatcg 360

agaagcttgg aattgaacaa cggaagccgt cgagaaattc aaatggtcat aacttatgac 420

acagatgtc 429

<210> 1553
<211> 396
<212> DNA
<213> Glycine max

<400> 1553

agcttgaaat tgaacaactt aagctctcga tatactcaaa tggtcataac ttatcacacg 60

aacgtccgat tcacgcgcat aatatatcga gacactccaa attgaacaac gtagggtctt 120

gagaaattca aatgttcata acttgtcaca cgaaagttca attcaggcac ataatacatc 180

gagaagctca aaattgagca acgaatgctc tcgtgaaatt cacatggtca taacttgtca 240

cacggaagtc tgattcatgc gcataatata tcgagacgct cgaaattgaa caaccaaagc 300

tctcgagata ttcaaatggt cataacgtgt tacacggaag tccgattctg ggccataata 360

tatcgagaag ctgaaattga caacgacgct ctctag 396

<210> 1554
<211> 377
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1554

agcttagcag ncacttgttg tcctccatcg ttatcctgat caccgtgaaa gtcctcaaca 60

accactctgt catgcacctt atacagagca tcctgagccg gagacacata attgcctcca 120

ccctcaacag cattagtctc atcactgaga ccataaatag taacaacgcg ctcttcgcac 180

cccggcacag tctcaccaat cctaatctta gccttagtct ccaccctcag ttgcttaaca 240

atctcacctc ccctaccaat aacactgcca atctttcgac ccgggcacac ataacgatac 300

acggtatcct ccgaatcaat cacaaactgc tctctatcat caccatgatt cctcctttta 360

attggcccat tatcatg 377

<210> 1555
<211> 378
<212> DNA
<213> Glycine max

<400> 1555

agctttggcc aaaccccagc agcagttgtt tccttagaga cttgccttag caccttgtct 60

ttgagactga ggataattac actgtgtgcc ttttgcagta gtgctttctt atccccatca 120

gccatcatct tttcaagttt ggcttctcca tcaagtgctt ccaccaggcc ctgctgaaca 180

agaagagctc tcatcttcaa tcgccataac ccaaaatcat tttgccctgt gaatttttca 240

acctcatact tggccgagtc catttcttga atcgaactca aaaatcgctc cacgctcacc 300

gcaccaattt gttgtgccaa gatcagattt tagttcacaa aagaatgagt ttcttgtatg 360

aacaagaata agcaaaat 378

<210> 1556
<211> 449
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 1556

tgcacacaag caagtcccat ttgattaaga tcagtaccaa atattgcaga tttcttctcc 60

ccagtagcac gaagcttcga cacagcattc ttgaaagtat tgtaagattc agtgtagttc 120

tccaacacgt agtacatgac tcccatctga gcttcaatac cagctattgt gttttgctga 180

ccagaggctt cattaagtat ctctagtgcc ttgtgaagta acttaagtgc ctgttctagc 240

tcattcattg actcataaat ggctgagaca ttcataaaac cactagcaac ctcctctgga 300

gggaccccag gcatgggatt ctcatagatn ntaagtgcac tctcacaata tgattttgat 360

tcccttatct tccatgtcct gcaatacaag tcagcaaggc gtacaaagac tgatcccaca 420

gaaggatgat tctcaccttt gtgagtcct 449

<210> 1557
<211> 432
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1557

agcttttgcc tcanaacgca ttgtttccaa catccaaggc tctggtaatc gattaccaga 60

agagaatttt gaagcaaagg gtttaaaaag ggttttgaat ttgaattttg agtcatgtaa 120

tcgattacta gatgtttata atcgattacc agtaatgaca ctttagaaaa cactttggaa 180

agacatgacc cttcaaaata taattgtgta attgattacc agaaatctgt aatcgattac 240

cagtgaataa ttttagaaaa atctttttga aaagacacat ctcttcaaac cattttgaaa 300

aggcacgaag ggcctatata tatgtgtgtc tgacttagaa aagcaagaga gagatattct 360

aagagaacat aattgccaaa ttctctctca acaactcctg ggcaaacact tganaatcta 420

ttgataattc at 432

<210> 1558
<211> 354
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1558

agcttacagc tttgtcgagc tattctgcta ttgcacagat atgtatatct atatccaaac 60

gcgatatata ggaacatgaa atacaactta gcaggattaa cttaagtata ataacatgtt 120

cttttacttt tatataatta gaaattattt tgtacatcga ttaataatta cttataaata 180

cagataaaat ataccaaaat atagatttga aaagcatttt aagaaaatac tagcttattt 240

actaaacata tgtgagaaga tccataatta catgagaaga gtatttntca ctctcaagaa 300

catgaagaga cggacttatt aaatagataa acaagtttta atatatctat gttg 354

<210> 1559
<211> 461
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1559

gactcttcgg ctggccgatt gctgaatcat aatcagctgc cggaataagt aggcaccacc 60

attcaatacc attatagaga atcaaataat atatatatca tcagaataaa attaaatatt 120

ttttattgat aggaattgta tatgagtatt aagaaattta taagacttcc gcaccatact 180

taactaagtt ataagaaaac ctattggatg ctttttttt ggtgatagga aatctgatgt 240

tgaagtttag atgaaaaaaa gtaaaacttt ctcatattat cggctaggaa atttaatggt 300

ttaaattgta ataaatgacg acatacaaga acataaataa taaaaaacat tgcaaaaatt 360

atatcatacg ctgagataat taaatntgtt gagataacta atanaacata gattattcca 420

aaatacacac attgctaaga atattatatg ctaatagaaa a 461

<210> 1560
<211> 345
<212> DNA
<213> Glycine max

<400> 1560

agctttcgtt ttcaattacg agcgactcga tatcctacgg gactcaatcg gacatccgag 60

tgaaaagtta ttgtcgtttg aatttactca gagcttccgt tttaaattac gagcgtctcg 120

atattctacg ggacacaatc ggacattcga gtcaaaagtt attgtcgttt gaatttgctt 180

agagctttag ttctcatttt cgagcgtctt gatatattac agggctcgat cagacatccg 240

agttaaaagc tattgctgtt agagttttct cagagcattt ggtttgaatt acgagcgcct 300

cgatatccta cgggacacaa tcggacatcc gagataaatg tattg 345

<210> 1561
<211> 394
<212> DNA
<213> Glycine max

<400> 1561

tggatttcct gttgtatgga atctttcctt cctaagatgg agccaaaccc agtccccctc 60

attaagaact agctcatttc ttcctctatt gcccttaatt gaatacacct ttgtttggtt 120

ctctatttgg gtcttaaccc tctcatgcaa cttctttaca aactctgacc tagattcccc 180

ttctttatgt ataaaagaag tgtcaagtgg gaggggaatg atgtctaagg gtgttaaggg 240

attgaaccca tagacaacct caaaagggga ttgcttggtg gttctatgaa cccctctatt 300

gaggcaaatt ctacatgagg aagatactca tcccaagact tatggttgcc ttttagaaga 360

gcccttataa gagtggatga agacctattc acta 394

<210> 1562
<211> 352
<212> DNA
<213> Glycine max

<400> 1562

agctttgaga taattcaaac gacattaaat tttttcttgg atctccgatt gtgtcctgca 60

gtatatcgac atgcttgaaa ttaaaagcag acgctatgag caaaatcaaa cgacaataat 120

ttttaattcg gatgtccgat tgagtcgtgt aatatatcga gacgctcgaa actgaaaaca 180

gaagctctgt gcaaattcaa acgacaataa ctttttactc ggatgttcga ttgtgtcccg 240

tggtatatcg agacgctcgt aactgagaac atatgctcgt agcaaattca aatgacacat 300

aactttaact cagatgccga ttgattcccg taatatatcg agacactcaa aa 352

<210> 1563
<211> 222
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1563

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ggatggcctt gattttctca gggtccactt ggaccccatt tcttccaact acaaaaccta 120

agaagactat attatctaca caaaaggtac acttctctat atttgcatag agggtgtttt 180

tgttggatcg agtggcctca aaataattaa gaaggggggg gg 222

<210> 1564
<211> 436
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1564

tatcttcctt gtgataacaa tatctctaag ggctaccggg tctacaactc gctaactaag 60

aaactcgtca tcagtcgaga tgttgaagtt gatgagtatg cttcttggaa ttgggatgaa 120

gaacaagtga agaagaacgt tcttataccc gctcaactac ctcaagaaga agctgatgaa 180

gaagacccan gtgaaccacc ttcaccttca ccataacaac aagatcaaaa actatcatca 240

ccagagtcta ctccaagaca agtaagatct ttggtggaca tatatgaaat cagtaacttg 300

gccatacttg aactttggaa gcttgaagaa gcgtcaaagc aggaagtatg ggtcaaggca 360

atggaagaag agatacagat gatcgaaaaa aacaacacat gggagttagt aaatcgtccc 420

catgggaaag atgtca 436

<210> 1565
<211> 359
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1565

actcagctta acatcagacc acttgcaggt gctggaacta cttcacatgg acttgatggt 60

gcctatgcaa gttgaaagcc ttggaggaga gaggtatgcc tatgttgttg tggatgattt 120

ctccagatgt acctgagtca actttatcag agagacatca gacacctttg aagtattcta 180

agagttgagt ctaagacttc aaagagagaa agactgtgtc agcaagagaa tcangagtga 240

ccatggcaga gagttcgaat acggcaagtt tactgaattc tgcacatctg aaggcatcac 300

tcatgagttc tctgcagcca tcacaccaca acaaaatggc atagttgata ggaaaaaca 359

<210> 1566
<211> 484
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1566

cctatcagac tcagcttaca catcgatccc tcaactgtag ccttattctt gactatattc 60

ttgaaggagt gtaaaaacct aacattaata tgaataagta tttctttaaa aatgactata 120

tatataatac aatggtgtat aaatgattac tcatttatac ctctcgaaag gatacatcca 180

atgatattgg actggaccac caagtcttgc ctcataaggt aaatgaactg gaaaatgctc 240

cattgaatca aagaagcttg gtgggaaata ttgttctaac ttacacaaca acacaggtat 300

gttattntcc ataactctta gttgttcaac atttaatgtt gtcgaagtta gttctttgaa 360

aaattggcta agttcaacaa gtgacttcca aatagggttt ggtaatgagt caaatgcaat 420

nggaaagcaa ccgtgcatga aaacatgaca ataatgactn ttcattccat tgaagtttcc 480

cttg 484

<210> 1567
<211> 420
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1567

ttgtataaac tcacatgtcg tatcacttct gattttatct tattagaata aattccattn 60

tgtattatat atacgtnttt ctctgaaatt ttaaaagaat aatagtggct gtacattggt 120

agcgataaaa taatgccgat aacaatcata acaaaatgta aaatatacta ctttaaagtc 180

ttacaaaaat aaatgagcaa caaaaacctt atcaactaat taacaatatt aaggacatat 240

ttttttaaaa tattaacaag cttattaaaa atgtagaaat aagcttcatg ataaatcaag 300

attgattcaa gggagtttga tgataacaaa gatgatgaca aacaactcan aagtcaagat 360

cacttcatga taacaaagat gatgacattc aagattaagt tcaagaatga gtcaagaaca 420

<210> 1568
<211> 400

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1568

agctctggta ccgcttgtta aacaagtggc ctcaattatc ttaagaaagg gggttgaatt 60

aaaatacaaa aactatcccc ttaattaaaa atttaacttt tttatattaa aaatgcaacc 120

cttattatga gttactctaa gaacaattca aaacaaactt ctttaaagcg aaatataaac 180

aataataaat aaaagaagtt taagggaaga gagaatacaa actcaatttt tatactgggt 240

cagtcacgcc ctatgcctac gtccagtccc caagcaacat gcttgagatt tccactatct 300

tgtataaagc cttttacaaa gtgtgaacca cacagtagca acccttccct tgtgtcaaat 360

aaccttacaa cttaagagaa cctnggcctt taaacagatc 400

<210> 1569
<211> 382
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1569

gtattataag ttataacctc aaaaaatggg gtatatgtaa catgaattat attctcctgt 60

tctttaaaag cttgaaatca acgtagtaaa taaaatttac ctgaggaatg caaagacttg 120

caatagtgag accagatatt aaatctcctc taaattattt aaggttgtaa cttcttcccc 180

aactaagtat tgggaatatg gcttcaatac cgagcctgat cttccttgat ctanngtgat 240

ctttgaaggg tcttacagga tcatcacaaa agaacgtttc ttttatagtg tcttggaatt 300

cctcgaagag gttctgtctc ggaggaattg ccatttgtgg gcttgtggtg cctgaccaaa 360

tgaagaagat ggcatacttc tg 382

<210> 1570
<211> 424
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1570

cagcttaaga ataatggcct caacaaactt cttattccca aaaggatatt caataaatag 60

gcctcctatg tttaatggag agggttacca ctactggaaa acccgaatgc aaattttcat 120

tgaggcaata gacttaaaca tttgggaagc catagaagtt ggaccttatg tacccaccat 180

ggtggctgga aatacaacaa tagagaaacc tagagaagag tggtttgaag atgaaagaat 240

attagtgcag tacaatttaa aggctaaaaa catcattact tctgccttag gaatggatga 300

aatatttang gtctgaaatt gtaagagtgc caaggatatg tgggatactc tacaagttac 360

acatgatgga acaattgatg ttaaacgatc tangataaat actntaactc atgagtatga 420

atta 424

<210> 1571
<211> 362
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1571

cagctttgga atgcagatta gctctattgg ctctctggtt gcattctttg aaccttngat 60

gtattatctg atatgttatc gaagatattc ttggttacta acttactctc cctttatatc 120

tcaattnttt atgtgtgcac gtgagctgat gagcatgcca atgactgatt actattgttt 180

gaattttact tgattgagat ataggaggtg aagatgtcga ccccggcaag gaagagactg 240

atgagggatt ttaaaagaat gcaacaagat cctcctgctg gcatcagtgg ggctccccaa 300

gacaataata ttatgctttg gaatgctgct atctttgggt gtgtaggagt atataaatca 360

tg 362

<210> 1572
<211> 395
<212> DNA
<213> Glycine max

<400> 1572

tatatatatt ataaataaac atctatcaat caatgtctac aaagtacata tattaatgtc 60

tgaaatcgat cacaaagact aaaattatga attttataaa atagggagac acaatgtctt 120

aattaaaaat gagagactaa aattataaat ctttttaaag tggaagatga aatatctcaa 180

ttaaaaagtg agagaactaa aatcatatat ttgaaaaaat aggggaacaa aaagtatatt 240

ctagtctaat tatctttgtg tatgaatttg gatttgaaat tgtgtataag tgaatataga 300

tttgggttaa tcactttagt gcttgaattt ggatctgggt tagacaatat gtctacgacc 360

atttaattaa acaagttagc aagtaatttt ggatc 395

<210> 1573
<211> 358
<212> DNA
<213> Glycine max

<400> 1573

ctgagaatgc gaatttagct ctattgtctc tctggtgcat ttcttgaacc tttgatgtat 60

tatctgatat ggtatcgaag attttcttga ttactaactt actctccctt tatatctcaa 120

ttctttatgc gtgcacgtga gctgatgaac atgccaatga ctgattacta ttgtttgaat 180

attacttgat tgagatatag gaggtgaaga tgtcgacccc ggtaaagaag agactgatga 240

gggatcttac aagatagcaa caagatcctc ctgctggcat cagtggagct ccccagaaca 300

atgatattat gcttcggaat gctgttatct atgggtgtgt aggagtatat aaatcatg 358

<210> 1574
<211> 305
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1574

agctttcgtt ntcaattacg agcgactcga tatcctacgg gactcattcg gacatctgag 60

tgaaaagtta tcgtcgtttg aatttactca gagcttccgt tttaaattac cagcgtcttg 120

atatactacg ggacacaatc ggacatccga gtcaaaagta attgtcgttc gaatctgctc 180

atagctctcc tcccatttac gagcgccttg atatattaca gggctcgatc ggacatccga 240

gctaaaagtt attgtcgtta gacttatctc agacgctgcg ttcccaattt cgagcgtctc 300

gatat 305

<210> 1575
<211> 328
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1575

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ttagtgccac tctcattttg aactcatcta aaccttgtcc agacttcttt gaaagccttt 120

tcacagctaa cgctttccca tctataagtg tgccctgaaa gttatcttct gccatagtta 180

gaaagattnt aaggaaaaca gaagtttgtg aagttttctt agtcaccttg tataccggcc 240

cacatccacc ttcttcgagc ttatattttg ttgagaagtt tttagtcaca ttagctaaga 300

ctgttggcaa gtcaatgtct tctgttcg 328

<210> 1576
<211> 402
<212> DNA
<213> Glycine max

<400> 1576

agcttgtgct cgaggccttg acctcataat tgtttcatca ctgtgtttga tccattctga 60

gagtttccag ggcttctgcc acttccattt aaactgtagc agccattgat gatgacttct 120

cttccacttc caaagtattc cggcttgtcc tatagctgct agcctcttcg ttgacaactc 180

tccaatgggt atcatctgga tataaaccca ttaaaactta ttgagaaata aacactatca 240

tcatcatcat cagggaaata gaatctagca aacatacctt tcgtgcttca tctaaaaatg 300

tagctgactc cctgcctgac caattaacaa ctccaggagt gaatttgagt tgctttggtg 360

cacgaagcga cattggagat aacggaccac tcatctcatc cg 402

<210> 1577
<211> 330
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1577

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ccaaatcctt caacttctcg tcttccccag ctgcctccat aagtttcaca aaatctatca 120

aactcaaaaa cacatcacca tcagaatcca actcctcaat caactgttca gcatctttgg 180

tcaacaactc accaccaatc atgcctagcc ggttcctaaa ctcacatgga gaaatcttac 240

catccccatc ctcatcanaa tacttaagaa cacgctcaaa ctctgtgttc accctcataa 300

ctatagaaaa tacacgcata aatattgatg 330

<210> 1578
<211> 447
<212> DNA
<213> Glycine max

<400> 1578

ctcagcttaa catcagacca cttcagggtg ctggaactac ttcacatgga cttgatggtg 60

cctatgcaag ttgaaagcct tggaggaaag aggtatgcct atgttgttgt ggatgatttc 120

tccagattta cctgggtcaa ctttatcaga gagaaatcag acacctttga agtattcaaa 180

gagttgagtc taagacttca aagagaaaaa gactgtgtca tcaagagaat taggagtgac 240

catggccgag agtttgaaac ggcaagttac tgaatttgac atctgaggca tcactcatga 300

gttcttgcac catccaccca acaaatggat agtgaaggaa aacggacttg aagaactgca 360

ggcatcttat gccaaaattc ctatatttgc tgagcataca ccatgctttt cacaagccac 420

taagaggctc acccctgtta attgaag 447

<210> 1579
<211> 387
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1579

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tctagagttc catcaccaaa catctgccac cattctccag gttgcataac tnttctagtg 120

tcctttgcct cttccataga caaaaaccct ctagcaaaat caaactcaac aagttgcaaa 180

ataattnttt ttcctttcta caacatcctt gaccaatctt ctcatacaca tgtgcaaccc 240

ttctttcacc tgagggtcat catgtctaan actaggttta taatgcaaat gaggattact 300

ataatacgca gttgtatgca aaggcttgtg aagctaatga tctcacctct cattgataat 360

tntctaaaca ggctcataga tacatca 387

<210> 1580
<211> 394
<212> DNA
<213> Glycine max

<400> 1580

agcttgcaca caagattctg cttggctggc acttcaaaac cttctggttg ggtcttatag 60

atgtcttcct ctaaatcccc atgcaagaat gcagttataa catgtagctg ctccaagaaa 120

agattctctg ccgcaacgat actcaaaata actctgatgg tagtcatctt tacaactgga 180

aaggagtctc tgagatatca attccctgtt tctactgaaa ccctctcacc acaaggctcg 240

ccttgtatct tcttctaccg tcagattctt actttatcct acagacccac ctattttgta 300

acgctatctt tccttctggc aatctattta aagaccacgt cttattcttc tgaagggatg 360

tcatcttatc tttcatcgct agcttccact caat 394

<210> 1581
<211> 354
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1581

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tgggagggga aaacccaact ggccgcatgg ggggtntcag agggatccgt ttcccactcg 120

cattacccgg cgtggaaatc aacggtgacg acacccccaa accaccagcc tggttctgat 180

taagactcaa tccctgagct tgcaaatgag cctggagttg agcatgagct gcagctgctg 240

cttgggcctg ngcctgggcc tgggccttgg actgagcttg gacaatagca tgggcctggg 300

acagtggaaa ctgtccttga taaccaacag gaatctgggc ctgtccttgg gact 354

<210> 1582
<211> 374
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1582

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tggaaggcct ctcatnttgt acatggggtg tatgctgggg caacatgatg aatccggaaa 120

gaaagagcgc gctatttact acctaagtaa gaagttcacg acctgtgaaa tgaattactc 180

cttgctcaaa agaatgtgtt gtgctttagt atgggcatcc catcgcctaa gacagtacat 240

gctgagccat actacctggt tgatatccaa gatggacccg gttaagtaca tctttgaaaa 300

gccagctctc acgggacgaa tcgcccggtg gcatgtcctg ctatccgagt ttgatatagt 360

ctacgtcacc caaa 374

<210> 1583
<211> 454
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1583

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tatggagttg cctcattcga ggtgcgtact aatgcacgat agccatgtgg tgcaaaggga 120

agcatgtcat gtcaatcctt cttgatattc ttgtttgctg cttctaccac cccattcatt 180

ttttggcgat atggcacaga attgcgatgt tgtatcttga agctatcgca caattctttc 240

atcatattgt tggtcaaatg ggtcccatta ttagtaataa tgtggcttgg cagacatatc 300

aatagatcaa atctcctttg atgaatctga ccactacatt ccttggtaca ctatcataag 360

atgctacttc aatccattag tgaaataatc aatgggacta cgatgaaacc atgccctatt 420

caatggctta ggttcaattg acanatcaca tcta 454

<210> 1584
<211> 434
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1584

gtgtgcattg ttngagttta gtattggagt acatttattg aattgcatag ttactttatt 60

atttgtcact ttgaattgaa ttcatagaat gtggattatg tttgttgaca cttgacttat 120

ttgcattaat tttttaatgg attgagtatc ataatatttt acactaaaaa ttatttattt 180

tcaagatcac attctttcta tagaaaatac aaaacataaa taccgaataa ttcatcttat 240

gtgagtcatc ttatgtgagc agacgagaat gctaatctaa agtttgagaa aatgactacc 300

acttattggt ctttcaattc ttataacata tgtgttgatt aataagtaaa tgtgcattat 360

tngagtaaag caagttcttt agtgtgcatt actagactat ntatcacttt gaactaaatt 420

ccatatatta actg 434

<210> 1585
<211> 445
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1585

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aagttgtaaa aattacctaa ataatgctag attaaatgtc attttagttg atcattcata 120

gctgtgtaag tttgatactt taagtttctt gcaatttata agttgtttta agaacttgtg 180

gcatttgccc cttcacatac tgagagaatg actaaagagc ctttctgctc tgccttttct 240

ctttcttaac acaaaatgat gttcaacctt catatacggc aggtttgcaa tcttgtctgg 300

tccaaaaatg tcaatgaact agtaagcacg catggctatt cccagaacca gataattgtt 360

tggagatacc tctccatgtc aaaggtacac tatatctact gtgataagcc gaatctctct 420

tatttttact taattntaac atgtc 445

<210> 1586
<211> 445
<212> DNA
<213> Glycine max

<400> 1586

agcttgcaca caagattctc cttggctggc acttcaaaac cttctggttg ggtcttatag 60

atgtcttcct ctaaatcccc atgcaagaat gcagttttaa catctagctg ctccaagtaa 120

agattctctg cagcaacaat actcaaaata actctgatgg tagtcatctt tacaactgga 180

aaggagtctc tgtgatatca attccctgtt tctactgaaa ccctttcacc acaagtctcg 240

ccttgtatct tcttctaccg tcagattctt cctttagcct acagacccac ctattttgta 300

acgctttctt tccttctggc aatttagtta aagaccacgt cttattcttc tgaagggatg 360

tcatcttatc tttcatcgct agcttccact caatagtgtc attcccctgc atagcctcac 420

tgaaacattc tggctcacca acatc 445

<210> 1587

<211> 439
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1587

ctcagcttgt caagttccat actgcctgca natgtagccc aaggcaagaa cccaacttgt 60

tgcacctttc gcttcctcat tatttcatag aaagctgttc tcatgactga aatactggtt 120

ttttcagctg aggctataac accgtgagca acagctcaaa tcttttcagc agatactgct 180

gccttcatga tgccagatgt tttggctcct gaagtcgcaa tccctggagc cacaacttta 240

taatggccag atgcaaaagc cagcactttc tgcatctggc tgagactgat tatgagtgaa 300

gttggaattt tgaaagtgat aaccttcacc agtgttgatg cagggactac tntggtcaga 360

gatgaagctc caanaactgc tgtcgcccag actctactgc accataggtt atctgtaata 420

accacttttc tcactatga 439

<210> 1588
<211> 400
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1588

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aagctgtgag caaattcaaa cgacaatatt tgtttactcg gatgtctgat tgagtcccgt 120

aatatatcga gacgctcgaa attgaatgtt gaacctctga gccaattcaa acgacaataa 180

ctttttactc ggatgtctga ttgagtcccg caatatatcg agatgcttgg aattgaatgt 240

tgaagctctg agacaattca aacgacaata actctttact cggatgtctg attgagttcc 300

gtaatatatc gagacgctca naatcgaatg ttgaatgtct gagccaatta aacgacaata 360

acttttttact cggatgtcct attcagtgac gtattatatt 400

<210> 1589
<211> 480
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1589

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tggttcctaa gaaggcagac ctcacaatga tcaagaatga gagggatgag cttatcccca 120

caagagtgca gaacagctgg cgagtccgca ttgattatag gaggctgaac caggcaacca 180

gaaaagatca ttgtcccctg ccattcattg atcaaatgct tgagcacttg gcaagtaagt 240

ctcattactg gtttcttgat gggttttctt gttatttaca aattcatatt gctcctgagg 300

atcaagataa taccacattc acctgtccct ttggcacttt tgcctatang agggatgccc 360

ttggcctatg caatgccccc ggtaccttct agcgatgtat gcttagcatt ttcagtgact 420

ttttagagag ttgcatagag gtgttgatgg atgaatctac tggttatgga tcctcttttg 480

<210> 1590
<211> 448
<212> DNA
<213> Glycine max

<400> 1590

agcttagccc atcatcaata ttgatttcaa gaaacaaaaa agcaagtaga tatatcagtg 60

aactgagcca gaccaaggaa aaatacatca aagaaaataa ataatctagt atagctaatt 120

ttataatcag ataaagcatc tgagacctgc tgccatgtgg tatcaacagg aggctgccgc 180

cgagcatcgc cagcatcaaa atccagtaca ccataatccc tcaaccgaat ctacacagca 240

ataactaaaa tcagaagtct ttttgaggat taaatgcatg gcattatcta taagacacat 300

ttttcaaatt gagacaaacc cgaaggaagg cacggattct ttgcaaattc ccaacaccac 360

caccaagagc agcctaccat tagataaaaa agcaagcaga aattaagtgt tgataacaaa 420

tacaaattca tgcttgctct cttatatg 448

<210> 1591
<211> 397
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1591

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ctatctaatt ctcgtttaca taccttgatc tttttacctg gtgctaataa ttatagagta 120

aatagttaat ttaatcctta atttatatca cgttatttta gtctttaaaa ttaaagaaaa 180

cttaaaacaa ttggttgact agtttgactt tttattaatt ttagagactt aaatgacaat 240

aaagtataaa ttcaaagact aattatctaa aaaaaaacta tctatttaat aattacatga 300

agataaagaa gacacatttt caacttttt aaaaaaataa atatacattc tctctctcta 360

tatatactta aaaagtcttt nggcattaaa aatatat 397

<210> 1592
<211> 451
<212> DNA
<213> Glycine max

<400> 1592

agcttgtcat tcattcagga tagaccagtg agcctcacgt tcaaagggaa gctagtattt 60

gaggtgaaca ggtatggctt cactgatggt ggagcttggg ttgatgggaa cctaaactaa 120

tgcaatccta ccccgcaagg gcattggata gaaaactcca agtagattaa gccagagatg 180

caagagaagg ccctaggatt cttatgagcc ttagggtaga tttcgggccc atgggctaag 240

tatgagccca cttatctttg taaatattag attaaggttt cattattttt gggccttgta 300

tttagagctc cataatgtag gtagggtacc ctagaaatat aggatttttc agcccttgta 360

ttctagggca cctagactag tctttgtatt aggggtagtt ttggaatctc acatgcacta 420

agtggatatt tgatgtgtgt ggctggagat a 451

<210> 1593
<211> 458
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1593

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tcagtgaggt gctgcttcaa actctttgtt agctcactag atgattctga gtcacgacca 120

aatggctttt caacaataac ccttgtccat ccatcttttg aagaagcttt aagactagcg 180

catctcacca catccacaaa tatgtttgga ggtattgaca aataaaacaa tctgttngat 240

agctttccac cctagaaaag gccattgtca aatatatcta agcatagttt caagagcaat 300

tattcgtata aatttaattc tgggaaatat aagatgcctt aaattttatg attgataata 360

tcacccttt gtagcactac ggttttaatt ntcaaatcac catctgctct aaaggttttt 420

gcactctatt ctacacagaa gaaagatctc ctaaactt 458

<210> 1594
<211> 482
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1594

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ccaagagatg gttgcattca ttctagggca acagtttaaa gactagggat aaggttgttg 120

agaagtttct aaaaaaatat ttcccagagt ctaaaactgc aaagggaaaa gctgcaattt 180

cttcattcca ttagtttccc gatgaatctt tgagtgaggc attaganaga ttccatagct 240

tgctgcggaa aactcccact catggttttt cagagcctat acagctgaac atcttcattg 300

atgggttacg accgctgtca aagcagttac tcgacgcttc tgcaggagga aaaattaagt 360

tgaagacacc tgaagaagcc attgacttaa ttgaaaatat ggtttctagt gaaccacaca 420

atttgcatga gagagttcat attcctacca ataagagntt attggagcat tcattacaag 480

at 482

<210> 1595
<211> 450
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1595

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tggaaggcct ctcattttgt acatgacaat cttggacgag tcaatggggt gtatgctggg 120

gcaacatgac gaatccggaa agaaagagcg cgatgtttac tacctaagta agaagttcac 180

gacctgtgaa atgaattact ccttgctcga aagaacgtgt tgtgctttag tatggacatc 240

ccatcgccta agacagtaca tgctgagcca tactacctgg ttgatatcca agatggaccc 300

ggttaagtac atctttgaaa agccagctct cacgggacga atcgcccggt ggcaagtctt 360

gctatccgag tttgatatag tttacgtcac ccanaaggcg ataaaaggaa gcgccttagc 420

agattatntg gctcaatagc ctcttaacga 450

<210> 1596
<211> 455
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1596

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ttaaaagatg atggttggca agctctgctg aaagatgtgg tattgttttg tgagcaacat 120

gacatttata ttcctgattt caatggtacc tatgtagcac atcatgggcg ctctcgatat 180

caaaaagatc atatcacaat agaacatcat ttcagagtga acacaatttt tattgcagtt 240

gataagcaat tgcaggagtt aaatgctatg tttagtgagc aaacaatgga agttttaact 300

ntaatctgtg ttntagttcc taagatattt ttatacaact tttcaatgtt gatgatatat 360

gcactattgt gaacaaattt tatcctttaa ttttagtaaa cacgagaaga tagttagaaa 420

tttaacttca cttttatttt gggtgctcta ctcat 455

<210> 1597
<211> 259
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1597

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taactnttaa ctcggatgtc caattcatgc gcatcacata tagagacgct aaaaaatgaa 120

caacggaagc tctccagaag ttaaaatggt cataagtttt cacaaagatg tccgattcag 180

gcttgtatta tatcgagacg cttcaaatta aacatcgaaa gctctcgaga aattcaatgg 240

gcataacttt tacttggat 259

<210> 1598
<211> 319
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 1598

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ggagaataat tctaggattt tagaattcca gtttttatta ctgttcatgc acactgtcca 120

cgtataataa aatccattnt ctgcaaatga tctctaatcc atacattttt taatactatg 180

gactttcttt attttctttt gatatactct gtgctttaac gacttaaagt caatatgaat 240

ttgcttatca attatttttg gatttgtaca ttacttatac gaaattttat aagtatcttg 300

ttctagttag tatttcact 319

<210> 1599
<211> 269
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1599

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gtgaagttgc taaatacaac gcatgattag tggccaaagg gttactgcaa aaatatgttc 120

tggattacca tgaagtcttt gttctagttg caagaattga actaattaaa cttatggttg 180

caatcgctag ctaacggggc tggtcattgg atcaactaaa tgtgaaatta tcattctttt 240

atgggccctt ataaaaagtc tatgtatat 269

<210> 1600
<211> 578
<212> DNA
<213> Glycine max

<400> 1600

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ataagaaaga taggcaggaa aattccaagc atgcaaaggc tttaatgatg acgaaggtag 180

atcaatgtaa tgtggctcta atgggagtta aaatcatggc agatcaaagt ctcgaagaag 240

aaagaacctc aaatactata attgtggcag gagatgacac ttaaagaaag attgttggca 300

taaaaagagt ggaggagata aactatagag aatcgagctc tcaaggttgt gttgctagca 360

cctcaaataa tatggaagcc atgtgtagtg aaacaccaat tggttttaga ggtggaagac 420

aacttcatga ttgttggata ttagatttag gtgcagcttg gcacatgact ccatgttgag 480

attgttttta cacttatgaa cttatcttgg aaggatatgt gttcatggaa aatgatcatg 540

cccttggaat tgctggggtt ggtactggtc aaataaaa 578

<210> 1601
<211> 483
<212> DNA
<213> Glycine max

<400> 1601

agctttgact tgagtcatca agagactata aatatgtgac catggcatga gtttcaaaaa 60

aaaaaaaaac aatcaatcat ctttgaatca tctatctttt acatcatctt ctttcaacat 120

ccttcaatca atctttcaac atctcttaat attttctttt atctctttca acactttcaa 180

cagaactttc taattgattt ctcttcatct ttctaaaagt ttttggtcaa cactgtccct 240

tccaagaaaa gttctttgat aaaaaactta tgttattcat cttgatgtaa gctccatttg 300

agcttgtagg cccaggatct tcttcataaa tggattcctt tgcttcttgg tagatgaatg 360

gcagcaaaat ggagaaggaa gggagagagg agacgccact tcaaggagaa gatgagtcta 420

gaagaagctc accaccatag gaggccatgg ataagagctt ggaggaagaa agagatgaat 480

gaa 483

<210> 1602
<211> 405
<212> DNA
<213> Glycine max

<400> 1602

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atacatcgaa acgctcgaaa ttgaaaacag aagctctgtg caaattcaaa cgacaataca 120

ttttaactcg gatgtccgat tgagtcccgt aatatatcaa gacactcgaa attgagaata 180

aaagctctga acaaattcaa acgacaataa ctttttactc ggatgtccga ttgagtccag 240

taatatatct agacactcga aattgagaat agaagagctg agcaaattca aacgacaata 300

acttttttact cggatgtccg atggagtccc gagcgtttcg atatattatg cgcctaaatt 360

ggacatccgg agttataggt atgacaattt taattgctcc aaagc 405

<210> 1603
<211> 562
<212> DNA
<213> Glycine max

<400> 1603

agctttagtc aaacagaata atccgaaaat gtcaaagaat tgggtgttga aaaagcataa 60

caacactttc tgtgattggt ttaaagatac aatctttgca gatgagaatg cttcaaaaag 120

attaagaaag ctagcagatg ggcctaaaag aaatgttata atctggcaag gatacgacat 180

aaacaggtat tcattttaca caaaagcaca agatgacaaa agtacaatgc agaacagcgg 240

ggtcacccta agggctgaat ctcaacactt tgcaagtgtc aatgatgcca atccctatgt 300

agcttccatc cattactttg ggttcattga tgaaattcgg gagcttaatt atgtgaaatt 360

tacagtatgt gttttcaaat gtaaatgggt tgacagcaac accggtgtgc acaccgatga 420

tataggattt acgctggtag atctaaagaa acttggttac cacaatgacc ctttcatcat 480

ggcaaaacaa gcttgacaag tattttacgt gcaagaccct tgtgatgaaa ggtggtgcgt 540

ggttctacaa ggcaaaacag tt 562

<210> 1604
<211> 581
<212> DNA
<213> Glycine max

<400> 1604

agcttattga acgtgatgat gtgctatcct gtttgtagag taatacttag caaactcttg 60

attattcata tttttttag cttgaaggct atagagaaag ccatagttag ctctgatctt 120

ggtatgactc caaataatga tggagaattg atacgactga gcatcccaca gttgacatct 180

gataggagga aggtattctc cagttccatt gatgctgcag tgtctaagtt tatttttct 240

ctgtcaatta cattcttgtt ctcattgact gaaagtaata ttcttaattg gttttcattt 300

cttatttaac tattaacaaa atcgcataga atcacctctt ctacagtcat gacccatgag 360

aaaactgatc tctacagtga cttaatatgt tgtttgccat gattccaata gttttagtta 420

tcaatttatt ttgtttatga gattgtaccg ttttatataa aggtcctata tgcataaatt 480

ttaatgaata tttgaaggtc taaatgaata tgttgatttc ttgaaggcat ctgaataact 540

taaggtctgt ttggtttttt tccccaaaga aaagtgtttt t 581

<210> 1605
<211> 489
<212> DNA
<213> Glycine max

<400> 1605

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atagtttcaa tatttttcat atgtaatcct ttatgtagat gttggggtga atgcacacta 120

agatggaaga gactcgctaa tatgcccaac gttcctactg caatataatg agaagctata 180

ctgaaacaaa aagataaaaa ccttccacgc ctcacacaga tttactgatt gtatccttct 240

ggtcaatcca taaggatcca ctactacaaa agcaattatt taagtcacga gacctacgac 300

ggttgtgcaa aaccgcctta atataaggca cagtggcaat tttgtaatta aggggagaaa 360

ttttattttt taagtcgcac gttctaaggc ggttacgaat aaccgactta gaatgagttg 420

ttattgtaag acaacgacgg tcttacggta agcccgtcgt tgttcctcac ctggcccgta 480

cttgacttt 489

<210> 1606
<211> 177
<212> DNA
<213> Glycine max

<400> 1606

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atctagcaac tgcattttac ttcttgcttc tccatgaaat caagtcacct ccaacaagaa 120

cacattagcc agaggtagat cttttatctg atgatgatcc tgcccaatta gcattag 177

<210> 1607
<211> 552
<212> DNA
<213> Glycine max

<400> 1607

agcttgtggt gtctcagcat tataatagtc tttcttttga cactttatat gagttggcca 60

agtgtttgaa cactgatatg gtgcctctga tagttaactg gctaccaaaa gttcttgctt 120

ttgctcttca tcaaactgat gaccagcagt taatttttgc cgtgcagttt taccatgcac 180

agactggttc tgacaagcag gaaatatttg cggctgcttt acctgctctt ctagatgaac 240

ttgtatgctt tacagattgt ggggattcag aagagataaa tagaaggtaa tttgtgtaga 300

tttctggaac ttgattttaa tttgattcct gagtggaaaa ctttcacacc tggatattaa 360

tttttggaat tcacgtgttt gtcttggaaa ctatgttgct ggcacctcag atttagctat 420

attaatgatt atatacgtaa tttgttttta tttattcact catcattgat taacagaatt 480

tgatttggtt actggccatt ggataaccaa tatatttgaa tctcacattt ctttctttca 540

tgggacttgt at 552

<210> 1608
<211> 493
<212> DNA
<213> Glycine max

<400> 1608

agcttccatt accgcaacca tctatctagg tttgtaagtt aataggaatt ttatttggat 60

tctaagtttg ttgttccata aattactatt attgttcata aaaaatatgt gcattgtgag 120

tgaaccctaa tttcccgttt gagattccat accatgatta atacggatag tttggattag 180

ttgtggtatg gattcttgaa ttgtccgttc ggacagtttg ggaactctct ttttttttact 240

tcattcatag tgttagtgtt tagctctact gagctttaaa agattggcta agattttgtt 300

aaaacataag cacttagaca atgaaggaaa gctggagttg ctgcacatga tgtccaacgt 360

tatgtcaagg aatgagatcg ggctgcacaa tgtacaaggc aagataaaat gtcaaatgaa 420

gaattgaagt tgcacgatcc acgatgtcgg ataacatgtc ctgacatcct gccccgagaa 480

tactggagtt gct 493

<210> 1609
<211> 561
<212> DNA
<213> Glycine max

<400> 1609

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ttgtaggtgc cataaaatgc gaaaaataat ccagacaata atacaataga atccaaggct 120

ttttgccaga tgggtagaga agagccaaat aactttaagt gaaatgtggc tggcataaca 180

aatgagagca ttgcacataa ggtgctccct acaaatgagg caaatacaga aaattctggc 240

acaaatgaag ctatgactgc caatccaacc accacaatcg cccggctaac gtatatgcac 300

atattttcta gtcccattga atcattattg tttctgagga tgattttgag tttcccttcc 360

acaatctcat taattgggtg aaacatgact gggagtgtga atgcaagccc cacacataat 420

cctacctgtc aaatgtagca aaaacttgaa gataatggaa ttctggcaaa ataaacgtag 480

tattctgcaa agtgtactat cctagtagac atggctaagg acaaagtaaa atacacccca 540

acatatatta tgcagtgcac a 561

<210> 1610
<211> 545
<212> DNA
<213> Glycine max

<400> 1610

agcttgtcaa aaagggaagc aagttagaaa ctcttttcaa agcaagaaca ttgtttctac 60

ttcgaaaccc cttgaactac ttcacactga tttatttggt ccctctaaaa ctatgagttt 120

gggttgtaat tactatggct tagttatagt agatgattac tcaacgttca catggacttt 180

gtttttgaaa acaaaaaatg aagcttttga tgcttttcgc aaacttgcca aggtgattca 240

aaatgaaata ggtcttaaca ttgtttcact tagaagtgat catgaaggtg aatttcaaaa 300

tgagtctttt gaaatatttt gtgaagaaaa tggaatttac cacaattttt ctgccccaag 360

aacaccccaa caaaatggtg ttgtggagag gagaaatata tcccttgaag aaggtgccag 420

aacccttcta aatgaaacaa agttacccta gtacttttgg gctgatgctg tacatactat 480

ttggtacacc ttgaacagag tacttattag acctattttg gagaaaactc cttatgaatt 540

gtata 545

<210> 1611
<211> 496
<212> DNA
<213> Glycine max

<400> 1611

cttaaaggaa gtgaacaaat agtatttgtc taaatgtctc tgattgatcg gcatatctgg 60

tccccaaatc ttggaaaact gccaagaccc cggtaccttc agcatacctt gtattatagg 120

gaacaggaag tttgacaatg ccatgctaaa tttaggagct tctgttaata ttatgcctct 180

ggctattttt aattctctat ctctaagtcc tctgcagtca actgatgggg ggattcattt 240

agctaataga agtgccgcct atcctgctgg ttgtaaaaaa gatgtcttat ttagagatgg 300

tgagctgatt ctgcctcttg aattttatat tctgaatatg gaggagggat tttttaaagg 360

atcagttcct atcattctaa gcagaccttt tattaaaact gctacaacta agatcgacgt 420

atatgcccgc acactatcta tggagtttgg tgatacaact gttcatttaa tattcttgat 480

gctatgaaac acccat 496

<210> 1612
<211> 451
<212> DNA
<213> Glycine max

<400> 1612

agcttgacat aatgaaatcg ctttttactt ttttatataa aattacacta aaaataaaat 60

atatttatta atgtatactt atttgctgtt gaaaaagagt attttagctt attataactt 120

taatttttt aaatatacca tataaaacat gtgtgtatat attaatatac tctataaata 180

ttcgctgatt tatttttaa aagaaaattt taaaaaggta taatttcatt tttttaaata 240

cattcaaaat gtaaattgtt caaattttcc ttcttttata aaacgagtac atgtgcatta 300

cctaatctca ataaaaaaat aatatttctt tatttaataa ataagaaaga ctaataagag 360

aataccaaag caaaaattag atttttttttc aattggaatt tgttattcga aatgagaatc 420

ttctaccaaa agatacactt ttttggtact t 451

<210> 1613
<211> 369
<212> DNA
<213> Glycine max

<400> 1613

agcttacgtt gttcaatttc gaccatcttg ttttattatg cgcctgaatc tgacatccga 60

gttaaaagtt atgaccattt caatttcacg agcgcttaca ttgctcaatt tctagcggct 120

ctatatatta tgcgcctgaa tctgacatgc gagtttaaag ttatgaccat ttgaatttct 180

cgagagattc cgatattcaa tttcgagcgt ttctatatat tatgcgcctg aatctgacca 240

tggagtgaaa acttatgacc atttgaattt ctcgagagaa tccgttgatc aattacgagc 300

atctcgatat attatgcgcc tgaatcgaac ctccgagttt gaagtgatga ccatttgaat 360

ctctcaaga 369

<210> 1614
<211> 578
<212> DNA
<213> Glycine max

<400> 1614

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gcgcaaaatc tcttgaacta ggaagatgtt gtccatcatc tttctgttct taatgaaagc 120

agtttgagtt tccccaataa tagtctcaag cactggggct atgcggttgg ccagaatttt 180

agatacaatc ttgtataaca aattacagca agatatgggt ctaaaatggt taacctggga 240

ggcctgatca tgcttaggaa taagcgcaat aatagcatgg ttgagttgct ttagaatttt 300

tccagttgta aagaattcat taaccgctgc aaagatatca tcaccaatga tattccaagc 360

cttcttgaag aataaaacat tgaaaccatc tggcccagga gctttattat tatccatcac 420

agaaataacg ttccaaacct cttgcttata agtaggacaa agtaaggcca caaagcaatc 480

gatgggaacc ttatgacccc tgttgcagat caaaatggat ggagtttggg tcagctcatg 540

aacactaaac aaattcctaa agtgattcac aaaagcag 578

<210> 1615
<211> 522
<212> DNA
<213> Glycine max

<400> 1615

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gaatgtatgt atactttgga aattcaaatt caaaagtcat aacccttcaa attataactg 120

tgtaatcgat tacacaaaca ttgtaatcga ttaccagtgg aaagttttca gaaaatctgc 180

cagcagtcac atcttttcat tagatttgtg aatggccatc aaaggcctat aaataggtga 240

cttgggcacg aattttaaaa agagagtttt gcttggcaaa aatgtcttat cctctcaaaa 300

gacaatgaga gagattctaa aagaacttca ttgtcaaatg ctctctcaaa agaaatcctt 360

gaccaaacac ttgcaaaatc tataaggatt cctacatgat ctttattgga atattcttct 420

cttgaagaaa gaattcttct tccattcttc ttattcaatg agattggtta agagactgtg 480

agtctcttgt tgtaaaggat tcctgaacac aaaggatggg tt 522

<210> 1616
<211> 554
<212> DNA
<213> Glycine max

<400> 1616

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tgtagtctcg cccttgtggc ttatgtcctt taaaagatat ttcccctatt gttcttgcgc 120

ctccatatga gcttcaatct gatgtagttt gtattgttcc agcaagtcac cctatggtga 180

ctcgtgctaa agctggtatc tacaaacctc gtcactttgc agatataact acttatcggc 240

catcttctct tttacatgca ttactcacca cttctgagcc aaaaggtttt aaatctgcta 300

ccaagcatcc tggctggctt gctgcaatga atgaagaact cacgtcctta cactccaaca 360

agacttggga acttgttctt cgaccaccta acactaacat tgttggctcc caatgggtat 420

ttgttagtcg gtgaaaacga ctaacttttg tgtataaaac ttgtataaat tgtatcacac 480

tcttccaatt tatggttatt ttggagtgtt ataaggaatt tctattaagt ataagtaata 540

aatacttagt attt 554

<210> 1617
<211> 469
<212> DNA
<213> Glycine max

<400> 1617

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gtggcctcaa atatcttaag aaggggggt tgaattaaga tatcacaaac tatttcccca 120

attcaaattc tatttcactt tctattcaag ttacaaattc cctttataat gaacttctta 180

aatattgatt caaatagaac aatctgaata taaatataaa acaataataa ataaaagagt 240

ttaagggaag agaaagtgca aacttagatt tatactggtt cggccacacc cttgtgccta 300

cgtccagtcc ccaagcaacc cgcttgagag ttccactatc ttgtaaaatc cttttacaag 360

ttctaaacac acaaggacaa tcattccttt gtgtttagaa ttcttttaca ataagagacc 420

ctcggtctct taatccctta gagaattaga aagagaaaaa gaatgaatc 469

<210> 1618
<211> 575
<212> DNA
<213> Glycine max

<400> 1618

agcttgggga atagcattaa ctggtaatct tgacacatgc attggtacaa cagtactact 60

gtggccacaa tgcaacaatc atgtggtact cgtactgaca tgacctaaca cgctagcacc 120

atggtttcac aagacggcaa gatgccaatc gtacttatac tttgatgtga gttttcacca 180

tggatagcat ctagttgtaa tggacaaaag caaatggctt cagccgttat caatgttata 240

aaagaataaa agattatgtt ttgttttgat caagagtgaa ataaaagtga aagaaacagg 300

agagaaagat ccaaatgtat aaggatagaa ataaagagag aaatagagaa atttgtcttc 360

aattgtttag atgggtacaa tattaaaagt gaaaaataac aaacgatatg agtttctatc 420

ggttggattg attattacca taataaaaat gaatcttact tgaaaaaatt ttattttgtt 480

tcattaagca ccttataatt tattgaactt aagttttgat aaaacgctaa tataaatttt 540

tttatactat caatttaatt aaaaattatt ttaat 575

<210> 1619
<211> 417
<212> DNA
<213> Glycine max

<400> 1619

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gatgtccgat tctcgggcca taatctccat ctaagatggc ttcgaaatat gaaacattct 120

ggaaagcctc tccgagaaaa ttccgatatg ggtcaataac cttttcacac ggatgtccaa 180

atttaggaca taatatatcg agacactcga aattgcacaa cggaagcact cgagaaattt 240

gaatggtcat aacttttcac acggatgtcc gaatttggga cataatatat cgagacgctc 300

gaaattgcgc cacggaagcc cctcagaaat tcgaatggtc attaactttt tcacacgaat 360

gtttggattc cggacataac ttatttagac gctcgaaatt gacaacggaa gctctcg 417

<210> 1620
<211> 602
<212> DNA
<213> Glycine max

<400> 1620

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ctatgcaagt tgaaagcctt ggaggaaaga ggtatgccta tgttgttgtg gatgatttct 120

ccagatttac ctgggtcaac tttatcagag agaaatcaga caccttgaa gtattcaaag 180

agttgagtct aagacttcaa agagaaaaag actgtgtcat caagagaatt aggagtgacc 240

atggcagaga gtttgaaaac ggcaagttta ctgaattctg cacatctgaa ggcatcactc 300

atgagttctc tgcagccatc acaccacaac aaaatggcat agttgaaagg aaaaacagga 360

ctttgcaaga agctgccagg gtcatgcttc atgccaaaga actttcctat aatctctggg 420

ctgaagccat gaacacagca tgctatattc acaacagagt cacactttga agagggactc 480

caaccacact gtatgaaatc tggaagggag gaacccactg tcaagcactt tcacattttt 540

ggaaagtcat gttacttttt ggcgattgaa accaaggaga aagatggatc ccaaaagtga 600

tg 602

<210> 1621
<211> 444
<212> DNA
<213> Glycine max

<400> 1621

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gactaaatcc tcactatata atgtgtgtgt atgaaaaata aatttcacac tttattattg 120

tagaatttca aaccaaaaga tatagtgcat ttaatacatg aaaattaaat ttttatcact 180

aaagttgaag tggtttaaat gcaaatggac aattgaattt tacgagctag ataaagacta 240

tttgaatgga tacattgaaa attatttttgt ttcaattttt aatagaactt atttatttta 300

gttggtgaaa atcttcacta taaatagaaa agagaattag tggagaaaat tactttgttc 360

agagaaaagc gtatttgtgt gaatgttatc atttttttgta actattgaat gtggtactag 420

gatttgttga gtaatacaca attt 444

<210> 1622
<211> 629
<212> DNA
<213> Glycine max

<400> 1622

agcttaagct cctttaactg cacaagactc ttaatatttg aagagtatcc ttgtggaacc 60

ttaacccgac aaagacactg acaaaaactt atcttctcct ttttggacaa agtatggcaa 120

gctggggcaa gtaaattttc ttcccatcag accttggatg caattgtgat cgtatcccca 180

tatcagctag atcttgacgg gtattcaagc catccttcgt cttgccttga atgttaagga 240

gcgtcccaat cacactgtca caaacatttt tctccacatg cataacatca atagaatgtc 300

taacgtctag atcagaccag tacggaagat caaagaaaat ggacctcttc ttccatatgc 360

aactattact tttatccttc ttttggatct ttccaaaaac attattcagg tgttgaaccc 420

gctgatatac ttgttcacca atcaacagta ttggcgcaat atcatgctct tggattccat 480

taaaagcttt tttcagtcgt ctgtaaagat gattgggtgt taaaaaacgg aaatgcctac 540

tgtagactat tttttttcc tgttttaatt ggttgtagct tttggtttct tcacagatgg 600

gggatgcatg aagaaccttt aacattgta 629

<210> 1623
<211> 584
<212> DNA
<213> Glycine max

<400> 1623

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accgtcttca gcaatttgta gctaatccac agattctgct ccgcttcctt tctaaagaag 120

atcgttaggc tggaattgag aatccagcgt atgaatcttg ggagaaacaa gatcaggtgc 180

tcctcacatg gcttcaattg acctttttcta cattgatttt atctcgagtg ttataggatg 240

cacacattcc tatgaagttt gggagtgcat tcatgagtat ttttacaaac aaactatcac 300

cacagcaagg caacttcgca ctgaattttg agcaacgact cttgcgggta agtcaatgca 360

cgagttcctg ttgcagattt gcgcaatcgc agattctctt gcctctgttg gaagtccaat 420

tatgcttcag gagcatatcg attccattct tgaaggtccc tcactgaatt atcatccgcc 480

attattgaaa gcaagtttta acccccgcgg agtaacttga accaatggtt gccaccactg 540

cagcatacac caccatacca aaaatcaact cgtcataccg aaaa 584

<210> 1624
<211> 597
<212> DNA
<213> Glycine max

<400> 1624

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ccttgtccgc ctctattccc cttactgaaa ttttatgccc cagcactatt ccttcttgaa 120

ccatgaaatg ggatttctcc cagttgagaa ctagattgga ctcttcacat atttgtaata 180

ctctttcaag gtttgatagg caccccttaa aagatggccc aaaaatagag aaatcgtcca 240

tgaaaacttc aatgcatttt tccaccatat caaaaaagat tgccatcata caccgctgaa 300

atgtagctgg ggcattgcat agaccaaaag gcatgcacca atatccgaat acacctatag 360

ggcaggtgaa agcaatcttt tcttgatctt tgggatctac aacaatctaa ttatagtcag 420

aatacccatc cagaaaacaa taataagatt gccctgcgag tcgttcaagc atctggtcca 480

taaaggaagc aaataatggt ccttccgaat ggcatcattc aacttccgat agtcaatgca 540

caatctccaa cccgtgataa tccttgtgga tattaactca tatttatcaa tttttat 597

<210> 1625
<211> 418
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1625

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aatagtccaa aaggtgattg ttatctttta taaaattgac ttatatttat ttaaaaaaac 120

attgtttatc atcataaaaa taaaatttac taacttagat cttaaggagt ttataacaaa 180

taacgcacag tatttaacta actcacttaa attccttgat gttgaattta agtatagtcg 240

ataatataaa attttagata acttttctat tactaataga tgttaaaata attaaataat 300

attgaattta atattatact taaattttat cttctttttt attaaaccat cttgtaataa 360

ttatatattg tctttaaaaa agntactana ttaatcttat ttttatctac tcttatta 418

<210> 1626
<211> 391
<212> DNA
<213> Glycine max

<400> 1626

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acgagacatc ttgcccaaca tagtcatgat aacgataact cgcctatgct ttctcttaca 120

tgctatatgt agcaaagcca ttgatccaat aatgtttgat gagttggaaa atgacgccga 180

aattatactg tgccagtcgg agatgtattt tccccctggg ttctttgacg tcatgatcca 240

cttgattgtg catctagtta gagaaatcaa ctgttgcgga cctgtttatc tatggcggat 300

gtacccactt gagcgataca tgaagatctt attagggtgt acaaagaatc tatatcgtcc 360

acaagcatct attgttgaga ggtacattgc a 391

<210> 1627
<211> 419
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1627

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cgcaagaagt gaaggacaac gcctccaagg agaacaaggc gccgctcatc gacgtcacgc 120

agttcgggta ctttaaggtt ctcggaaagg gcgttttgcc gcagaaccag cccgttgtgg 180

tcaaggccaa gcttatttcc aagatcgctg agaagaagat caaagaggct ggcggcgccg 240

ttgttctcac cgcttgaatt tgacggtatc actttttga acgatttang ttttgttctg 300

atacgttttg ttttggatta tgttgntgnt tagtctctgc tatatttcan gagtaaattg 360

aaggtttatt attttaattt gcgcgaataa ctatgccagc ctgatgacat tagaatcta 419

<210> 1628
<211> 489
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1628

tccatcaatc tatctctcta accatcaagg ccgatatatg tatggatatc ctactcaagg 60

cgtcagccac tacattggct gtgccggggt ggcaactaag ctcaaaatca taatctttaa 120

gaaactctaa ccatctcttt tgacgcatgt tcagctcttt ctgactaaac aagtacttaa 180

ggctcttatg atcactaaac acctcaaact tggagccaaa caggtaatgc ctccacatct 240

taagggcaaa aactacagca gctaactcca agtcgtgagt gggataattc ctctcatgag 300

tctttagttg tctagaagca taggctatta cttggccatt atgcatcaac actcctccta 360

tacccatctt tgatgcatca caatacacct canatggttc cctcgggtta ggaaaaacta 420

gcactagagc ggtcgtcaat ctttccttaa gggtcgtgaa actatgctca cactaggtgt 480

cccacccat 489

<210> 1629
<211> 487
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1629

tagatgaaga tgaatccgtg gccacctcat ggactcctct aaggacaata gcatcatttc 60

ttgcactgaa ttgttgggag ttggaagcca tcttctcaat caaattccta gcctcagcag 120

gggtcatatc accaagagct ccaccattga cagcatcaat catactcctc tccatgttgc 180

taagtccctc atagaaatat tgaagaagga gttgctcaga aatctggtgg tgaggacagc 240

ttgcacacaa tttcttgaat cttccacaat actcatacaa gctctctcca ctaagttgcc 300

tgatgcctga aatgtctttt ttgatggcag tggtcctaga tgtagggaag aatttctcca 360

agaacaccct cttaaggtca tcccagctga naatggacct gngagcaagg tagtatatcc 420

aatcttttgt cacttccttc aaagaatgan gaacagcctt tagaaagata tgatcttctt 480

ggacatc 487

<210> 1630
<211> 452
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1630

agcttgcttc tacagtaagt gttgatagtc aattagcact tagtcttagg aaaaaggtaa 60

ctgtgtttta aaatttgcag atacgaaaaa ccaacttgca gacatcttca caaaaccact 120

aaccaaagat tctttctaca ccattagaag ataattagga cttctagatg caagtgactt 180

agacaaatga tttatgtttt gatgacttat ttgttattta tgcacatatg cttctattat 240

aatgtgagga taatttatta tcttgtttga tttctataag cttctctctt ttcttgttta 300

attattatat ttttttaac ccttgtattt ggctatgttn ttatgacatt tgaatactta 360

gtatttcttt tattatttga ttagtatgac tggacatgat gattatattt acttgctttt 420

gggtgttatg gtatgaagtt taaacttatt tt 452

<210> 1631
<211> 436
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1631

agcttgacaa gagggtctgt ntaactaaca ataataataa taactttatt ttatcaaatc 60

ttatcttatc cagattttat tccatccaga ttttattccg tctagatttt atttcgtcca 120

gattttattt tatccatctt atcttatctt gtccagattt tattttattt cgtttatggg 180

cttggactta aaatagattt gtaagctttg tggctaagaa cctcatccat acatttttta 240

atagtatgct ctttttattt tcttttgata tactttgtgt tttaacgact tgaattcaat 300

atgattttgt ttatcaatta tttttggatt tgtacattac ttatatgaaa ttttataagt 360

ttatttttt agttagattt cactaggttt taaaataata aattaattaa aggcgtcttt 420

aaacaaactt ttaaat 436

<210> 1632
<211> 404
<212> DNA
<213> Glycine max

<400> 1632

agcttcagaa ttcaatttcg agcgtctcaa tagattacgg gactcaatca gacatccgag 60

caaaacatta ttgtcgtttg aattagctca gagcttcaga attcaatttc gatcgtctcg 120

atatattacg ggtctcaatc agacatctga gtaaaaaagt tattatcgtt cgaatttgct 180

gagagcttca acattcaatt tcgagcgtct cgatgtttta tgggacttaa tcagacatcc 240

gagtaaaaag ttattgccgt ttgaatttgc tgagagcttc aacattcaat ttcgagcatc 300

tcgatatatt acgggactca atcagacatc cgagtaaaaa gttatcgtcg tttgaatttg 360

tcagagcttc aacattcatt tggagcgata catatatacg gact 404

<210> 1633
<211> 361
<212> DNA
<213> Glycine max

<400> 1633

agcttaataa atctatatat ggtttaattc atgcttctcg tcagtggtac cttaagtttc 60

atgggataat ttcttcattt ggctttgatg aaaaccccat ggatcaatgc atataccaca 120

aggttagtgg gagtaaaata tgctttcttg gtttatatgt agatgatatt ttacttgcag 180

ccaatgatcg gggtttgcta catgaggtga aacaatttct ctctaagaat tttgacatga 240

aggatatggg tgatgcatct tatgtcatcg gcattaagat tcatagagat agatctcgag 300

gtattttggg tctatcacag gaaacctata ttaacaaaat tctagagaga tttcggatga 360

a 361

<210> 1634
<211> 357
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1634

ctgtagagga atccatcgga gttgtgtttg gtcgacatcc catcataccc gaatcagata 60

atatgtccaa agtatacttt ctttgcgaca aatggattcc cttagaggaa cgcgcgattt 120

ccaggccaag gaagtacttt aagtttccaa gatccttgat cctaaaagct tgatcaagca 180

atgtgagcat ctcctgtatt tcagtgttgc tgttgcctgt taaaataatg tcgtccacat 240

atactaagag tatcgtggtg actgaaccat taaagcggag aanaagggaa tggtctgagt 300

gagactgttg gaacccatgc attggtagga tacccgatag cttcacgaac cattgac 357

<210> 1635
<211> 388
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1635

agcttctata gaaggttcgt tcctaatttc tctacaattg catcacctct caatgagctg 60

gtgaagaaga atgtggcatt tacctgnggt gaaaaacaag agcaagcctt tgctttgctc 120

aaagaaaagc ttactaaggc acctgttcta gctcttcctg acttttctaa aacttttgag 180

ctagaatgtg atgcctctgg agtgggagtt ggagctgtat tgttacaagg tgggcaccct 240

attgcttatt ttagtgaaaa acttcatagt gccaccctca actaccccac ctatgataaa 300

gagctttatg ccttaataag agccctccaa acttgggaac attatcctct gttcaaagaa 360

tttgtcattc atagtgatca tcaatcac 388

<210> 1636
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1636

ntngacggac tataccaagc tctaggaacc agggacggag aaagatctat atatatgctt 60

gctaatggta gagagaggaa gactagagat ttggatcaag taaagtgtgt taaggatgaa 120

gaaggcaaag tcttagtgca tgaaaaagat atcaaggaaa ggtggaaggc gtatttccac 180

aacttattta atgatggata tggatatgac tctagcagtc tagacacaag agaagaggac 240

cggaactata agtactatcg tcggattcag aaacaggaag taaaggaagc gttgaaaaga 300

atgagtaatg gtaaggcggt ggggccagac aacataccta ttgaagtgtg gaaaactctt 360

ggagatagag gtcttgagtg gctcaccgaa ctctctaacg aaattatg 408

<210> 1637
<211> 372
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1637

tgcagcttcg ttgtcaattt cgagcgtctg gatatattat gtcccaaaat tggacatccg 60

tgtgaaaagt tatgaccatt cgaatttctc gagagcttcc gtagttcaat ttcgagcgtc 120

tcgatatatt atctccccga atcggacatc tgtgttaaaa gttatgacca ttttaatttc 180

tcgaatgctt ccgtttttca atttcgagca tctcgatata ttatgtccag aaatcaaaca 240

tcagtgtgaa aagttatgac cattcgaatt tctcgatagc ttccgctggt caatttcgag 300

cgtcttgata tattatgtcc ccgaatcgga catctgtgtg aaaagttatg accattcgaa 360

tntcttgaga gc 372

<210> 1638
<211> 288
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1638

agcttcttgg caatcctcat tccagcgatc agtttggttn ttgcgtaaga gcttgaacaa 60

cggctcacaa atggcggtga gctgcgatat gaatctggca atataattca agcgtcccag 120

gaaacctcgg acttgcctct ctgtacggng ttctggcatc tcaaggatag ccttcacctt 180

ttcggngtct acctctatcc ctttctggct tacaatgaaa ccaagcaatt tcccttattt 240

gaccccaaaa gtacacttgg cggngttcaa ccttaattga tatttctt 288

<210> 1639
<211> 477
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1639

tcatgcaaga attattaatc ttcttggcca actaataacc attgtgaggn ggaggcatat 60

gacgaaagtt aagaatcttt ntatttgact tccaatttag gtaaacaaaa tgggtagtca 120

aagttatgaa acccttagta ttaatagatg tccataaatc agaagttaaa cagatcctgc 180

caggaatagc acacaacagt tctttactga tggttttctt cctctcatat attctcaaca 240

tattagtctt aaaagtattt ctagaaattg gttaattgag gacacaaata acttatcaaa 300

gcctgaaact ctggatactt aacaaaaatg aagggcaaat tacgcctaat cattagatta 360

cacaacaatt cgcgtgccat cattngatct atctctttgg ccttaaactt tccttgcatg 420

tctaagatca tttgactcat atcttcanag ttttttatct cacatctgcc attatga 477

<210> 1640
<211> 325
<212> DNA
<213> Glycine max

<400> 1640

caatttcgag cgtctcgata tcttatgcgc ctgaatctga cctccgagtg aaaagtgatg 60

agcatctgaa tttctcgaga gcttccggtg ttcaattgcg agtgcctgga gataatatac 120

gcctgaatca gacctccgag tgaaacatta tgaccatttt aatttctcga gagcttccgc 180

tgctcaattt ccagcgtctc tatatgtgat gcgcctcaat ctgacctccg cgagaaaagt 240

catgaccatt tgaatgtctc gagagctctc gttgttcaat ttcgagcggt ttgatgtatc 300

atgcgcctga atgcgacctc cgagt 325

<210> 1641
<211> 396
<212> DNA
<213> Glycine max

<400> 1641

actcagctta cagttccgtc actttggata atacacaaag aaggctgttc gatgttagaa 60

gacaatctca acaggttagg gatacagtgg tggaaatgca atctaaaatt ggtagtaatc 120

gagtgacgtg catggagtta caagtagaac ttgagaaaga aaggtattta gtctgtaata 180

atgtgtacaa aatttttctt cgaatgattt ggtacacaga agttgtgaac cttcttgtct 240

ttctatatct aggtttgcca agaaaagagt ggaagaggat ctggaggtcg ctaggagaaa 300

gtttacgcgc cttatagagc agaatgaggg ctcttcagta actgaaaagc ttcaagagga 360

acttgaagag tacagggaca ttatcaagtg cagtat 396

<210> 1642
<211> 315
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1642

agctngaaga caagactata cgaggtatct ttcttgggta tagcaatatc tctaagggct 60

accgtgtcta caacttgcaa actaagaaac tcgtcatcag tcgagatgtt gaagttgatg 120

aatatgcttc atggaattgg gatgaagaaa aagtggagaa gaacgttctt atactcgttc 180

aactacctca agaagaagat gaggaagana acccaggtga accaccttca cctccatcac 240

aacaacaaga agagatggag tatccataca gaannaattg caccagtagc tcgtcttaat 300

aagacaaagc tcaac 315

<210> 1643
<211> 404
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1643

ttgattcaag atntcttcaa gatcaagcct tgcctcataa cgaaaggttt caagtcatcc 60

aaggcacatg taatcgatta ccaatacgtg taattgatta ccaatgattt gaaagtgtgt 120

aatcgattac tagagactct gaatgttggg aattcaaatt ttaaatgaag agtcacagct 180

gttcaagata aataactatg taatcgatta cactaatgct gtaatcgatt agtggagagg 240

attttcaagg aatatcgcca atagtcacat cttatcattt ggattttgaa tggccatcaa 300

aggcctatat atatgtgtga cttgtgacaa aattggaaga gagttntgct ggtccagaat 360

gtcttatcct ctcacaagaa aatgagagag attccaagag aact 404

<210> 1644
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1644

agcttaatct taatgatcaa tcattaattc acgagacatc ttctgtttgt ctcctgatca 60

tgcactgcag aaaatctaga agttgctgca agaggttcaa ataaaatggn gaaagctata 120

atgaactggc catccacctt gtcctcaggc tccttttctt cattttcatt agcaggactg 180

tccttgtttc cttctgctgc atcttcctct cctacaggct tctcatcagc aagaaccttt 240

tcagtttcat tcaccacttc ctcagtcacc ctatgaaatt aacatcaaaa ggaacaaata 300

attaataact gccaattaaa aacatgagac tcttggatga aaattctaat ctgaacttca 360

ttattattaa nattaagaat taanantatg aatacaaaca attactta 408

<210> 1645
<211> 413
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1645

agcttaactc tcaaattccn cttcatccca ttctcttttg atataggcat tccttcatta 60

gggacaacaa cctcagcacc aggtttgaca atatctgtca atgggatcat gagactcctt 120

ccgtccaagg tggtgagatc caacgtttta ccagtaaggg cctcaagaag ggttatctct 180

tggttgatca ccaaatcatt accatccctt ctataaagag catgcggctt ctcatctatc 240

acaaaaatga gatctgctgg gatgacacca ggctcacggt tacctttctc tgggaaggta 300

atttttgttc ctttcttcca gccaggtttt atctcgatag tcaaaatctc ctccacatcc 360

ccacatttgc tgaaatggaa ttgcatgtgt caaatattgt caaaaaacac aaa 413

<210> 1646
<211> 343
<212> DNA
<213> Glycine max

<400> 1646

agcttgctta agtccgtata ttgaattctt tattgtgcac accacgtgtt cttttccttc 60

aactgagaat cccattgggc tggtccatgt acacattctc ctctaaatct ccattaagaa 120

agatattttt cacatgcatt tgatgtagct ctaagtcata ataggctact agcgccatga 180

taattctgaa ggaatccttt cgtgacactg cgaaaaatgt ctctttataa tcaacatcat 240

ctgtctgagt aaaagtctta gtaacaacag ttggcctagt aatgttcaag gttgccatga 300

gagtcacatt tagtcttaca gacccatgta caaccaactc tat 343

<210> 1647
<211> 255

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1647

tctcgatata ttatgcacct gaatcagact tccgtttgan aagttatgac catttgaatt 60

tctcgagagc ttctgctgtt caatttcaag cttctcgata tattatgcgc ctgaattgga 120

cttccgtgtg acaagttatg accatattaa tttctcgaga gcattcgctc ttcaatttcg 180

agtgtctcga tatattatgc gtctgaatcg gacttgcgcg tgataagata tgaccatttg 240

aatgtctcga gagct 255

<210> 1648
<211> 433
<212> DNA
<213> Glycine max

<400> 1648

cattgacagg acatgcctat tatattcttg ttaaacagag ctcatacatc tgtgagcatt 60

attaagctcg atgcaagatc tttcatatgc cccctagatc cttcttacca attgaagttt 120

tgaacaacat ggattgagaa ggtataatca tgaagaggag atacttaatt cactacagag 180

caaaatggtg taccataaga tgatttttt ttttcacgca attatgaaaa ctactaaata 240

acaaactaga agaataaaat gaaggcaaat agtacacagt acacacccat cttgccgtga 300

ttcgctccct gagttcaaat tttggttcaa tggggcgtct tcctgtgaca agttcaacaa 360

gcaaaactcc aaatgaatac acgtcactct tttcagttag ttgataagtt ttcacgtatt 420

cagggtccaa gta 433

<210> 1649
<211> 366
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1649

ntatagaaat tcaaatggtc atgactcttc acacgaatgt ccgattcggt gaaataataa 60

atcgagacat tcgaaatata acaacgaaag ctctcaagaa attcaaatgg tcataacctt 120

tcacgcggat gtctgattcc gacacataac atatcgagac gctcgaaatt gaacaatgga 180

aactttcaag aaattcaaat gatcataaca tttcacacgg atgtccgatt aaggcgcata 240

atatatcgag acgctcgata ttgaacaatg gtcgatattg aacaatggta gctctcgaga 300

gactcacatg gtcataactt ttcactcgaa tgtgcgattc ggagacataa tatatcgaga 360

cgctcg 366

<210> 1650
<211> 372
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1650

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ctgttagtgt tttataagat ggttagtaag ggactgttgc ctgacgtcaa gaattgcaat 120

agggttctta gattgcttag ggatagggat aataacatcg acgttgcgag ggaggtttat 180

aatgtgatgg tggagtgtgg aatttgccct accgttgtta cttataacac aatgttggat 240

tccttttgca agacagggat ggttcangaa gctctgcagc ttttgtttca gatgcaggcg 300

atggtgtgtt cgcccaacga tgtcacgtat aatgttntgg tgaatggttt gtctcacagt 360

ggggagatgg ag 372

<210> 1651
<211> 429
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1651

agctataagt gaggccttgn gagaggatnt gtccaaaccc tccaacacca gtacttgtag 60

taataaagct gacactacta ctactaaggc aaggataaga tgcagcatcg accaaagctt 120

tctgaagaac aaatctgtaa agggtaccac ggaacttctt gaacagcatg tgtggaggcc 180

ccagagaggg ttgccagagc gtgcagtggc aattcttaaa gcctggttat ttgagcattt 240

tcttcatccg tatgtttgtc tctatctatg tctcttatta ataatttttct tgctccgtga 300

ctctcttttc tgcattctaa agagacattt ggattgaatt gtggcctttt tttgctgttg 360

ttgaatttct tttcagttac cctacagaca ctgataaaca catgctggct agtcaaacag 420

gtctttcac 429

<210> 1652
<211> 277
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1652

ttctctttcc catgtcaact atgcagcttg cggtcaacat gaacggcctt cccaagatta 60

caaggatgtc agtatcttca gagatatcca taaccacaaa gtctgctggg aagataaaat 120

gttntaccct gaccaacact tcaatcactc cacatgacct ggtaatggag cggtcagcta 180

attgcaaagt cattcgagtg ggcataatct ccaactctcc cagccttctg cacatggaga 240

gtggcatcaa attaatagtg gcttccagat caatcat 277

<210> 1653
<211> 337
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1653

agaacgcatg aacganaatg cttttcatgg tgctccgaan aagggttgag gatggagaat 60

cgcactaaga aatcactacg catggctcca aactcgtggg tggaggacgc atgaacgaaa 120

acgcaattca tggggctccg aaaaagggtt gaggatggag aatcacacta agcaatcact 180

acgcatggct ccaaactcgt gggtggagga cgcatgaaca aaaacgcatt tcatggggct 240

ccgaanaagg gttgagaatg gagaattaca ctaagcaatc actacgcatg gctccaaact 300

cgtgggtgga gggcgcatga acgaaaacgc aattcat 337

<210> 1654
<211> 400
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1654

agcttatgga gtagataaac aaaagcttgt tgaggagatt actcgtgcct atgcccacca 60

aatatatatt gatggattnt tcaatggtga tcctcatcca ggtactctct ctctctctcc 120

ctctacgttt gtgcttatgt atgcatgtgc atatgatgta acacttccga ttgttccatg 180

tgctcatgaa ctattttggc tctcttactg gaatcatcat aggaaatttt cttgtgagca 240

aggaatctcc acatcgtcct attttacttg actttggcct tacaaagaaa ctatcaagca 300

ccattaagca agcacttgca aagatgtttt tggcttctgc tgaggtntgg tttggctttt 360

gtgcttttca tgattatgtg gatactaata acatcatata 400

<210> 1655
<211> 382
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1655

tatagaatat ataatataag aacagtgact attgaagagt ctatacatgt ttcctttgat 60

gagcctaatg ccattcttgc aaggaaggat tatttagatg atatttcaga ttccttagaa 120

gatacacata ttcatggaaa tgactctaaa gaaaaagatg aacgaagcaa tgaggattct 180

caagataatg gggctagagg aaataatgaa cttccaagag aatggaaagc ctcaagagat 240

catccnctcg acaacattat tggtgatata tcagaagggg tcacaactag acattctctt 300

atagatttat gcaagaatat ggctcttgta tctatgattg aacctaacaa tatgggagaa 360

gtcatagtag atgataactg ga 382

<210> 1656
<211> 252
<212> DNA
<213> Glycine max

<400> 1656

tcccggcaac attgtttgta ttaatgaatt caacattatc cttgaatatc agtaaacgtt 60

tttgcttctc tgcagcatcc ttatatacct tcccatattt cttcatccac tgctcatgtc 120

tttcggacat ggatgcctca tggaggttgc gggacattac ttgggaagtg cacattgaga 180

gaaggagcac aagagctaaa atgtgctgct ttttgcccat ggaacccatg tcttttctca 240

acaatgtatc aa 252

<210> 1657
<211> 312
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1657

acactatgat actcagctta ccactgtccg gttactcctt gcccttgttg ctcttcataa 60

ctggcacctt caacaattgg atgtaaacaa tgctttcctt catggngatc ttaacgaaga 120

ggtttatatg aagcttcctc caggacttat tgtggataat cccaaccttg tttgtcgcct 180

ttagcattcc ttatatgggc tcaaacaagc cagtcgctaa tggttcacac ggctctcgtc 240

atttcttctc tcccacagat tccgacgatc ttcagcagat cactcgttta tatatactct 300

gataatgacc at 312

<210> 1658
<211> 451
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1658

agcttgtaat tttcttattg cctttgcttg ttattacatg gttnttatag aattcctaat 60

atggaataat cctaggaata ttacaataac cgttttattg ataagaattg ctcagcagga 120

tcacaattcc aagcaaggcg atctgggaaa ggatttgcag aagcttctgt tttggcagga 180

ttcttcaaac gaagtcgtga aggtaagtgg gcctcttcac cttacgtttg ggctttactt 240

cgttatgcac cccctgtttt gtaattccca cctccgagct catctaagag ctcatctatt 300

gtgggaattg ngaactggtc ttggaccatg acagcattga gggccctgta gtccatacag 360

aaccttcagc tcccatcatg tttccttaca aggaggacga gtgaggagaa agggcttgta 420

ctangttgga tcaatccttt ttgaagcatg a 451

<210> 1659
<211> 428
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1659

gctatgctgc ntatattaca atagaacttc cttcacctca gcagcanaat caaccacagc 60

agaacaatta tgacctctcc agcaacaaat acaaccctgg atggaggaat caccctaatc 120

tcagatggtc tagccctcag caataacaac agcagcctgc tccttccttc caaaatgttg 180

ctggcccaag cagaccatac attcctccac caatccaaca acagcaacag cccctgaaac 240

agccaacagt tgaggctcct ccacaacctt ccctcgaaga acttgtgagg caaatgacta 300

tgcagaacat gcagtttcaa caagagacca gagcttccat ttagagcttg actaatcaga 360

tgggacaatt agctacacaa ttgaatcaac aacagtccca gaattctgac aagctacctt 420

ctcaagct 428

<210> 1660
<211> 297
<212> DNA
<213> Glycine max

<400> 1660

acagcagaat aattatgacc gttcgagcta ctgatacggg ccatgatgga ggaattatcc 60

taaactaaga tggactagtt ctttacaaca acatcaacct gtccctccgt tccagaatgt 120

tgctagtaca agcaagcctt atgttcctcc tacaatgcag caacaacagc tgtctcctca 180

tagactacag gcaactgagg ctcctactca accttactta taagagtgag cgaggcaagt 240

gaccatccat aatatgcaat tttagcgaga gacatgagcc tccgttcaga gactgac 297

<210> 1661
<211> 398
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1661

agctnttcaa agccaatttc atcagagaag tcaggtactc tacttgactc gccatcgtcg 60

tcatggtcaa aatggccaat ggcaagtggc gaatgtgcac caactacacg tatcttaaca 120

agctagttga tggagcgtcc gagttccaag tactgagctt cctggatgcc tacacatgat 180

acaattagat ccggatgcat gccctacatg aagagaaaat gacattcatc tttgaagatg 240

ccaacttctg ttatagggtc atgccctttg gcctataaca tgtaagcact acatactaga 300

gagtgatgga ccatantatt caatagcaaa ttggatgaaa tgtcgaggtc tgcgtcaatg 360

acatggtcat caaatcacat accactagcc cacatgtg 398

<210> 1662
<211> 429
<212> DNA
<213> Glycine max

<400> 1662

tatacagata tacatatttt ccagcaacat cttgatggct ctattcaata caacatacat 60

cacatggaaa tattagatta cagccagaca caatgcatag atgctactgt gttgggtgct 120

ttgctacatt gccacatgat tttctggtac aagaactgtt tggaggggat caaattcaat 180

aaagaatgtc cgaatcttca tcggagcaag ttcaaccacc aacttcgtag gatcaacagg 240

tcctcctctc accaccttcg gctcttcaga ggagccttct accttccaat ctagcttcct 300

cttttccatt tgagctcttt cttgattagc agacaaactc atctctgtca ctttattgat 360

ctgaaaagat tgagtagtca aaaggaaact atacatgagt acatgatgtg tgaaaaatac 420

taacttgga 429

<210> 1663
<211> 180
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1663

gaggttntga ttgatcaaaa agaagaanct acttcatacc gatatgccct taggcacggc 60

aatacataac atagaaatca canctcgaaa gggtggacca atagctagag cagcaggtgc 120

tgtagcgaaa ctaattgcaa aagaggggaa atcggccaca ttagaattac cttctgggga 180

<210> 1664
<211> 440
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1664

cttgtgtgta aagagtcaca acttanaatt ctttttttcaa gtctaaagag tcacaactct 60

ttagaaaaat aattttgtaa tcaattacac cattttaata atcaattatc agtaaggaat 120

tttcaaaaat aactcccaac agtcacatct attcaaatgt ttttgaatgg ccatcaaagg 180

cttatatata ggtgacttgg gacacaaaat ttctcaagag tttttactgc acaaagagtc 240

tcatcctctc aaaaactaaa ttatcttatc ctctaaaaca ttctttggcc aaacacttgc 300

aaattcaata aggaatcttg agtgatcttc aattgttata tctttatctt anaagagaga 360

attcttcttc ttcctcttct tattcaaaga gattgattaa gggaccgaga gtctcttgaa 420

gttgtaaaaa ttcttgacac 440

<210> 1665
<211> 357
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1665

gctacacaaa tccngtctaa tagctaagct caccccccatg cgcaaaaata catgaaaata 60

aaaaaaaagc tcctactaca aagactaccc aaaatgccct gaaatacaag gcttaaaccc 120

tataatacaa gaatggccaa aatacaaggc ctaaaagaag gaaaaaccta ttctaatatt 180

tacaaagata agtgggctca tacttagccc atgggctcga aatctaccct aaggctcatg 240

agaaccctag ggccttccct tggatctctg gcccaattta cttagagtct tctatccaat 300

gcccttacaa ggtagaattg catcagtagg gtcggtgctg cttaccctca acgatca 357

<210> 1666
<211> 329
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1666

taatatcacc aggaactatc acattaacaa aatcacagcc tctaagattt cgacanatta 60

ttaggtagcc ttgaagcatt atgtttttat gattctaatc taccattctc tntatatata 120

atacataact atatttttta atttgtaatt tatttataat attcaattat gttatgtaaa 180

aaaatagtta aaataattaa cattataatg attttagact atctaataat ttctagtaag 240

attttaatgt ataacanacc tggaagcaca gaaggctacc acataatccg tcccagaaca 300

agtgaaaata ctagttggat catcataag 329

<210> 1667
<211> 400
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1667

acttaagtga ttattttata attttaatag ataaatgact aaattatcag ttaanaataa 60

aagttaaaga accaaatgag taatntaatc aaataattgt gatgtttgac aacactcaca 120

agacttatat attgtaattn tgataattca ttaagatata atggataata ttaattcttc 180

tcacttttg cattaaaaca ttctcactaa ttatttaatc ttttcttttt aacataaaag 240

gcaaaacctc gctagataga gagagaggac ttaaatttgt gttgataaaa tttactgtga 300

agcttattaa aatatttata aaaatcataa atcattttaa caagcttaac aaaatacata 360

ctcattatta ctataatcaa ataagtttca tacaaactcc 400

<210> 1668
<211> 372
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1668

agcttccact tgantaatct taaccattgt ttttttttcaa ataatatctc atcaatttgg 60

tgactagccc atccatttgt gtagttttct cggcaggatc tggtcttgag gtatctatgt 120

ccaaaaaaca ccaccagggg aagtttcact tatggcattt tctaatcttt caattccaat 180

taaatggaaa aatagtttgg ttgatagctt atcatattag ttgaaatgct tagtttgcag 240

gaattcttcc ttgtttctat tnttgaacct aatgatctgc gttggcagat gctgtgattc 300

ccatcacttg cttcatactg gtgtgtttgg ttgcactaca acactatgga acacataggg 360

tgggattctt tt 372

<210> 1669
<211> 269
<212> DNA
<213> Glycine max

<400> 1669

ataataaccg gaagtgcaac gatataagga cctagagcag attggactga ggaagacaga 60

agattactac aatataattt aaaggccaaa aatattatta catctgcctt aggaatagat 120

gaatacttta gggtttcaaa ttgtaaaagt gctaaggata tgtgggatac aatacaagta 180

acacatgaag gcacaacaga tgttaaaaga tctacggata acactctaac ttcgtgatat 240

gaacttttac gatgaatgta ataaaagta 269

<210> 1670
<211> 206
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1670

ctttttttcct cgcagcaaat caaccacngc ttaacaatta tgacctcttc agctacagat 60

accaccctgg atggaggaat caccctaatc ttaaatggtc cagccctcag caacaacaac 120

agcaggctgc ttctttcttt caaaatgctg ctggcccaag cagaccatac attcctccac 180

caatccaaca acagcaacaa ccccag 206

<210> 1671
<211> 352
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1671

agcttttata cggagtttaa agataaatac atatatattt atagaaaagt caaacttctc 60

tcttttttaaa atgcatatcc cttaaanatg cttgagaaat aataatgtta ttaaatagtt 120

atagttatga aaaattatta aggacaaaat ttagatacca attgttaagt gcttttagag 180

atttatttga ataatttggc ataataaaat ttatattaaa tattactctt ttcggttcta 240

tttataagac tcaattactt aatttagtta gattaaggag agtgattagt ttagttgata 300

ataagaaata tgttcaagat catattcttt tttctaaaac taccattgtc ta 352

<210> 1672
<211> 316
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1672

agctngaaga ccccataagg ctcctattgt ttatggtgca gcaactatct tcattatctt 60

ccagtaatct ccctcctaag aatgctgtca cacacctgat tggccctcta tggcccacta 120

gaactgccag acacgtgtgt ngaccatctt gttctctagc ccaaaccctg ctcgttgagt 180

cagccgagcc actcactaca tatttggcca cacttgccag acacaacact gcatgcgtgt 240

gcccttggat ggagccaccg tattgtaact gccccgcana ccaacccttg tgccagtagt 300

gtatgtagcc atcagt 316

<210> 1673
<211> 471
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1673

cgcgctntca tatctaatat tacaacttgg tctaagaact ctattaccta tcttgtcctg 60

acaacaggtt gggatttttg agatagcccc atccaagcag tcattgcagt ctttctcaga 120

caagtcaggg gtgcactctg ccataccata tatggtctga aaacttgaag cagttacatt 180

atccgtggca tacttacgac gagagtcacc cgatgcggct acacctttga ggtttctcat 240

taagttcgcc agagcttgac tgaacttatc cggttccgtt acattgttta tgttcatcaa 300

ggattggcta ggttcaattt ccatgatgcc aaatatcgag cggggtgagt agcgcaacat 360

gcatttgcta gtgttcaacc acagaagtgc ctctttctgg tttggacaaa actgtttaat 420

tgtgactctg gaatcattga ggcaactgcg gcactcatgt ggctcaacat c 471

<210> 1674
<211> 448
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1674

acctgtctga gcaatcttat gttctggttc tcaccttcat atcctctnga ccttctccca 60

ttacctgcaa gcaaacattg tgttctggag taggcttgtc ttccacagac aagtcgaaat 120

caatttttgg gtcttcaaaa cctaactcca gctttctctt ccccatgtca actatgcagc 180

ttgcggtcaa catgaacggc cttcccaaga ttacaaggat gtcagtatct tcagagatat 240

ccataaccac aaagtctgct gggaagataa aatgttttac cctgaccaac acttcaatca 300

ctccacatga cctggtgatg gagcggtcag ctaattgcaa agtcattcga gtgggcataa 360

tctncaacta ctccagcctt ctgcacatgg agagtggcat caaattaatg ttggctccca 420

gatcaatcat agcctcttcc acatttac 448

<210> 1675
<211> 326
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1675

tcaccattag tgacgggaac cttactcttt cttatggagg ccactataac ctgacacatg 60

cgagtgaggg ggctaccacc gggcttctga atccgataca gactcgtacc ggataagaag 120

ctcaccacag caattgccat ggccactgct ggaaagacaa atccccaccc ccaacttaca 180

gtagtaagga cccacaccac caaagaagca gcaacgcgac caccactatt tattgacaag 240

cagaaccact ngaagaaaga gctcttgtgc tcnctctcag cttcatcagc atcacaaatt 300

gagtgcacca aagaagagac acaagc 326

<210> 1676
<211> 465
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1676

actaagcttt acctttagtt taacccttag aacttcccgg ccaaattgtt atatataaag 60

caatgttgat gttcaaagga cactttacat gcctttntaa tcaactgacc tacgcttagc 120

aagttctggt caatgttagg tacataaaga acatctgata ttaatttgat acctgaacac 180

gttgaaattg caacagttcc ttttcctttt ataggaatat agccaccatt cccaattctg 240

acctttgaga cattagttgg cttcaaatcc ttgaataaag tcttatcata tgtcatgtgg 300

ttcgtacaac cactatcaat caaccaactt tcacttgatt cactactcaa ggttgataat 360

ttttcttttt atccttacct ttgatatgga tgattgcact attttcgctg cttgctggct 420

ggatcttcta gaanaaatgc tttntgcttt catcaacttc atgat 465

<210> 1677
<211> 624
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1677

ttctccacta agttgcctga tgcctgaaat gtcttttctg atggcagcgg tcctagatgc 60

agggaagaat ttctccatga acaccctctt aaggtcattc cagctgaaaa tggacctagg 120

agcaaggtag tatagccaat cttttgtcac tccctctaga gaatgaggaa aatcctttag 180

aaagatatga tcttcctgga cattaggggg cttcatggtg gaacaaaaaa tatggaactc 240

cttaagatgc ttataaggat cttcacctgc aagaccacga aacttgggca gcaaatgtat 300

tagtccagtc ttgagaacat atggaacacc ctcatcagga tattgaatgc acaagctttc 360

ataagtgaaa tcaagtgcat ccatctctct aagagtcctt tcacgaggtg gaggttgagc 420

catgttctca gtatgaaaat tagcagcgga atgttcaaaa tcacaatatt cagaatcacc 480

ctcaacagaa tgctcaaaat gcacataatg accaggatgc acactatgcc taactaatct 540

atgaaagggt ctatctattn tatgatcaaa gggttgtaaa tcacctagat tgcccctagt 600

catgcactat atgcagcaaa tagt 624

<210> 1678
<211> 563
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1678

tcttatccaa ggcaattctt ggtggtgaag ctccttcttc cttggcttat tccctagtgg 60

atggtgcctc ccctatcctc ttctcctttg ccttccgctg catctccatg gtgaaaaatc 120

accattgaag gacctcattg aagctcaaag atccagcctc catagaagct ccacaagcaa 180

gcttccatca cttttcacac agaggtcaga ttcgggcaca taatatgtcg agatgctcgg 240

aattgaacca cggaagctct cgagtaattc aaatggtcat aacttttcac acagatgtcc 300

gattcgggcg cataatatgt cgagtagctc gaaattgaac aacggaagct gtcgagaaat 360

tcaaatgggc atacttttтc acacctgcct cacattcngg cacataatat gttgagatgc 420

tcggaagtga accacgaaag ctctcgagaa actcaaatgg tcataacttt tcacacggat 480

gtccgattca ggcgtatcac atatacagac gctcgaaatt gaacaacgaa agctctcgag 540

aaatacaaat ggtcataact ttt 563

<210> 1679
<211> 402
<212> DNA
<213> Glycine max

<400> 1679

agcttgaatc ggacctgagt gtgaaaagtt atgaccattt gaatttctcg aaagctttcg 60

ttgttcaatg tcgagcatct cgacatatta tgcgctcgaa tcgaacatcc gagtgaaaag 120

atatgaccat ttgagtttct cgagagcttc cgtggttcaa ttccgagcat ctcgacatat 180

tatgtgcccg aatctgacct tcgtgtgaaa agttatgacc atttgaattt ctcgagagct 240

tccgatgttt aatttcgagc gtctcaatat attgaaagcc tgaatcggac ctcagtgtga 300

aaagttatga ccatttgtat ttctcgaaag ccttccttgg ttaaattccg agcatctcga 360

caatatatgt gcccgaatct gcctttgggt gaaaagtatg ac 402

<210> 1680
<211> 599
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1680

taagaatatg gaattgaaca aagttaacaa aaatggtagc atgcagcaag cttcatgtgc 60

ttaggataca gtagaacatg aaagtttgta ttagagtcaa gttgcgaact caactcattt 120

ctagactttt ttttttctga attctcattt agtgtcaact atccctactc taattttatt 180

tattatgttt taatatttaa tgttctatac ttttgtagat ttaatttatt gttttaaata 240

tactatagca atgtgtgtgc gcacacgaat ttatgcattt ttaggtttgg tgtatatttt 300

ttatcaacaa ttattaatat acctcctcta attgtttact tttttttaa tcccaaattc 360

aaaagctagc ctccataatt ctatattggg ttatccgatt ttaacctttg caatcatatt 420

ttattgtatt ctcaatgtcc cttggtccat atgtctctca attgaacacg agagtaagaa 480

tgtgttattc tcgtaaagtt atgatcattg attcttttat acttgagtga aagagtaaac 540

acaaatatgt canatatcac atattggtat gcatggtcac acatatttca tgttctact 599

<210> 1681
<211> 359
<212> DNA
<213> Glycine max

<400> 1681

tccattgttc aatttcgagc gtctcgatat attatgcgcc tgaatctgac tttggagttg 60

aaagttatga ccatttgaat ttctcgagag cttccgttgt tgaattagga gcgtatcgat 120

atattatgtg ccggaatcgg acatccgagt taaaagttat gaccgtttga atttcttatt 180

agcttccgtt gttcaatgtc gaccatctcg atgtattatg cgcctgaatc tgacatccga 240

gttaaaaggg atgaccattt gaatttcacg agcgcttcca ttgtgcaatt tatagcgtct 300

ctatatatta tgcgcgtgag tctgacattc gagtttaaag tgatgaccat ctgaatttg 359

<210> 1682
<211> 344
<212> DNA
<213> Glycine max

<400> 1682

agcttataag aaattcaaat ggtcataact tttaactcgg atgtccgact ctggcgcata 60

atatatcgag acgctcgaaa ttgagcaacg gaagcagttg agaaattcag atggtcataa 120

cttttcacac ggacgtcaaa ttcaggcgca taatatctag agacgctaaa aattgaacaa 180

cggatgcctt cgaggaatac aaatggtgat agcttttaac tccgatgtta aagtcatgcg 240

cataatatat tgagacgctc gaaattgaac aacggaggct ctccataaat tcaaatggtc 300

atgacttttc actcggaggt cagaatcgag gacataattt atgg 344

<210> 1683
<211> 582
<212> DNA
<213> Glycine max

<400> 1683

agcttgttac tggtttgctt ctctgcaatg gggttgtata aatgatgaaa tgcttataga 60

aggcttttct tgctttttg tccttgatac ataattaggt tggcaagaat cttcatgttc 120

tcagtcagat agagggtgtt gacctagata tgtacaaaga tgttgtgctt cccagagtac 180

tggagcaggt ctaattgctt tattgtttct atttctaatc atcaaagaca tggttaactt 240

tctaaccata aaaaaaaacg attccttttc ctcaattatc atgggcaggt tgtgaattgc 300

aaagatgagt tagctcagtt ctacttgatg gattgtataa ttcaagtctt ccctgatgag 360

tatcacttgc aaactcttga tgttttgttg ggtgcttacc cccaacttca agtcagtgaa 420

cttgcacatt tttttgtatt acttctggag gatgccttaa tgtatatatg ttttttctca 480

ctccgaaaca tgaaaattca ggttagtgaa cttgcacagt tttgttttac taatataata 540

atattatatt ttattgggaa aaagcccaaa ttaaatattg aa 582

<210> 1684
<211> 398
<212> DNA
<213> Glycine max

<400> 1684

agcttcatgt agctttttct agaagcttca ttaagaggct tcctccagaa gcttcctcgt 60

ggcttctttg agaagctttc tcaagaggct tctttgagaa gctagatcct tatctatcca 120

caccctcta ttaactaaat taacttcctt aaaaataatt accgatgaaa ataacgcaac 180

aaatattcaa acatcaaaca taattactaa tagtatatag atatatatat atcagggtgt 240

tacaactctc ccacccttt agaaatttcg tcctcgaaat ttaccttact caaacaagga 300

tgggtgagct tctcacatct gactttctaa ttcccatgtg gcatcttctc ctgatgcacc 360

tccccagatc accttgacca acagaatctc tttccctc 398

<210> 1685
<211> 303
<212> DNA
<213> Glycine max

<400> 1685

agcttgaagg caaactggat gcattggtta acttggtaac ccacctggcc ttgaatcaga 60

aatctgtacc tgtcccaagg gtttgtggtt tgtgctcctt tgctgaccac catacagacc 120

tttgcccttc catgcagcaa cctggagcaa ttgagcaccc tgaagcttat gctgcaaata 180

tttacaatag acctcctcaa cctcagcagc taaatcaacc acaacagagc aattatgacc 240

tcttcagcaa cagatacaac ccttggatgg aggaaatacc ctaacctcag atggtccagc 300

cct 303

<210> 1686
<211> 663
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1686

tgaaggtagg agaagatgag tggagggaga gggagtgaag aggcacgaaa ttttatgcct 60

caaatgaggt ctgaactttg aagtgtaatt ctcaaatgat caaagttaca acaagtgtta 120

cacatgcttc catttatagc ctaggtagct tccttgagaa gcttccttga gaaacttcct 180

tgagaagctt ctttgagaag cttccttgag aagctagagc ttagctacaa acacccctca 240

aataactaag ctcgcctcct tgagaaaatt cctagagaag ctagagctta gctacacaca 300

cccctctaat agctaagctc acctccttga gatgagaagc tagagcttag ctacacacac 360

tttctataat agctaagtcg tcatattccc acatggnttc ttcttctcca attntcaaca 420

aatatattca agggaaatga aacaccggaa agcataccgg gtcatcaagt atttaaaatt 480

aaaacagagt gatccgagta tcgaacttag ggaacttgct tattagacaa agttttatta 540

acgagtaagg cattgttgga acacacattg acaattgatg ggtaaaaaca gaaataaact 600

aattctatgg taagaataat aaatgcaagt aagttaaagt tgacaacaac aggtaaaaag 660

tgt 663

<210> 1687
<211> 557
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1687

ttggagtttc caagtgccaa ttcgtcttct tctttagtcc agtcttcttc tggcttcaat 60

tcattagagg gctttccttc tgtgtccagc atcttgggat gttcccagcc tttgatgaca 120

gctttccagg ttctgctatc cagtgatttg aggaaggcca ccatccttgc tttccagtat 180

tcatagttgg ttccatccag aataggtggt ctgttcactg gtcctccttc tttctccatg 240

ttcatcagaa tttatctccc tagatctcac tcagtgattt cgagtgccag ctctgatacc 300

aattgaaatt ctgatactgg ggacagatgt cgtacaggat gtcacgacat cacgcttcag 360

aacatgcaga ttatagttga cagtgtggac agtttaaaca agaagataac acaagagatt 420

ngttaaccca gttcggtgca accttaccta catctggggg ctaccaagcc agggaggaaa 480

tccactaaaa tagtgttagt tcaaggtcta acagccactg tttacaacct tctcacctaa 540

ccactacccg tgcgatc 557

<210> 1688
<211> 440
<212> DNA
<213> Glycine max

<400> 1688

agctttaaga ctattcacat aagttaacaa gaagcaataa aggatcaact gtgaaaatga 60

attgcattcc catacctaga tcttctccac aattccttcg aatttatata tgcttagatg 120

catgcaagaa aggattcaag gctaactgca aacctttttat tggtcttgat ggttgtttcg 180

taaaagggta ctatggcggt catttgcttg caacagtggg acaagatgca aacaatgcct 240

tttttgtgat tgcatatgcg gcagtaaata ttgaagataa agataactgg aagtggttcc 300

tcactttgtt acctgaagac ataggagact acaagcaata tggctggaat ttcatgtcag 360

acatccaaaa ggtgccatta aatataaaaa gttgatttca tgcctgcatg ggataatttt 420

gttgtcatgc tagcaatatg 440

<210> 1689
<211> 709
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1689

ttgagccaaa atcctgactc accataaacc ttgacccagg gtgagaatgt caatccttac 60

cctcggaagc aaaaaaggaa tagaagggaa atttccaatc aaagaaaaag agaaggaaaa 120

tttccaatga aagcaaaaaa agaaaggaag ggaaatttcc aatcaaagaa aaaaagaagg 180

aaaattcccc aatcaaagag tgggagaaag caaaaagaaa agaaaggaaa ttcccaatca 240

aagaatggga gaaagtaaaa aaggaagaag aagaaggaaa gaaagccctg atcggggatc 300

gaaggaaaaa acagaagaaa tatgcagaga ggtctttgga ccggacaata tctgaacaat 360

acagaattgt caccaaatga acaaaaaaga aggaaaggaa accacgacct aaaatggtct 420

tctcccttta attaccaacc aaaatcccgt gcgctagcga ccctttttt ttctcgcccc 480

gcactagaca aaaaaaaacg gaaaaaagaa aaaaagccag aaaaatcaaa agccaaaaac 540

acacaaaagc cgaaaaaccc accaaaagaa cccattccca agggaagccc tattgatcca 600

tgatcacgca tgtaatnttt gatttgatag gaagtaattt gcanagtcaa gtcatgacat 660

atctatggnt cngaattang atgaaacact tacctgtgcg agattgata 709

<210> 1690
<211> 409
<212> DNA
<213> Glycine max

<400> 1690

agcttgcctt gccccttgat atatttgagg gactcatggt cactatgaat gacaaattcc 60

ttgggataaa ggtagtgatg gcatgttttc aaagcccgta ctaacgcata caactcctta 120

tcataaattg aatagttaaa ggtaggacca cttaactttt cactaaaata agcaattgga 180

tggccttctt gcatcaacac agccccaatc ccaacattag aagcatcaca ctcaatttca 240

aaagattttt gaaagtttgg caacgcaagt atgggggcat tagttagctt ttgcttaaaa 300

acattgaaag cttcttcttg tttctctccc catttgaaac caacattttt cttgagcact 360

tcattgagag gtgctgccca tgtgctaaaa tccctctatt aaaacttgc 409

<210> 1691
<211> 584
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1691

ttttgagaga ttaaatttac cttatagaga gtattttgtg aatttgactg cataacaaat 60

taaaagtaaa acaataaata ttttaatgat atgagacact taaagaatta aaattaatca 120

aaatatttaa caagaataaa agtgtatttt attaatgtta ggagtaattt tacaaaaatg 180

cgttaatttt tttatcttaa taaattagtt aattgggtct taaaaattca gcaagagtaa 240

aaataataat aattnatact tcttccttct ctttttctat ttataagaca tttcttaaaa 300

agactatttg tacttttata taatactttt ttcaaaaaaa attattaatt atttttaac 360

ccanatatat ttattcattt tctcctgaac gccatanagt aactaaatac attctttttt 420

cttctctcgt aaaaaccaca caacatgact gaaacatatt aattccttac gcaaaaatta 480

agatttgctc tgcattatat atttgagtgt agattttagt gaacatatcc aattttggga 540

cgaacacatc atacgtcaag aattataaaa aaaataatgt attt 584

<210> 1692
<211> 552
<212> DNA
<213> Glycine max

<400> 1692

agcttccatt ttcaattgcg agcatctcga tatattacgg gactcaatcg tacattcgag 60

taaaaagtta ttgttgtttg aatatgctca catcttcagt attcaatttc gagcgtctca 120

atatattaag ggacttaatc ggacatccga gttaaaagtt attgtcgttt gcatttgcta 180

cgagcttccg ttttcaatta cgagcgtctc gatatattac gggactcaat gcaacctccg 240

acttcaaagt tattgtcatt tgaatttgct acgggctttc gttttaaatt tctagtgtct 300

tgatatatta cgggacttaa tcgaacattc tagttaaaag ttattgtcgt cagcatttgc 360

tcagagcttt cgtttcaaag acgagtgttt cgatatgtta cgggactcat ccgaattaaa 420

aagtattggc gtttgaattt gctacgagct tttgtattca acttaaagcg tcttgattat 480

gttacgggac tcaatcgaac atccgagtaa aaggtatatt gggttggatt tgctacaagc 540

ttccattttc aa 552

<210> 1693
<211> 640
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1693

ttaattcaag atcaagaaac taagatcaag agtcagataa agacttagtt tatttgttaa 60

aagaatctca cattggttaa taaggtttgg cctcaaaagc ttgattttaa aatgattata 120

taaagcttta aaagatgttt taccagcaca aaaataagtt tttttgcact ggtaatcgat 180

taccaagtat tgtaatcggt taccagagac aaattacata aaaatatttc tagaaggatt 240

ttgaaatttg aatttcaaat gttgtaatcg attaccactt gtctgtaatt gattatcagt 300

gacaaaactt cataagttaa ctttgaaaag tcatgacctt caaaacataa ctgtgtaatc 360

gattatcaag acattgtaat cgattaccag tgagagaatt tttgtaaaat attctgaaaa 420

gtcacatctc ttcaaaagtt tttgaaaagc caccaaggac atataaatat gtgacttgtc 480

tatgaaaata tntagagttt tctgatgcaa tcctaccccc acaagggcat tagatagaag 540

actccaagta gatcgggcta gagatgcaag agaagcccta tggttctcat gagccttang 600

gtagaattca agcccatggg ctaagtatga ctccacttta 640

<210> 1694
<211> 649
<212> DNA
<213> Glycine max

<400> 1694

tgaagtgtcc agttgtgatt tttgttttcc agttataatt ataaatttga ctttattttc 60

taactatcta aattcttatt ttatattatc agatagtctt tttggggata gacaacatcc 120

atgcgatgag agagagcttt gttcggctcc gagaatacat ggacactcat ggaagaacgt 180

catcagatgg aatgtcctct tttttggtta gtccgtgaat gttaaaacaa aatgtaatta 240

tcatttttca ggtagtgtaa atttatttgg ttcctatata gacctgcaca atatttatgt 300

tttagtcctt acaccttaaa attaaaaact acttgtttta gtcccaatac atacactttt 360

taagtcgctt aatccctata gcttctgcgt gacagggatt aaaacgggtt aaaaaatgta 420

tgtgtaggga ctacaacgag tagcttctag gtgtaggaac taaaacatac atatggtgca 480

taggtataag gacccaatga gtaattaaat catttatttt taatagtata tatttgatat 540

ttgaagagtg atactactat tagctgtata atgacacttg tagattagat atttaatctt 600

tcttcatgat gcttaatata tatcttaata ttatttaata ctttttttct 649

<210> 1695

<211> 583
<212> DNA
<213> Glycine max

<400> 1695

tatgaccatt cgaatttctc aagagtttcc gttgttcaat ttcgagcgtg tagatgagtt 60

atgtccccga atcggacatc tgtgtgaaaa gttatgacca ttcgattttc tcgagagctt 120

ccgttgttca atttcgagcg tctcgatata ttatgacccc gaatcggaca tctgtgtgaa 180

aacgtatgac cattcgattt tctcgagagc ttccgttgtt caatttcgag cgtctagatg 240

agttatgtcc ccgaatcgga cattcgagtg aaaacttatg accattcgaa tttctcgaga 300

gcttccgttg ttcaatttcg agcgtctcga tatattatgt ccccgaatcg ggcatccgag 360

tgaaaagtta tgaccatgcg attttctcga gagcttccgc tgttcaattt cgagcgtctc 420

gatatattat gtccccgaat cggacattcg tgtgaaaact tatgaccatt cggatttctc 480

gagagctctt cttgttcaat atcgagcgtg tagatgagtt atgtcctcga atcggacatc 540

tgtgtgaaaa gttatgacct tctattttat cgagagcttc cgc 583

<210> 1696
<211> 362
<212> DNA
<213> Glycine max

<400> 1696

agctttgatg caacatttgg agaggttaat gaaacaacga gatgatgcgc tccatgagag 60

gttggatcaa atggagaata gagatcataa tgaagaagaa aggaggagaa gagggaatga 120

tagtgttcct aaacaaaacc gaattgatgg tattaaactc aacattcctc catttaaagg 180

aaagaatgat ccggaagcct acgttgagtg ggagatgaaa atagagcatg ttttctcatg 240

caacaactat gaggaggacc agaaggtgaa gcttgccgcc acggagtttt ccgactatgc 300

tcttgtgtgg tggaacaagc ttccaaagga gagagccaga aatgaagagc caatggttga 360

ta 362

<210> 1697
<211> 605
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1697

tggccatatt cctaattctc ctctccttta actaaacatc ttgttaatat ttgggttatt 60

gtatatttct taatactcat aaaattctgg ctcaagtttc aattctcact ttcacggagg 120

taagatccta aattccaaat caatttatgg attatttgat tttaattgaa tcattgtgct 180

tatacaaaca cccactcata ttatgggtta ataatttgat tcatttttac gggtgttgta 240

agtagattat ggatgcaagg aaggtgttct atgaaatgcc tgaaagaact attgtttctt 300

agaactcggt tatgactgct tgtgttgaga gtctttcatt gngtgatggg attgagtatt 360

tttttaggat gtggggttgt gcgtttgagc ctaatgagac ttccatggtt gtgttgttgc 420

tctctacttg tgttcttcaa gctccatcca tttctatttc ttttttatta attactaata 480

atactatata tgctattgta attgtattaa taatgagtca ttaataatac tatatantgt 540

atggctacta tatatggcta ttactngtag ttgaattcaa tgacttattt tctgatctcc 600

gatgc 605

<210> 1698
<211> 675
<212> DNA
<213> Glycine max

<400> 1698

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gtatatttct taatactcat aaaattctgg ctcaagtttc aattctcact ttcacggagg 120

taagatccta aattccaaat caatttatgg attatttgat tttaattgaa tcattgtgct 180

tatacaaaca cccactcata ttatgggtta ataatttgat tcatttttac gggtgttgta 240

agtggattat ggatgcaagg aaggtgttct atgaaatgcc tgaaagaact attgtttctt 300

agaactcggt tatgactgct tgtgttgaga gtctttcatt gggtgatggg attgagtatt 360

tttttaggat gtggggttgt gggtttgagc ctaatgagac ttccatggtt gtgttgttgc 420

tctctacttg tgttcttcaa gctccatcca tttctatttc ttttttatta tttactaata 480

atactatata tgctattgta attgtattta ataatgagtc attaataata ctatatatgt 540

tattgctata ttatattgct attacttgta gttgaattca atgacttatt tctgatctcc 600

gatgcttatc ataatggtag agatacaatg tatttgtcct ataaaccttt ggttatatta 660

ctctatggat tttaa 675

<210> 1699
<211> 722
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1699

tgataagaaa gaagaaagta ttatgcaata acaagataaa ttaggtgtgg ctagtaaaga 60

aaataaacta tgaaagtaag caagaaatta aagtgaaaga aatgtaaact aggcggatcc 120

taagagtgtt tggatgacct catttaaggt ttccaacaaa atactcacta tcctaaagaa 180

aaattgccta aaagtattac acacaaatgg aagtagggtg acctattgga ggctcccaac 240

ttacttccaa tgaaaggcct ttttgttata aaatttgaaa gcaatgaagg taagtaaatt 300

ctcaattaaa aaaattacaa aaaggttctc aatttttggt gattgttctc tctttggtga 360

ttcactcaat ttggagtgct tcttagtcca atagctctta aggttgtttt ccccttgctt 420

cttgactcaa attcttcaag ggatgacacc aatcctcctt tccaattccc tatatggcaa 480

ctcacaaaca aggaaacaaa gagacaagca ataaccaaag acccaaaaaa tgaaatgaaa 540

gctaaaccaa tagagtttta acaagacaaa ttttcaggaa tttttcaaca attaaagcac 600

ataaaagaaa gctaggactc anagagaaac ttagaatgac tctagagtag agtanaanaa 660

acccaaatta aaaagactca ngaaacctcc tagttttgga acttgttttt cacactaatt 720

tt 722

<210> 1700
<211> 529
<212> DNA
<213> Glycine max

<400> 1700

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tactagaaaa accatcaaca agtaaagtct cattaaactt ttcatgccat tgtttaggaa 120

cttgttttaa accatatagg gatttcaaaa gtttgcacat tttgttctct tgaccatcca 180

ccacacaccc cttaggttga gtcatatata tctcttccgc taaatcacca ttcaagaaag 240

ttgtcttaac acccatctga tgaatcacta acttatggat tgtagctaag gctatcaaaa 300

tcctaatgga ggaaatcctt gtaataggtg caaaggtata aaaaaaatct atgttaggtt 360

tctaagtaaa ccctttagca atcaaccttg ctatgtattt atctataaaa tcatcacgat 420

tatacttcct cttaaagatc catttacatc caataagatt tgcaccctca aatagatata 480

ctaaattcca tgtattattc tttttaataa aatcaatttc aatcctaat 529

<210> 1701
<211> 584
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1701

ttgaataaat tgaaacgaca aaaactttat acacggatgt ctggttgagt cccgtaatat 60

atcgagacgc tccaaactgt aaacggaagt tcgtaggaaa ttcaaacaac aatatctttt 120

tactcggatg tctgattgaa tcgggtaatc tatcttgacg ctcaaaattg agactagaag 180

ctctgagcaa attgaaacga tattaacttt atacacggat gtccggttga atcctgtaat 240

atatcgagac gctccaaatt gaaaatggaa gctcttataa aattcaaacg acaataactt 300

tatactcgga tgtccggcag agtctcgtaa tatatcgaga tgctccaaat tgaagacgga 360

tgctcgtatc aaattcaaac gacgataact ttntactcgg atgtccgatt gagtcccgtg 420

atatatcgag acactcacaa tttagatcca aagctctgag caaatttaaa cgacaataac 480

tttctacacg gatgttcagt tgagtcccgt gatatatcga gacgcttgaa attgaaaaag 540

aagctcgtac caaatccaac gacaataagt tttactccga tgtc 584

<210> 1702
<211> 397
<212> DNA
<213> Glycine max

<400> 1702

agcttctagt ctcaattttg agcgtctcga tatattaccc gattcaatcg gacatccgag 60

taaaaagtta ttgtcgtttg aatttcctac gagcttctgt tttcaatttg gagcgtctcg 120

atatattaca ggactcagcc ggacatcctt gtataaagtt attgtcaatt caattttctt 180

agagcttcgg atcaaaaatt tgagcgtctc gatatattac gggactcatt cagacatccg 240

agtaaaaagt tattgtcggt tgaatttgat acgagctttc gtttttaatt tggagcatct 300

ctcgataaaa tacgacactc tgtcgggcat ccgagtaaaa gttattggcg tgtgaatttt 360

ctaagagttt ccgttttcaa tttgggagcg tctgata 397

<210> 1703
<211> 363
<212> DNA
<213> Glycine max

<400> 1703

agcttgtacg cgatgccata tggctattac ttgcaaatgc ctattctgaa gccaagacta 60

ctgcatggtt gaatgaattg tgcatgcctc gggtaactgc aataacttct tcgctgcttg 120

acgattgttt tgtggaggca tccaatgctc taatgtcaca accaattact aaaggagcct 180

atatatatgt atgtacaaaa aaaatgtact tattatgcaa aatatatttt tcctcaagca 240

attctttata tggaaatgtc taagcaacat gagttaaatt attagctaca agttaccttа 300

tctaatgccc atatgctgaa atgagcgcga tattcttctt gttgaatgcc tccattttca 360

act 363

<210> 1704
<211> 414
<212> DNA
<213> Glycine max

<400> 1704

agcttgaaag tgtgtaacca accattttct cattgtagaa caccggtaac gtgtatacta 60

tcattgtgat catcttttтc tctgtcattg aaggtgccac ttgagctgtc aagtccctcc 120

acctctgggc gtattccttg aatgactcat gctcttttтt acacatgttt tgtagttgcg 180

ttctatccgg agccgtatca taattgtact gatattgcct aacgaaggca accattaagt 240

ccttccaaga atagactcgg gaaagttcca agttagtgtc ataccctaat ttcgtccggg 300

gattattact tgacgacatg caacctttga ttggccgttt caagatactt ggcccccttt 360

gttgcacaat atgtaagtct tgagacccac cggagtcaaa aagaaccagg gtta 414

<210> 1705
<211> 524

<212> DNA
<213> Glycine max

<400> 1705

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gcagagcaat tatgaccttt ccagcaacag atacaaccct ggatggagga atcaccctaa 120

cctcagatgg tccagccctc agcaacaaca acagcagcct gctccttcct tccaaaatgc 180

tgctggccca agcaaaccat acattcctcc accaatccaa caacagcaac aaccccagaa 240

acagccaata gttgaggccc ctccacaacc ttccctcgaa gaacttgtga ggcaaatgac 300

tatgcagaac atgcagtttc agcaagagac cagagcctcc attcagagct taaccaatca 360

gatgggacaa ttggctaccc aattgaatca acaacagtcc cagaattctg acaagctgcc 420

ttctcaagct gtccaaaatc ccaaaaatgt tagtgccatt tcattgaggt cgggaaagca 480

atgtcaaaga cctcaacccg taacactgtc ctcatctgca aatg 524

<210> 1706
<211> 661
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1706

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aagatgcgga catagaacaa tagttgacag caccttattc tccttaacaa aatggcaccg 120

tagaaaggaa gaataggact attatggaga tggctaggtg tttgcttcat gaaaaagaat 180

tgccaaagag attttgggcg gaagccgcaa atattgcagt tttcatgctt aacagactgc 240

caacaaaagc tttgcaaaag aagacaccat ttgaagcatg gtatggctat aaacctgagt 300

tgctcaatct gaagatattt ggttgtttgt gctttttctt acattcctcg ggttaagaag 360

gacaaactat acaagaaagc agaagctgta acctttgtag gctatagctt aatttcaaag 420

gcctacatga tctatttgcc acatcatgac aaagtaattg ttagcaagaa tatgagattc 480

ttggagctgg atagttggaa ctgggaagat gacaagaaga ttgaatntca gaaggagaat 540

gagaacatag acaaagaacc tgccagagga acaagatcac tttttgatat ctatcanagg 600

tgtaatgttt ctctcatgga acctgcacga tatgaggagg ctacaccaat aaaaaatgga 660

t 661

<210> 1707
<211> 338
<212> DNA
<213> Glycine max

<400> 1707

agctttcaga aaatgtcaat gtcgagcata tactattttt cttccatgtt tcagttgtat 60

gtagcttgta tcttcttcac agatagggca tgcatgatgg tccttaacac tgtatccact 120

caaattcttg tatgccgaaa agccattaat gggaaaaaat agcattgcat gcaacttgga 180

tgcctcattt tgatacccat caaacatgac aatccctttg tcccataact ttgtcaagtc 240

tttaatcaag ggactaagat aaacatcaat gtcttttcct aagtgtcttg ggcccaatat 300

tatcataaac aatatcatgt attttcgctt catgcaca 338

<210> 1708
<211> 592
<212> DNA
<213> Glycine max

<400> 1708

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ttaagtttgc tatcaaagga gaagatggta agaggactac cctatattaa tcaccctgat 120

caactctgtt aaggatgttt acttggcaag aaatttagaa tgatttttcc aaaggagtca 180

aactcaagag ctaagaagcc acccgagcta atacatgtta acgtctgtgg gccaatcaag 240

ccccaagctc actacgtaaa aataaatatt tcctcttttt cattgattat ttttcaagag 300

aaacatgggt ctatttctta tagcaaaaat cataagtctt ttccaccttc aagaagttca 360

aagctgcagt agataaagaa aattggtgag agatcaaagc cataaggact gatcgaggag 420

gagaattcac ttgcaaaaag ttcaagagtt tgtgaagaga atgaattaga cgtcccctga 480

cagtctaaga cccccaatag atagtgtggc agaagataaa atagacgatc cttgatatgg 540

cttgaacatg ctcaaaagca gaactgccaa agaatttagg caaagctttg ca 592

<210> 1709
<211> 367
<212> DNA

<213> Glycine max

<400> 1709

agcttgaagg caaactggat gcattggtta acttggtaac ccagctggcc ttgaatcaga 60

aatctgtacc tgtcgcaagg gtttgtggtt tgtgctcctc tgctgaccac catacagacc 120

tttgcccttc catgcagcaa cctggagcaa ttgagcagcc tgaagcttat gctgcaaata 180

tttacaatag acctcctcaa cctcagcagc aaaatcaacc acagcagagc aattatgacc 240

tctccagcaa cagatacaac cctggatgga ggaatcaccc taacctcaga tggtccagcc 300

ctcagcaaca acaacagcag cctgcttttt ccttccaaaa tgttgctggc ccaaacagac 360

catacat 367

<210> 1710
<211> 654
<212> DNA
<213> Glycine max

<400> 1710

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actcccatgc tagttttgcc taacctgaga gaagcctttg aggtgtattg tgatgcatca 120

aagatgggtt taggaggagt gttgatgcaa aatggccaag tagtgaccta tgcttctaga 180

caacttaaga ctcatgagat gaattatcct accaatgatc tagaattggc tgctgttgga 240

tttcccctgt ggttactttt tgttccactt ttttcttcat acaaatatat tcaagggaaa 300

tctggtttgt cgaaaagtgc accagatcgt caagtattta aaaattaaaa cggatgaatt 360

cgagtatcga actcagggaa actagtctaa gatcgggtta aattcagaaa taatgcattg 420

ttgaaagaaa cattgataat tgatggttta aaatagaatt aaactgggtc taggataaaa 480

acagtaaaaa tgcaagtaag taaaattgac agcagtaggt agaagtgttg ggtctttcaa 540

acagacaagc tgatgcatat agggatgttt ctctaatcga tcatgctttt atgttctatg 600

atgtagcata aattactaaa cctcgatccc taattgactg aatcaatcca gctt 654

<210> 1711
<211> 503
<212> DNA
<213> Glycine max

<400> 1711

agcttatggt agattagagt gaagttcatc ctgatcccga gaggtatagg agacttgtaa 60

gaaagctcat ttatttcacc attacaagac ctgatatctc ttttgttgtt ggagtagtta 120

gtcaattcat gcagaattct catgttgatc attggaatgt tgtcatgcat attcttagat 180

atattaaaag agctcctgta caaggattgt tgtatgaaga caagggtaat acacaactat 240

caggatattg tgatgcagat tgagctggtt gtcctatgga taggagatct acatcaggtt 300

attgtgtctt cattggaggg aatattattt cttggaagag caagaagcaa gttgttgttg 360

cttggtccag tgcagaagtt gaatatcgat ccatggcaat ggttaaatgt gagctcatgt 420

ggattaaaca cattctccaa gaattgaaat tctgtgaaag tgtgcaaatg aagttattct 480

gtgataatca agctgctctt tac 503

<210> 1712
<211> 696
<212> DNA
<213> Glycine max

<400> 1712

tcacagcaaa tgatagaatg tctatagttt tatcatttga caatttattg ttattatatg 60

tcttatcctt catatatata gactcttttt tttcatcttt ttcaactgtg aatttttaca 120

taattcataa attttatttg ataccttgca tagcattgca tttagcaaat acaatttaac 180

atgcttggtt tataagtatt gacacaaaaa aggcttatga aaataccttg tattgcatgt 240

tgctagggct tattaaaaat atcaaataat tttacatgtg tctgtgaaat cagacttatt 300

aatgatgcga taaattatgt aactatcatg tctctcgttg atgttgctaa aaaaattgtt 360

taggaagtat atggattaaa agtgcattct tcaaaaagtt taaagatcga gaacataatt 420

aacccattaa attattatca ataaaataac cttaaattta aaatacaaac ataggtacat 480

gtaatttata ttatcaatta ttgataaaaa aaaatataat aatgtttatg tgaacaaaat 540

atttttttga ccaaaaaata aacgcatgtg ttttatattc aaaatcattt tacagtttaa 600

tatttaatgt gtataaaaca gtataattgt agcaagctga aaatagttta tgaacatata 660

tataagtgtt atcataagtc tggcaaacat gtttac 696

<210> 1713

<211> 469
<212> DNA
<213> Glycine max

<400> 1713

agcttgtgtg cagtaatata aaatgtgtcc acacacagtc acttgttgct atccagtgta 60

ttgttagcct ttttttcac attttttttt tgcttactcc cttttacttt ctttttctct 120

tttttgtttt ctattttatc ttgtaaaaca caagatgctc tagttttaat ttaactaatt 180

tttaaactag tcaaaataac ttataaccta ctgctcttaa aatgatttgc aaaatacact 240

gtttcacttt tgattaagaa ttacaaaatt cacacacaaa aagatgacaa tggaacaaat 300

tttatactat ctctatattg taattaaaat taatattata aagatttgat agttatatta 360

agttgttcat aaattatttt tttttatcaa tcattcaatt caattttgaa taaaactata 420

ataatggttt aaatcttgaa aaaataatat aaaatttta gaattaaaa 469

<210> 1714
<211> 470
<212> DNA
<213> Glycine max

<400> 1714

agcttgacga aatctagatg gcgatgcctc agcaacagct tgtacttgtt tctcgggcac 60

agcaaagcat acagaatgct cactactagc ctacataaat actgaaaatg attaatgcca 120

tttcttatat atcagcgtgg acaactagaa aaattgaaaa aagttataaa tgcacctgag 180

atatcatgat aacattagct ccaacatctt ttactgcacc aaaaatagca ctggccgtac 240

ctggaacacc agacattcca gttctgcaaa aaagcatcaa agaaaaattt attggaatct 300

acaacttgga caattaatat tggttaaaga aaaccttaaa ttaaatagaa atccctcggc 360

aggaaaaaat gccaactatt catcatgtaa cacaacttgc atttatgact caccccttga 420

cgtttacaaa tgccaaagtt gcctatggat gcaaaatctt tgacaaaatt 470

<210> 1715
<211> 439
<212> DNA
<213> Glycine max

<400> 1715

agcttctaaa ctttgtacaa gaatgaagct ctgataccac ttgttagaca agtggcctca 60

gatatcttaa gaaggggggg ttgaattaag atattccaaa cttttcttct aattaaaaat 120

ctatcttact ttttacttaa gttatgaatt cccttaatga caatcttctt aaatattaat 180

tcaaatgaag caacttgaat tatgaatata aagcaataat aaataaagga gattaaggga 240

agagaaaatg caaactcagt tttatactgg ttcggccaca cccttgtgcc tacgttcagt 300

ccccaagcaa cccgcttgag agttccacta acttgtaaat tccttttaca agttctaaac 360

acacaaagac aacccttcct ttgggtttag agattcttta caacaagaaa ctcacagtct 420

cttaatccct tagagaatg 439

<210> 1716
<211> 485
<212> DNA
<213> Glycine max

<400> 1716

agctttaaac tctattttta attctatttt tctctctaaa tgtatattac aatgcatata 60

tttgtaaata attaatgagc tcaaatattt aaaatgtatt ttttttacat aaatcttata 120

aaataagtgt tagaaacaca ttttttaaca ttatccttaa cacatttaat ggattgaaat 180

tgtttaaaaa ttacaaaatc atttcatgga gtcattaaat aagatgaatc acacaatttt 240

tttataattt taagaaattt caatcaagag gatgtgtatt taaaagaatg agtgaaaata 300

tgttactaat atttctcatc ttgtaatatt ttgagtctga ttctttctaa ttggataggg 360

aaatacacat tatttttgtg ggagccacaa taatattttc ttcgtcccgt tataaataat 420

gtttaaggtt tttttaaacc gattaaaaaa acaagtattt taaagtgttt tgtgtatttc 480

aaatg 485

<210> 1717
<211> 590
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1717

ttgaatgcac tattcaatgg agttgacaag aacatcttca gactgatcaa cacttgcaca 60

gtggccaaag atgtatggga gatcctgaaa atcactcatg aaggaacctc caaagtgaag 120

atgtccagat tgcaactctt ggctacaaaa ttcgaaaatc tgaagatgaa ggaggaagag 180

tgtattcatg acttccacat gaacattctt gaaattgcca atgcttgcac tgccttggga 240

gagaggataa ctgatgaaaa gctggtgaga aagatcctca gatccttgcc taagagattt 300

gacatgaaag tcactgcaat agaggaggcc caagacattt gcaacatgag agtggatgaa 360

ctcattggtt cccttcaaac ctttgagcta agactctcgg atggggctga aaagaagagc 420

aaaaacttgg cattcatgtc caatgatgaa ggagaagaag atgagtatga cctgnatact 480

gatgaaggtc tgacaaaagc agttgtgctc ccgggaaagc agttcaacaa agtgatgagc 540

agaatggaca ggaggcagaa gcccatgtnc agaacatccc tttcgacatc 590

<210> 1718
<211> 581
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1718

tcttatccaa ggctcatctt ggtggtgaag ctccttcctc catggcttat tccataatgg 60

atggcgcctc ctctcacctc ttttcctttg tcttccgctg catctccatg gtggaaaatc 120

accattaaag gaccccattg aagctcaaag atccagcctc catagaagcc ccacaagcaa 180

gcttccatca ccttgcccta atccatttgg tgaaatagtc aatggcgatt agtaggaatt 240

agattgctcc tggggctttt ggcagtggtc ctagtatgcc tattccctat aaggcaaaag 300

gccaagggga actcaagcta tggaggatgt cangaggggt gtgtggaatg tctacaaact 360

cttggcatcg cctgaacctc cttatgaagt caagggtgtc ggccaataat agccggcgcg 420

caccacttan gttgctaggg agcgacccct gatatggagg tcacagattc cttcatgtag 480

ctcttgcatg agatagtcta cttgttggtt ttttaggcat ttaagcaatg atgtgttcaa 540

ccctcttttg aatagctcac catcaaggat ggcgttgtat c 581

<210> 1719
<211> 406
<212> DNA
<213> Glycine max

<400> 1719

ttttgtctct cttattaggc aatggttggc cctctctctc tctattgtga aatcctcatc 60

ttttattctt ttctactttt gcagcaacaa caaatttaat catcttttca ccgacgagct 120

tgtccctttc aataccaacc ccgacaagat gctcgacctc caacacacca ccaccttcct 180

cccctgcacc aagatcaaag cctctgctga ttcctctgtc accgctgact ctgacctctg 240

cattttcact actggcgccc gccagatcac tgatgagtca cgcctcaacc tcctctagag 300

gaacctctcc ctcttcggca ccaccattct gactctcgtt cgttactccc ccaacgctat 360

tctcctcatc atttccaacc ctggcgacat tctcacctac acacat 406

<210> 1720
<211> 441
<212> DNA
<213> Glycine max

<400> 1720

agcttgctaa cccatggaag ctcctaatat ctcccacact ttttggggtg ggccattcgt 60

ggatggcctt gatttcccag ggtccacatg gaccccattt ctaccaacta caaaacctaa 120

gaaaactata ttatctacac aaaaggtaca cttctctata tttgcataga gggtgttttt 180

cctatggact gaaagaactt acctgagatg tcctaagtga tcatctaggc tcctattgta 240

cactaaaata tcatcaaaat aaacaactac aaatctacct atgaaatccc ttaagacatg 300

atgcataagc cttataaagg tgcttggtgc attactgagc ccaaaaagtt ggtcttgaaa 360

gcgaattttc actcatcacc ctttttcatc ctgatttcgg gataaccact tttaagaaca 420

atttttgaaa aaatattggc a 441

<210> 1721
<211> 381
<212> DNA
<213> Glycine max

<400> 1721

agcttgcttc tacacttctc cttgaagtgg ggtctccaat caccttttcct ctgtctccat 60

tccactacca ctgatcttca agaagcaaag gactccattg atgaaggata tccaaggcct 120

acaagttcta catggagcta cattatgtgg tatcagagta tcttcatcta ggtgatcttt 180

tgcttactct atcttttgtt cgggcaattc actttaattt ctttttgttc atcgtcttct 240

ccatgtatct cctccattgt ctagtggttt ggtgttggtt aaattacatt caaaaaaata 300

aaatgatcaa aacttagatc tacacttgtt cttgcatttc catggggtcc aacccatgcc 360

tcatcaatta aggaatgctt t 381

<210> 1722
<211> 519
<212> DNA
<213> Glycine max

<400> 1722

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atcgagacgc tcgaaatgga ataccgaagc tctgagcaaa tttaaacgac gataaccttt 120

ttactcggat gtctgattga gtcccgtaat atatcgagat gctagaaatt gaatgttgaa 180

gctctgatca aattcaaacg acgatgactt tttactcgga tgtccgattg aggctcgtta 240

tatatcgaga cgctcgaaat ggaatatcga agctctgagc aaattcaaac gataataact 300

ttctactcgg atgtccgatt gagtcccgta atatatcgga acgcttgaaa ttgaatgttg 360

aagctctgag ccaattctaa cggcggtaag tttttactcg gatgtctgat tgagtcccgt 420

aatatatcga gatgctcgaa atggaatgtt gaaactctga gcaaattcaa acgacaataa 480

tcttttactc ggatgtctga tggaggcccg caatatatc 519

<210> 1723
<211> 451
<212> DNA
<213> Glycine max

<400> 1723

agcttctaca ttcaatttcg agcttttcga tatattacgg gactcaatcg gacatccgag 60

taaaaagtta ttgtagtttg aatttgctca gggcttcggt attccatttc gagcgtctcg 120

atatattacg ggactcaatc ggacatccga gtaaaaagtt attgtcgttt gaatttgctc 180

agagcttcgg cattccattt cgagcatttc gatatattac gggactcaat cagacatccg 240

agtaaaaagt tattgtcgtt tcaatttgct cagggcttcg gtattccatt tcgagcgtct 300

cgatgtatta cgggactcaa tcagacatcc gagtaaaaag ttattgtcgt ttgaatttgc 360

tcacagcttc tacattccat ttcgagcttt tcgatatatt acgggactca atcagacatc 420

cgagtaaaaa gttattggcc tttgaatttg c 451

<210> 1724
<211> 618
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1724

ttgctggtaa aggtcttgaa tgaagctcac gtagcccaag acatctccgt agaaggcttt 60

gggggaatcg tcaataacat caaagccaac aactacctca ccttcgctga agaggaaatc 120

cccgccgagg ggagaggaca taaccaggct ttacatgtgt cagtcaaatg catggaacac 180

gttatggcca aagtactcat cgataacggc tctagcttga acgcgatgcc caaaagcaca 240

ttggagaaat tgccatttaa ctcttcccat ctaaggccaa gttccatggt ggtctgtgcc 300

ttcgacgaca gccgccgaga ggtaagggga gagatcgacc tcccagtaca gatagggcct 360

catacctgcc acgttacatt ccaagcgatg gatatcaacc cagcctatag ctgtcttttg 420

gggcgtccat ggatccactc agtgggagtt gtcccctcca cactccacca aaagctgaag 480

tttgtagtgg aaggacatat ggtcatagta tcacgtgagg aagacgtcct gntaagttgc 540

ccttcctcta tgccatacgt ggaagccgcg gaggagtcat tataaacgac tntccaatct 600

tttgaggtag taagcatc 618

<210> 1725
<211> 486
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1725

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gatttgaata ttacctcttc accatcagag ttgacagtgt tatcaggcta aggatgtatc 120

aaccattaga cataggttgg tttcttcctc attgtcctta tcagacaatg aattatccaa 180

gtcctcccaa gtgttcatga ggcttttaga tgcaatccta ccccgcaagg gcattggata 240

gaagactcca agtttattgg gccagagatc caagggaagg ccctanggtt ctcatgagcc 300

ttanggtaga tttcgagccc atgggctaag tatgagcccg cttatctttg taaatattag 360

aatagatttt tcctttgctt cgcgcccttg tatttggcca ttctagtaat atagggcttt 420

aaccctgtat ttcggggcat tttgagtagt ctttgtaaca acgacttttn ttgtttttca 480

tgtttt 486

<210> 1726
<211> 565
<212> DNA
<213> Glycine max

<400> 1726

agcttttggt acaaaagaag aagaagaata acttcaaaga gatttcaagg cttgtaaatg 60

attgtaagag attgttagaa agattgatta aaaatgcaaa acaaagcctt acttttatag 120

actcttcatg tatggtcaag aaagccattc agaagagtta taacttttag aaaaacttaa 180

aacccatttg aaagggtcaa aacctttttg aagagttaca tctttagatt tttcagaaac 240

aaacattggt aatcgattac caaataagtg taattgatta cacaaagatt ttgagtgaaa 300

caatgtgact cttcacattt aaatttgaat ttcaacgttc aaggacactg gtaatcaatt 360

accaaatcat tgtaatcgat tacagccttt tgaaaatatt tggaacgttg taaattcagt 420

ttgaaaactt tttcaaactc attttgctac tggtaatcga ttacaacaat atggtaatcg 480

attaccagaa gagtaaaact cttttgtaaa ggtttttgtc aaaactcatg tactattcaa 540

aagttttgaa aacctttaa tactt 565

<210> 1727
<211> 565
<212> DNA
<213> Glycine max

<400> 1727

ggctcaaaca cgctatgacc aactcaacct tattgaaggt aaacgcttga tggccatgtg 60

ccatgggcgc ctatatcaac aaagaatgaa gaatgtgttc gacaagaaag tgcgcttgcc 120

caagttccac gaaagggacc ttgtgctgaa aaagatgtcc cacgctgtta aagaataatc 180

gagggaagtg ggcctccaac taccaaggac ctttcattgt gaaatgggct ttttccggag 240

gggccttggt gcttgccaac atgaatggcg aggagctacc tttacccgtg aactctgatg 300

ttgtcaagcg atactatgct tagaatctgg ggcaattaag gatatcattg catgttcttt 360

tatttttatg tgttcttctt gggttccccc aaggattccc gtctgctgta tatttctcgt 420

cacagtcttt ttaaaaagaa gagaacaaga gtttgaggct tcaatcctca ctttgggctt 480

taaaccatgt gcagtttgtg ataacctgag ccttttttcct tagtccatgg gatgccccaa 540

gcgcttaatt aaaactgaac ctgac 565

<210> 1728
<211> 716
<212> DNA
<213> Glycine max

<400> 1728

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attcaatgca ccatatttaa ttaacttagt taaatatcct tgacaatttc taagctactt 120

aatttcactt cctggacaat aattcatatt atccaattta tactatctat aaggtaaaaa 180

ttacaaatac atgaaagttt gaaagcaccg taggatttgt taataaaaaa acatgaagca 240

agtgggttcg aagggaactt catgaatcct tataattttg ttttaatcag cataggtata 300

cgtatattaa tataaatgaa agacaaaaat gggtgcccca accattttcc gtataatgta 360

gattcatgga gaaaatttaa caatcaatat attttctgac atacttttt aatattgatt 420

aaaattataa attaaattta tagatcttga tttattttaa ctagtatttt aaatttgcaa 480

tttattgaat aaatttttat ttatatataa taataataat gtaaagttac caaccaatta 540

gatattttta acatttaata aaatattatt aattaaaaac ttggaaaaaa aaaaatttaa 600

aaatttataa attatatttt tgaatttatt actaaaaaat ttcaaatagg ggatattagg 660

taatttttt taaaaattaa aatgaatacg ggggttaaaa ataaaggatt ttttaa 716

<210> 1729
<211> 548
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1729

tatatactat atgatgaact aagttntata tagctcttag gtgtaataac tatttaaata 60

gccaaagcca agcgctaaat ataattaaac ttatattccg tccaagctta aaaacagcta 120

tttatataca agatatatct ttaaaataac aaccagtcac atggatattg tcaaataatt 180

gaaaacagtg tgtgggcctg ttattatcaa atcacttgta aaacttaatt atatgaagag 240

cacttaatga ttgataaact atttactatt aatatcagat aaaaattatt ggatagagat 300

tattttcttc cttcgacatg tttaatcatc atttgtttta aaaaccccct gatttataat 360

ttaattaaaa ataatgtttg tcctgagggc tacttccatc aaaagtggaa actatttttt 420

tatacttgcc ctttactcct catcaatcat aatctgtgat ttttaagata taaccctcct 480

ccgttgacat ccaatttagc atattaaaga aaaatggtgc gccattatac aacattgata 540

aataagtt 548

<210> 1730
<211> 455
<212> DNA
<213> Glycine max

<400> 1730

agcttaaaag aatcagaggg gctcaaacac gctatgactt actcaacctt attgaaggga 60

aacgcttgat ggccatgtgc catgggcgcc tatatcaaca aagaatgaag aatgtgttcg 120

acaagaaggt gcgcttgcgc aagttccacc aaggggacct tgtgctgaaa aagatgtccc 180

acgctgttaa agataatcga gggaagtggg cctcgaacta cgaaagacct ttcattgtga 240

aatgggcttt ttccggaggg gccttggtgc ttgccaacat gaatggcgag gagctacctt 300

tacccgtgaa ctctgatgtt ggcaagcgat actatgctta gaatctgggg caattaaaga 360

tatcattgca tgttctttta tttttatggg gtcttcttgg gttcccccag ggattcccgt 420

ctgctgtata tttctcgtca caagtctttt aaaaa 455

<210> 1731
<211> 400
<212> DNA
<213> Glycine max

<400> 1731

atactgaaac ttttgcccct attactcatc taaaagcaat acacatttta ctatcccttg 60

gtgctcatca tgggatgatg gtgtatcaaa tggatgtaaa aatcatattt ctcaatggac 120

taattaagga agaagtctat gtggaacaac ccctggagtt tgagaattct atctaccttc 180

atcatgtttt caagcttaaa aaggaccttg tatggtttaa aacaaactcc ttgagcttgg 240

tatgaaaagc taagtttggt tataactgaa aatggcttta aaagaggaaa agtagatact 300

actttgttgc ccaaaaatta tggtaatcaa ttcctaatcg gctagatata tgtggatgat 360

atcatatttg atgctcctaa tgactcttta tgccagcttt 400

<210> 1732
<211> 687
<212> DNA
<213> Glycine max

<400> 1732

gcttcccaag tttttaagtt attcctcaaa actgtcctaa gcaaagttcc caaagtccta 60

ttaacaactt ccgtttgccc atcggtttgg gggtgacaag tggttgaaaa taacaattta 120

atgcccaact tgctccacaa agtcctccaa aaacgcaaat catcaagcct aagtatagga 180

tgcctatatt taatggtgat gttattaagg gctctacaat cagaacaaat gtgccatgtc 240

ccatccttttt tagggaccaa aatcactggg acagcacaag gactcatact atctcttacc 300

caacctttgc taatgaattc atccacttgt ctttgaatct ctttggtttc ttttgaatta 360

cttctatagg ctggcctatt gggcaaagaa gctcccggaa tgagatcaat ttgatgctca 420

attcccccctc aaggaggtag tccacttggc acatttggtg gaaacatgtc atgaaaatcc 480

tgcaaaagaa ttttaacact agaaagcact taaaatcatc aaaagtgtta ggggcaaaat 540

ctgatttttg cataacaaga tatagaacga ctgtttaaca ccaaacaacc ctcttgacct 600

cacttttttgt gggttaatac ctctccctca ctctaagggt tccccctttc ttttggaccc 660

tcttttttccc tcccagtggt tccctca 687

<210> 1733
<211> 437
<212> DNA
<213> Glycine max

<400> 1733

agcttgaacc aagatcaatc tcaatggtct tgtttctaat gagaccatcc ctttttttca 60

gataagctct ttctgcctct cccacttctc gcttggcaca agcacaatga tccaaccaaa 120

tccccaacac ttgcttggaa atggggtcca aatggtccct gatgatctcc tccatgcgtt 180

ccactccgcc attttccgtc agaacgcgaa ccattatggc tgtaggagaa gaaacagtgc 240

ggatgtaaag ggaagaagaa aagtatggtt gaacctctgg aactctctcc agagtctgcc 300

tatgtttgtc tagttgagtg tcctcataga aagttttgag gtcatctggc caaagcacat 360

ggtctttccg gggaggccaa tcaagaatga gaagtagcat tgttggacta ctggggatca 420

tttcaaacac aaaattt 437

<210> 1734
<211> 505
<212> DNA
<213> Glycine max

<400> 1734

tcctatacat atgatagaga gggttcacat caataatgtg gttctatcat atgctaaaag 60

ttttacgatt ccatgcaacc atatacatct aggatacatg tgggcatgtg catttgagtt 120

ttgcttaaaa taaccttatt ttctatccag aagtcccata tgtgtaatac tattatccca 180

aagaaaaatt ataatttttg ctatattaga ttactaatag aaactttctt attaactatt 240

atgaataaat caatatggag attatagtgt ttatctattt tttaattttc aaaatccttt 300

atgttgaata gaatgaatga atggctatag aataattagc catatgaaaa acccaatgta 360

ctatgacaga aattcctaag aatgatatca tgactttacc tagccattga accaatttgc 420

ccaattaatg aacatggaga tgtacccaca tgtagaggta tacatgcatc accattattt 480

catttttaat ttattgtgca aaaat 505

<210> 1735
<211> 395
<212> DNA
<213> Glycine max

<400> 1735

aaggtctatg actcagtctc atgggttttt ttggattata tgctgcaaag aatgggtttc 60

tgccacaaat ggagacactg gatgtctgcc tgtctcagtc aataagcatt tctattctta 120

tcaatggcag tcctaccaag gaatttgctc ctactagagg tttgaagcaa ggtgatcctt 180

tagccccctt actctttaat ataattggag aaggcatcac aggattgatg aacgaagcag 240

ttcagaagaa cttatataga agctatatgg gtggaaagaa aaaggaaccc attaatattt 300

tgcagtatgc ggatgacaca atttttgtgg gtgaggctta ttgggaaaat gttattgctt 360

ttaaagctat gctcaaggga tttgaattgg cctca 395

<210> 1736
<211> 516
<212> DNA
<213> Glycine max

<400> 1736

agcttcaaaa aaaagatggc ctcggcaaac tccttatttc cagaagggaa ttctatcaat 60

agacctccaa tcattaatgg agagggttac cactactgga aaacccgaat gcaaattttt 120

attgaggcaa tagacctaaa tatttgggaa gccatagaaa tagggcctta tatacccacc 180

acagtagaaa gagttacaat agatggcagt tcatcaagtg aaagtataac aattgaaaaa 240

cctggagata aatggtctga agaggataga aaacgagtac aatacaattt aaaagccaaa 300

aacataataa catctgccct gggaatggat gaatatttca gtgtttcaaa ttgtaagagt 360

gctaaggaaa tgtgggacac tctttgatta acacatgaag gaactacaga tgttaaaaga 420

tctaagataa atgcactaac tcataagtat gaactaatta gaatgaatgt caatgaaaat 480

attcaaagca tgcaaaagag atttacacat atagta 516

<210> 1737
<211> 408
<212> DNA
<213> Glycine max

<400> 1737

caatagaaac tatatgactt ggagaattct atgccacttc aacctttga acaacaagtg 60

aaggacctca agataaccca agctgacctt tgggaaaagc tactatgcag gagtctattg 120

tgaggcagaa atcaagatgc atatggatca aagaggggga caacaacaca tcctattttc 180

atagagttat taatttgagg aggaggataa atgctttgag gggggtgcag attggtgaca 240

cctgggtgga aaatcctaac attataaagg ctgaaaccct tcatcatttt cagaacaggt 300

tcaatgagcc tcacttgagc agacctaact tggatggggt ttcatttaaa agtctgactt 360

ctactcagag agaaactatg attgaaccct tttatagagg aagagata 408

<210> 1738
<211> 445

<212> DNA
<213> Glycine max

<400> 1738

agcttatgct tttaatttag cccatttaaa tataagtatg agcaaccttt ctttttcaga 60

agccaagctt gaacttcaag tgttcaactt ggctagatag acttgtttgc acctttactg 120

ataaatgact aatcagaaaa ttaaattcac atagaggaat acaatcatta tactaatgta 180

taggtgacag acacacctta cttttgcatt taaccttgta gactgcctct ctgaatgatg 240

agacaaagct gttattaatt ctgatctgcc aataaaaagg caggggaaat aaaaagtatt 300

agctgtgaaa tatagaggtg agaataagaa cagaaccaac ctgtgcatga tgaagatctg 360

gctcaatgtg tttcctaaat aatggaaaaa tgctatcaat aaggtaatcc agtgaacaag 420

aatctccaat gtcatagcga acttt 445

<210> 1739
<211> 213
<212> DNA
<213> Glycine max

<400> 1739

tctcagcttc accttaggag acggaccatt ccaagtgttg gagaagatca acgactatgc 60

ctacaagatt gacttgccta gtgagtatta tgtaagtgcc actttcaatg tgtctgacct 120

atctcttttt gatgcagatg gcggagcctt tgatttgagg acaaatcctt tttcagaaag 180

ggggagggat gaagacataa cccaggacca tga 213

<210> 1740
<211> 416
<212> DNA
<213> Glycine max

<400> 1740

agctttgagc taattcaaac gacaataatg ttttgctcgg atgcccgact gagacccgta 60

atacatcgag acgctcgaaa ttgaatgttg aagctctcag caaattcaaa cgacaataac 120

tttttactcg gatgtctgat tgagtcccat aatacatcga gacgctcgaa attgaatgtt 180

gaagctctca gctaattcaa acgacaataa ctttttttact catatgtctg attgagtccc 240

gcaatatatc gagatgatcg aaattgaatt ctgaacctct aagctaattc aaacgacaat 300

aatcttttgg ctcggaagtc tgattgagtc cccgtttcta ttgagacgct caaaatagaa 360

ttcttaacct cctagctaat taaacgacaa taacttttt ctcggatgtc tgattg 416

<210> 1741
<211> 433
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1741

tctgtggtgc acaagaattc tattatttaa atattcaatt tcccaaacaa aaatttgggc 60

atcataggtc tttcatatca aattatttct ttaatcaatc tatagctttt ggaaagctct 120

tcaagagctc caaanatatt tacataatct acataaacaa cagttatgaa aaatctattt 180

tttcatattt tcatgaaaaa tacatggaca aataagatca tttctatatc cttcctttag 240

caagtactca ctaagtcaat tgtaccatgt gcgacttgat tgccttagta ttattctcta 300

gaatatgcat tattgggtca attatatcct tcaggaagtt ttatgcaaat atcattatca 360

agagagtcgt ataagtaaat tgtacaacat aaaaacatcc attagatcta aactaagtcc 420

tccatgggct act 433

<210> 1742
<211> 394
<212> DNA
<213> Glycine max

<400> 1742

agcttaagct ccttcaactg cacaagctct taatatttga agagtatcct tgtggaacct 60

tcacctgacg aagacactga caaaaactta tcttctcctt cttggacaaa atatggcagg 120

ctgggggcaa gtaaattttc ttcccatcat accttggatg caaatgtgat tgtataccca 180

tatcaggtag atcttgacgg gtattcaagc catccttcgt cttgccttga atgttaaaga 240

gcgtcccaac cacactgtca caaacatttt tctccacatg cataacatca atacaatgtc 300

taacgtcaag atcacaccaa gtcggaagat caaagaaaaa ggacctcttc ttccatatgc 360

aactctgact tttatccttt ttttggggcc ttcc 394

<210> 1743

<211> 432
<212> DNA
<213> Glycine max

<400> 1743

taaaggtgtg tagcccacca tcttttcata gtagaatact gtttatgtgt ctactattat 60

tgtcatcatt tgtttttcca tcattgaggt gccacttgag ctgccaggtc tctccacctt 120

tgggcgtatt cttttgaagg attcgtgccc ccttttttgca catgttttgt agttgcatcc 180

tatccgaagc cattatactg acactgccta acgaaggcaa ccattaggtc cttccaagaa 240

tggactcggg aaggttccaa gttagtgtac caagtaacag ctaccccagt aagactttct 300

tggaaggaat gtatcaacaa ttcctcatct tttgcatatg cccccatctt tcaataatac 360

atctttagat ggttctcggg gcaagtagtc cccttgtact tgtcaaagac cagcaccttg 420

aacttgggag gg 432

<210> 1744
<211> 457
<212> DNA
<213> Glycine max

<400> 1744

tcaacatcag accactttca gggtgctgga actactttta ttttttgat ggggcctatg 60

cacgttgaaa gccttgtagg aaagaggtat gcctatgttc gtgtggatga ttttctccag 120

acttacctgg gtcaacttta tcagagagaa attagaaacc tttgaagtat tcaaagagtt 180

gagtctaaga cttcaaagag agaaagattg tgtcgtcaac aaaatcacga gtgaccatgg 240

cacagagtta gaaacaacag gttcactgaa ttctgcacat tctgaaggca tcactcatga 300

gttctctgcg gccattacac cacaacagaa tggcatagtt gagaggaaaa acaagacttt 360

gcaagaggct gctatggtca tgctttatgc caaagaactt cctaatatct tctggctgaa 420

gccatgaaca cagcatgcta catcccaacc gagtccc 457

<210> 1745
<211> 255
<212> DNA
<213> Glycine max

<400> 1745

tgctggaact acttcacatt tatttgatgg agcctatgca cgttgaaagc ctctgaggaa 60

agaggaatgc ctatgttgct gtggatgatt tctccagatt tacctgtgtc aactttatca 120

cacagaaagt ccaatccttt gaagtattct acgagatgag tctgagactt caaagagaga 180

aagattgtgt cttcaagaga atcacgagtg accatggtag agagtttgaa aacagcatgt 240

tcactggatg ctgca 255

<210> 1746
<211> 589
<212> DNA
<213> Glycine max

<400> 1746

agcttatagg gagccatgcc aatggtaaag tgaaaactat tgttataagt taactctatc 60

aatggaagaa aactctccca acttcccttc ttctccaaga cacacgccct caaaaggtcc 120

tccaatgact gaatggtccg ttcagtttgt ccatcaatct aaggatggta agctaaactt 180

aatctaagct tggttcccaa tgctctgttc aagctctccc aaaatctaga ggtgaatcta 240

ggatctctat cagatactat gctagatggc acaccatgta atctgacagc ctcacatata 300

tacaaggagg tcaacttctc caaggaaaat ctgatattaa tgggaatgaa gtgagcagac 360

tttgtcaatc tatcaacaat aacccagata gaatctaaac ctctaggggt tctaggtagt 420

cctaccacaa aatccatgga aatactgtcc cactttcact ggggtatctc taaaggttgt 480

aacttccctg aaagtctctg atggtctatc ttagccttct gacagactag gcatgcatac 540

acaaactcac taacctcttc ttttatgttg ggccaccaaa acatcggct 589

<210> 1747
<211> 414
<212> DNA
<213> Glycine max

<400> 1747

agctttgagc caattctaac gacaataact ttttacttgg atgtccgaat gagtctagta 60

atatatcgac acgctcgaaa ttgaatgttg aagctctaaa cctattcaaa caacaataac 120

gttttactcg gatgtccgat tcagtgacgt aatatattgg gatgctcgaa attgaatgtt 180

gaacctctga gccaattcaa acgacaataa ctttttactc ggatgtctga ttgagttccc 240

tcatatatcg agacgctcga aattgaattt tgaacctctg agccaattta aacgaaaata 300

acgttttact cgaatgtctg attgagtccc cgaatatatt gaggacgctc gaaattgaat 360

gttgaaactc tgagccaatt catacgacaa ttacttttta ctcggatgat tgat 414

<210> 1748
<211> 509
<212> DNA
<213> Glycine max

<400> 1748

aaactttcct ttcttattaa tcactttgaa tgttatatca caaaataaat tatatttaaa 60

catttaaggc aaagctattc cgagtaatgg gagagttgac cttttggtat attcttcaaa 120

ctacaaaata tgtttggaac aaagaaatct tttcttgaac ttggatataa atatagcact 180

aaggaatata ccaaatctga gatacttctc aatactagtt tgtaaaagct aaatttctaa 240

catactccat attttaattt ctagttttca gcaaggtatt tttgttgctt ttaaagtgta 300

aatcggtttg aaaatctttt taatatttag ttctaatcaa gtttattatt agatattatt 360

caatcaaaac taattaaaca cacaacacaa acttgagaag caaggaaagg atattgaaca 420

tgagaatttt tttattgatt cacctataac cctgggctat acattcagtc attacaactt 480

aattatagga tcttctacgt ggaaaaaaa 509

<210> 1749
<211> 516
<212> DNA
<213> Glycine max

<400> 1749

agcttcaaga attatggcct catcaaaata cttgtttccc gtaggaaatt ctataaataa 60

acctcccatc tttaatggag tgggttacca ctactggaaa acccgcatgc aaatctttat 120

agaggcaata gatttaaata tttgggaagc catagaacaa ggaccttatg ttccctctat 180

aataaccgga agtgcaacaa tagaaaaacc taaaacaaat tggactgagg aagaaagaag 240

attagtacaa tataatttaa aggccaaaaa tattattaca tctgccttag gtatagatga 300

atactttatg gtttcaaatt gtaaaagtgc taaggatatg tgggatacac tacaagtaac 360

acatgaaggc acaacagatg ttaaaagatc taggataaac actttaacgc gtgagtatga 420

actttttaag atgaaatgta atgaaaatat acaagacatg caaaagaggg tcacacacat 480

aggtaatcat cttgcatctt taagaaaaac cttttc 516

<210> 1750
<211> 404
<212> DNA
<213> Glycine max

<400> 1750

agcttttgag caaattaaat ggtcataact tcttactcgg aggtccgatt gaggcgcata 60

atatattgag acgcttcaaa ttgaaaaatg gaagctcttg aaaaaatcaa atgggcataa 120

cttgtgactt cggagtcgaa ttcacgccca taatatatcg agacgctcca aattgaacaa 180

tggaagctct tgaacaattc aaatgggcat aacttttaac tcggaaggtc cgattgaggc 240

gcataatata tcgaaacgcc tcaaattgaa caatggaagc ttttgagcta tacaaatggt 300

tattactttt cactcggaaa tccgattcag gcacataata tatccaaacg ctccaaattg 360

aacaccggaa gctttttgaa caattcaaat ggtcataact ttta 404

<210> 1751
<211> 538
<212> DNA
<213> Glycine max

<400> 1751

ttaaaatttg aattaaaacg ttcaataact gctagttaat cgatttacca tcccaggtgt 60

aatcaattac acaatttaaa atttgaattc aaatttctaa tagctgtttt aaatagtttc 120

aactgctggt aattgattac aatacttatg taatcaatta catgctttca aaagtattca 180

aaatcatttt aaaagcattt caggaagcat tttggccact agtaatcgat tacatcctct 240

ggtaatcgat taccagagag taaatctctt gtaaaaacat tttaacttat attctttggc 300

caaacctctt gttgtctcaa cttggaattc ccttcctaag tctctagaga ttatcttgat 360

catatatctt gaatttcttg gattcttgtg ttgaattaaa cttgagaagc gcagcatgat 420

cctcttgaat taaacttgag aagcacatgg tccttttgca tcatcaaaaa cataaaatgg 480

cctttgtttc tacaaaatta tctttgattt ggtatataga gctcttgcgt tggacaaa 538

<210> 1752

<211> 556
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1752

agcttgtata accatgtcta gatatgaagt tattgaaaca atcaagaatg ttcttttaat 60

gaatattggg gctcttatac caatattgag aaggaaataa taacattata ttctctaaca 120

ccttttgaca cacttttta tttggtgaaa ttgatgtaag tctcactaaa tgagactcat 180

ttcttatttg gcgcatctcc ttttaaacta gtggaattca aataaatttt aaccaatatc 240

agaagagagt ctattagaaa gagaattata attatgttac acgaggctga agtgccctga 300

atagcagact gataaaagac aagaaatttt gtttgcaggt acttactcct tcgtactcac 360

tccaaggagg ctttccccgt gaacatttca ataattgtac aacccanact cccaatatta 420

acagcgaaag ccaggtcaga gctgttatct ttttgcacaa ccgcttgaaa aagctgcatg 480

tatgaggaat aagtgtctat agagaacgca tgagacatcg cggagttata gagttataaa 540

ccttaataga tatacc 556

<210> 1753
<211> 469
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1753

agctattcct ctagtngctc tgatagggtt tcctagtcat tatatagaaa gagaatggat 60

tggagcctca attatattgt ctctgtgcga ggggcatttc tttctctaca aacattattt 120

tgcacatccc aacggtggga atatgcggaa atgagttccg aatgtggtga ccaaattcta 180

tgatgctcca atggttaatg aatatgggat catactttta cttacacaag tttgggtgta 240

tgcatgtttt gggagaggaa gaagcgataa ctaanttgag aggaagaaag agcgcataga 300

cgtatccgat gtgtcaaaac tgacctaatg tgtccattta taactatgag accgagtcta 360

ctatatatnc tatctgttgc tataattaat tactncataa aaagagagct ctattatact 420

ctctatcaaa tacataaata taacatcctc ttatgttcta aaaacacat 469

<210> 1754

<211> 431
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1754

ataactttca ctcggaggtc cgtattangc gcataatata tcgagatgct cgagattgaa 60

caacgaaagc tctcgagaaa tttaaatggt cataactatc aacttcgagg tccgattcag 120

gcgcatacta tatcgagatt cacgaaattg aacaacggac gctctcgaga aattcaaatg 180

atcataactt ttctcacgga tgtcatgatt aggcgcataa tatatcgaga cgctcgaaat 240

tgaacaacgg aagctctcta aaaattcaaa tggtcattac ttttcactga gaggtccgat 300

tcatgcgcat aatatatcga gacgctcgaa attgaacatt ggaagctctt gagcaattca 360

caatggcatt acttttcact cggaggtccg aatcatgcgc atactatatc gagacgctcg 420

aaattaacaa c 431

<210> 1755
<211> 182
<212> DNA
<213> Glycine max

<400> 1755

gccactgcaa ctgaattctt acatgattac ccgaagtagc ttgtgtgcac ttcacagatg 60

gagcatgcat gaggaccctt gacactgtca ccgtatggat tcccataggc gggactgcca 120

ttattggttc caatcagcat ggctcgcatc ataaacgtct cattgcgaaa cgcatctaac 180

ac 182

<210> 1756
<211> 458
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1756

taataagtcc atctatggat tgaaacaagc ctnccgccaa tggtatttaa aatttcatga 60

ggtcatttct tcatttagct ntgaagagaa tgtcatggat cactgtatat accagaaggt 120

cagtgggagt aagatttgtt tccttgtatt atacgtagat gacattctgc ttgcgactaa 180

tgataagggt atgctatatg aggtgaaaca atttctctca aagaaacttg atatgaagga 240

tatgggagag gcatcttatg tcataggcat aaagatccat agagaaagat ctcgaggcat 300

tntaggcttg tctcaagaaa cctatatcaa caaagttnta gagagattaa tatgaaagat 360

tgtcaccaag tgtagctccc attgtgaagg gtgacanact tgctttgagt caatgcccca 420

aaaatgattt tgagcgggaa cacatganaa atattcca 458

<210> 1757
<211> 371
<212> DNA
<213> Glycine max

<400> 1757

agcgtctcgt tgtcgaagtt cgagcgtctc gatatatcat gcgctttaaa cggacctgcg 60

agatgagagc tatgaccatt tgaatttctc gaaagcttgc ggcgttgaag ttcaagcgtc 120

tcgatatatt atgcagcgtg aatcggatgt acgcagggag aagttgggac catatggatt 180

tttagagtgc ttccgttggt caatatcgag cggctcgaga tattatgcgc ctgaatcgga 240

cctccgagat agaagtcatg accatttgaa ttcctcgaga tgtctcgttg ttcaatttag 300

agcgtctgga catattatgc acttgactcg gacctccgag tgaacagttt gaccatttga 360

atgctcaaga g 371

<210> 1758
<211> 294
<212> DNA
<213> Glycine max

<400> 1758

agctttaact cggaggtccg attcaagcgc atatatatat cgagacgctc gaaattaacc 60

aacggaagct ctcgagaaat tcacatggac ataactctta actcggaggt ccgattcatg 120

cgcataatat atcgagacgc tcgaaattga acaacggaag ctctcgagaa attcaaatgg 180

tcataacttt gcacacggag gtctgattca ggcgcataat atatcgagac gctcaaaatt 240

taacaacgga agctctcgag aaataccaat ggtcataact tttcactggg atgt 294

<210> 1759
<211> 419
<212> DNA

<213> Glycine max

<400> 1759

gtacagcaga tgccactcta ctccaaattc ttgaaggata tgttaacaag gaaacataag 60

tacattcacc aggaaaacat tgtagtggaa ggaaattgta gcgttgtgat tcaaaagatc 120

cttccaccta agcataaaga ccctgggagt gtaactattc cttgttcaat tggagaagtc 180

attgtgggaa aggctcttat tgacttggga gccagtataa atttaatgcc actctccatg 240

tgtagaaggt tgggagagtt ggagatcatg cccactaaaa tgactttaca actggctaac 300

cgctccatta ctagaccata tgcagtaatt gaagatgcgt tggtcagagt gaaacatttt 360

atcttcctgg tagactttgt ggtaatgaat atctgtgaag atactgacat tgctgtata 419

<210> 1760
<211> 490
<212> DNA
<213> Glycine max

<400> 1760

agtcacctgc ggcatgcaag cttcattcta cacctgaaaa agaggatgag atagttgcac 60

aaaggagaaa gcttcctaac aaaaattttc atgcaggtgg accttcttct agtaattcta 120

acttaccgca gcctcctatc cctcttccat tcccacctag agcaattcta gacaaaaaaa 180

tggaagaagt ggaaaaggag atcttggaga ccttcaggaa agtagaggtg aacatacctc 240

tgctagatgc catcaagaag attctaagat gtgccaagtt tctaaaggag ttgtgcaccc 300

acaaaaggaa gctcaagggc aatgaaagga ttagcatggg cagaaacgtg tcagcattga 360

taggtaaatc tgttcctcac attcttgaga aatgtaagga cccaggtact ttctgtatac 420

cttgcattat tgggaacagt aaatttgaga atgccatgct agatctagga gcatcagtta 480

gtgtcatgcc 490

<210> 1761
<211> 244
<212> DNA
<213> Glycine max

<400> 1761

agcttgtagg ccttggatct tcttcatcaa tggagtcctt tgcttcttga agatcaatga 60

caatggaatg gagaaggagg aaaggtgatt ggagactcca cttcaaggag aagataagtt 120

gagaacaagc tcaccaccat aggaagccat ggataagagc ttgaaggtaa gagaagatga 180

gtagagggag agaagaggga gaatgaggtc ttaactttga agtctaattt ctcaaatcat 240

caaa 244

<210> 1762
<211> 459
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1762

gacaacgatc agaagacaac cttttcctgt aagatataat tgaaacttat tgagtcttac 60

atcctgggtt tgaaagatga gatatatcat gtgactaaat tatcattcat ctcgatcaat 120

acattgataa gcaacccttc aattcatgtt ataccttaaa gttgaattct tcatctttaa 180

ccttatcgta aatttgggat tcatttcaca ccttatcttt gcaaagccga aaaaattatt 240

ttattcttga tccgtaaaaa gaatactctc taaatcattt taaacaatca ccttttttac 300

ctttatctgt atgtttaatt ttttgtctat tcttttcaaa tattatattc tttatcaatc 360

taaaaattaa tgttcaatat tctattaaat gagaatgtca ataattaaaa ataactctat 420

attggaactt aaattgattn tataaatcta cgtgctcta 459

<210> 1763
<211> 259
<212> DNA
<213> Glycine max

<400> 1763

agcttctccg gtcaatgtca gaccgtaccg ataccctcat tatcagaaac aagaaattga 60

gaatcaggtt gatggcatgt tgcagcgagg cttcatacaa ccaagcacaa gcccgttttc 120

ctcacccgtg ttgtttgtca agaagcacga taggtcttgg cgcttatgcg tcgactaccg 180

tgctttaaat gctttgacgg cgcatgatca gtttccaagt gcgactgtgg atgaactctt 240

ggacgaatat gaggcgcca 259

<210> 1764
<211> 394

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1764

ctacgccnaa catgagacca cttccagggt gctggaacta cttcacatgg attcgatggg 60

gcctatgcaa gttgagagcc ttggaggaaa gaggtatgcc tatgttgatg tggatgattt 120

ctccacattt acctgtgtgg actatatcag agagagatca taaacctttg aagtattcag 180

agagttgaaa ctaagacttt aaagagagac agactgtgtc atcaatagaa tcacgagtga 240

ccatggctga gaataagaat acagcatggt cactgaattc tgctcatctg aaggcatcac 300

tcatgaggtc tctgcagcca ttacaccaca acagaatggg atagttgaga tgaaaaacac 360

gaccttgcaa gaggctgttc tggtcatgct tcat 394

<210> 1765
<211> 364
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1765

tgtctattac tcccaataga cgtcctcctg gtgttgcaac cttcttcaac ccaatagaca 60

tggctntgct gtcagctgtg aagcaaggta cttttgtagt tcaagcagca ggaaatactg 120

gaccatcacc aacaagcatg ttctccttca gtccatggat ctatactgtt ggtgctgcct 180

ctcatgaccg ggtttatagc aactccatat ntcttggaaa taatgtgacc atacctggag 240

ttggtcttgc acgtaagttt ttgtttctca attcctggta aatggttaac cttataagaa 300

tttattntag actaactcac cagaggggg gtaatgttac tgactttaat gattggactt 360

tctc 364

<210> 1766
<211> 205
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1766

agctttntcc aagttaataa aaaccatatg taagtctctn tctttgcttt ggtaactatc 60

catcaatccc tgttaaagat aaatgacttc tgttgtagac tttcttggta taaaccaaat 120

tgattctttg caattcttat ttcttatcta tgaccaatca cttgttctca taatttcata 180

gtgtggtaat taacgttgaa agtga 205

<210> 1767
<211> 463
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1767

agcttgatgg tgttgagaag aaatcacatg tttgtcatca tcaaaaaggg ggagaatgtg 60

aatgtatgta tacatgattn tgatgatgtc aaaagaagaa tcaaacaagg ctcattntgt 120

ttaaagatta atacaagatt gtttcaacaa acaaagcctt gattcaagat ttcttcaaga 180

tcaagccttg cctcacaatg aaaggtttca agtcattcaa ggcacatgta atcgattacc 240

aatacatgta atcgattact aatggtttga aagtgtgtaa tcaattacac atcatatgta 300

atcgattacc agagacaatg aacgttggga attcaaatnt taaatgaagg ttcacaattg 360

ttcaagaaaa acaactgtgt aatcgattac actaattctg taatcgatta ctagagagga 420

ttttcaagga atatcgccaa cagtcacatc ttatcatttg gat 463

<210> 1768
<211> 478
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1768

gcatgcaagc tntctgctca tagaacanna tttnttcttc ctctcttaat tctccaacat 60

ctgaattcaa tttctcaaaa gtgtgcctaa attctctctt cagggcactg taagagtgct 120

tcagcctctc tttaagctcc ccttgcttcc tactgttgta ttttggcata gaccaaatct 180

gtccagtaac aacttcctct tctcttttca ctttgtattg gccaagtagc ccactcaatt 240

ggccatcata tgagcatttt tgctcccacg catcagcaat aaaatcagca gatcctggaa 300

cttcaagatc tttatcatac ggtatatcgc cagtcacaaa gttcaaatag ggagcatcaa 360

tatcttcatc ataagcatct ttgatacgcc ggtaaagtct acccaggaat ttcttcgacc 420

tgtaagactg gtgccgctct ttccccatga natcagggta caattttggt ttcagatg 478

<210> 1769
<211> 455
<212> DNA
<213> Glycine max

<400> 1769

acacatttta attttatagg gataaaaaat atatacaaaa ttttacatag ataagattta 60

aacattttaa tatttattgg aatataaaaa catattttag tgcaatatat atgactggat 120

tatgaaagaa acagcaaaga gaatattaaa aacatctaat ataaaagcaa cttttccaac 180

taagaatata tataagtgaa tattggatgt aatatttaat ttcttaaaat caaatcaaat 240

taactcttgt gatgatcgga acaaaaagga agttggcatg aatgcagcct tctggcgtac 300

tacctgtaat attgtggtaa gcgcttctgt acttgatcgt atcaattatt ctttataaat 360

aaaaaaaaca atcgaagtta gtatcgacgc gtatattttg aaagttgaag acgtgtttgg 420

ataaattgtg aaaccgacgg tgaccttaca cttga 455

<210> 1770
<211> 430
<212> DNA
<213> Glycine max

<400> 1770

agcttgtata ttctgtttgt ggtaggctgg aactatagtt cttacacaac catggcatga 60

tttgcactgc agaatagatg gacctgctgc atatgatgtt cttattaatt ttgagcagcg 120

atggagaaaa gcaactaagt ggaaagagtt tgcgatcctt ttcaaaaata tcctctcaat 180

ggcatggcga tgctttaata agaatagaac gcatctgaaa ggataaattg gattattata 240

ctactctagg ggatgaccct gtagtatggg tttctagtga agctgatcct gataatagca 300

tgttcaggat ggacaatgca atcttagttt tgagtgacgt cacttgcttg ctatattttc 360

ttgattgtgg agataaatac tttcattaca ttgtattcca acccttacag atcttacact 420

ccgttgactc 430

<210> 1771
<211> 454
<212> DNA

<213> Glycine max

<400> 1771

agctgccttg tcccttgata tatttgaggg actcatgatc actatgaatg acaaattcct 60

tgggataaag gtagtgttgc catgttttca aagcccatac taaggcatac aactccttat 120

cataagttga atagttaagg gtaggaccac ttaacttttc actaaaataa gcaattggat 180

gaccttcttg catcaataca gccccaatcc caacatttga agcatcacac taaatttcaa 240

aagatttttg aaagtttggc aacgcaagta tggcggaatt agttagcttt tgcttaagaa 300

cattggaagc atcttcttgt ttctctcccc atttgaaacc aacatctttc ttgagcactt 360

cattgagagg tgctgccaat gtgctaaaat ccttcacaaa tcgtctataa aaacttgcta 420

agccatgaaa actcctcacc tcggtcacgg actt 454

<210> 1772
<211> 462
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1772

ntgcataccc caaggatcca ttaggaaatt acttgtgaaa gagagccatg agggtgggct 60

catgggccac tttgggatag acaaaaccct tgtcttactc aaagaaaagt tttattggcc 120

ccatatgaag aaagatgtcc ataagcattg cactaggtgt gtggcttgtt tacaagccaa 180

gtctagggtg atgcctcatg ggctatacac acccttaccc atcccatctg caccttgggt 240

agacattagt atggactttg tccttgggct tcctataacc caaagaggtg tagactctat 300

ctttgtggtg gtggataggt ttagcaagat ggcacacttt ataccatgcc acaaggtgga 360

tgatgcttcc cacatctcac aactctnttt cagggaagtt gtgagactac atggtatgcc 420

tatgaccatc gtgtcagata gagatgctaa gttccttagc ca 462

<210> 1773
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1773

ngagctngca aaagaatgct acaagaatgc tctcgcaatt atgcacacaa gagctcatga 60

aggtgtggca cgcatttatc atcagaaaaa tcaaagaaaa gctgcatatg atgagatgac 120

caagctaatt gagaaggcag agagcaatgc ctcagcatat gagaaaagat cacaatactg 180

tgaccgtgag atggctaacg ctgatcttga tgttgtaaca taacttgatc ctttaaagac 240

ctacccatat agatacaggg cagcaggtac tctccctagt agctcactct actatctgcc 300

atttgagctt atcaagtaac catgttcaat ttaaccatct gtagttagat tactacttaa 360

caagtttggc atcagcattg aaattaatca gatagtgtgc gggatctg 408

<210> 1774
<211> 482
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1774

tcttaagtca cctgcangct gcagctntat agaactccnt taaaaaatca cttcggaatt 60

taagtttgat tatgcacacc atgctgataa aattntattt aaaacaagtt catcagttta 120

tcttaaaaaa attaatatac aatgtaccgt tgaaaataga aacaattatc aaaagtctat 180

tttttctaat ttggtgggta tggtaaacat aacactcatg attgaaaatt agatagatga 240

aaacatcatt ccatcatatt aatggtgcag gtatatcaaa tgttacacca attagaaagc 300

attatgaata tgattagtaa atgtgtgatt atacatttaa attatttttt aacatcacaa 360

gtgactgctt cagaaatcag aattgatgat antttactag aaaacaaaaa ggaacttgag 420

acattattaa taactatcca gtgttattac aaaagcatat atgttattat caatcaatta 480

cc 482

<210> 1775
<211> 448
<212> DNA
<213> Glycine max

<400> 1775

agcttgttct gaactatagc tatcgaatgg ccaacatata ttgagatgct atgagcatgt 60

cgactacata gagtagtata tagatgtggg aaccatcctc caccttacta tgataaacac 120

atgagtcaca gggactttcg atgtcccatg agagacaatg aaatcattaa atctcttgta 180

ccactgcctt agtgagtgct tcaacccata aagagatctc tttaatctac agacataatt 240

ttcctttcct ttcacttaaa aaccttcagg ttgtagcatt agaatgtctt cctctagtct 300

tccatggaga gaggcagtta tgacatcgag ttgctctaac tccaagtcct tagttgccac 360

tagggccagc agaacacgta tgaaggtgtg ttgactacca gatgtgcttt ataacatacg 420

tgctgtataa aagatgactt cttcagtc 448

<210> 1776
<211> 463
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1776

tcaagaataa tggcctcaac aaacttctta tttccagaag gaaattcaat caatagacct 60

ccaatcttta atggaaaggg ttaccactac tggaaaaccc gaatgcaaat ttttattgag 120

gcaattgact taaacatttg ggaatccata aaaatagggc cttatatacc caccacagta 180

gaaagaacca caatagatga aagcacaaca agtggaagca caacaataga aaaacctaga 240

gatagatggt ctaaaaagga tggaagacga gtacaatata atttaaaagc caaaaacata 300

attacatcta ccctaggaat ggatgaatat ttcagggttt caaattgtaa gagtgctaag 360

gaaatgtggg acactctaca agtaacacat gatggcacaa cagatgttaa aagatctagg 420

ataaacacat taactcatga atatgaacta tntangatga atg 463

<210> 1777
<211> 472
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1777

tactaagctt aacatcagac cacttccagg gtgctggaac tacttcacat ggatttgatg 60

gngcctatgc aagttgaaag ccttggaggg aagaggtatg cctatgttgt tgtggatgat 120

ttctccagat ttacctgngt caatttttatc agagagaaat cagacacctt tgaagtattc 180

aaggagttga gtctaagact tcaaagagaa aaagactgtg tcatcaagag aatcangagt 240

gactatggca gagagtttga aaacagcaag tttactgaat tctgcacatc tgaaggcatc 300

actcatgagt tctctgcagc cattacacca caacanaatg gcatagttga aaggaaaaac 360

aggactctgc angaggctgc tanggtcatg cttcatgcca aagaactgcc ctataatctc 420

tgggctgaag ccatgaacac agcatgctac attcacaaca gagtcacact ca 472

<210> 1778
<211> 491
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1778

atcttaagca cctgagctgc agctatgctg aaacattaca atagacctct tcaacctcaa 60

cagcaaaata agccacaaca gaacaagtat gacctctcca gcaacaggta taatcccggg 120

tggaggaatc atcccaacct tagatggtcg agtccttcac aacaacaaca acaacaatag 180

ccttattttc ataatgctgc tggcccaagc agaccatacg ttcctccacc agtccagcag 240

caacaacaac aacagcagca acagcaacag tcccaaaaac aacaaacagt tgaggctcct 300

ccacaacctt cccttgaaga acttgtgagg caaatgacta tgcaaaacat gcagtttcaa 360

caagagacca gagcctacat tcagagctta actaatcaaa tgggacaatt ggctacacag 420

ctaaatcaac aacaatccca gaattctgac agattacctt ctcaatctgt ccagaatccc 480

aaanatatga g 491

<210> 1779
<211> 413
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1779

ctagataatg gacacacatg aacagcgcta ggcaatgaca ttcatggtgc tccatacaaa 60

ggtggagagt ggaggatcgc cttgagggtc ctctcttagg caatcatgaa actcagctcc 120

aaactctaaa gtggaggaca catgaacagc cctaagcaat aacattcatg tggctctgga 180

aaaggatgag aatggaggat tgccttgagg gtcctctctt angcaatcat ggaacacaac 240

tccaaactcg aaagtggggg acacatgaac agccctaagc aataacattc atgtggctcc 300

ggaacaggat gagaatggag gattgccttg agggtcctct cttacgcaat catgaaacac 360

agctccaaac tcgaaaatgg atgacacatg aatgacaatg caattcattc atg 413

<210> 1780
<211> 361
<212> DNA
<213> Glycine max

<400> 1780

agcttctggt gggacatctt gacttgcttt ccaatctgac attcaccaca gattctgcct 60

tcttctattt tcagattggg aatgcctcta acagcacctt tgtcaatgat attcttcatg 120

cctcttaagt gcagatgtcc aaatctttga tgccatattt tgacttcatc ttctttggag 180

gatggacatg tggaggagta actggtttct tgaggtgtcc ataggtagca gttgtccttt 240

gatctgttgc ccttcattag aacttcattc ttctcatttg tcaccaagca ttctgacttt 300

gtgaagtcta cattgaatcc ttcatcacac aactgactga tgctgatcaa gtttgctgtc 360

a 361

<210> 1781
<211> 343
<212> DNA
<213> Glycine max

<400> 1781

agctttgagc aaattcaaac gacaataacg tttactcgga tgttcgattg tgtcccgtag 60

aatatcgcga cgctcaaaat tgaaaataga agctctgagc aacttcaaac gacaataaat 120

ttttactcgg atctccgatt gtgtcccata atatatcgag acgctcgaaa ttgaaaacag 180

aagctctgag catattggaa cgaccttaac ttttttctcg gatgtacgat tgtgtccctt 240

agtatatcaa gacgctcgca tttgacttcg gaagctctta gcatactcaa acgacaatat 300

tctttacctc ggatgtccga tagagtcctg caatatatta aga 343

<210> 1782
<211> 458
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1782

tctaaactnt atacaagaat gaagctctga taccacttgt tagacaagtg gcctcagata 60

tcttaagaag ggggggttga attaagatat tacaaactat ttccccaatt aaaattctat 120

ttcactttct attcaagtta caaattccct taataatgaa cttcttaaat attgattcaa 180

atagaacaat ttgaatataa atataaaaca ataataaata aaggagttta agggaagaga 240

aagtgcaaac tcagatttat actggttcgg ccacaccctt gtgcctacgt ccagtcccca 300

agcaacccgc ttgagagttc cactatcttg taaaatcctt ttacaagttc taaacacaca 360

aggacaatcc ttcctttgtg tttagaattc ttttacaaca agagaccctc ggtctcttaa 420

tcccttagag aattagaaag agaagaagaa tgaatctc 458

<210> 1783
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1783

gttgacggac tataccaagc tctaggtaac caggacggag aatgatctat atataggctt 60

gctaagggta gagagaggaa gactagagat ttggatcaag taaagtgtgt taaggatgaa 120

gaaggcaaag tcttagtgca tgaaaaagat atcaaggaaa ggtggaaggc gtatttccac 180

aacttattta atgatggata tggatatgac tctagcagtc tatacacaag agaagaggac 240

cggaactata agtactatcg ccggattcag aaacaggaag ttaaggaagc gttgaaaaga 300

atgagtaatg gtaaggcggt ggngccagac aacataccta ttgaagtgtg gaaaactctt 360

ggagatagag gtcttgagtg gctcaccgaa ctctttaacg aaattatg 408

<210> 1784
<211> 378
<212> DNA
<213> Glycine max

<400> 1784

gcttggccat attagactta ataatttgat tgttcgagta taacattaca aggaaatgtt 60

tttaaagaaa tcataacatt gatctggtac tacaaaaaaa ttagagattc aactttcttc 120

actaataatt aacaactaag atttattgat aaaaaaatga tatattattc tagaagtatt 180

catagatcaa tcaaatgtat tgataaaaaa catagatcaa tcaaatttta tgaagattgg 240

aaaaactcaa tatggaaaag tgaaaaaaga aatatgtagt attaaacata tttatttaaa 300

agcatgtaag ccaagtctaa ttacattaat aaaaaattaa cataaaaaaa tgtatcccaa 360

acattcagtt tggaaaat 378

<210> 1785
<211> 472
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1785

tatggatgat gaagacgcaa gttttgtgta tcatatttca tacacagatg acagttctgt 60

atgcttacca acccatccag gatgcttctg cataataaca gcaaaagcag tcatctgttc 120

taagataatg aaatcaatca tggaagtatg gttggctaca aaaacctgct caacaaatga 180

agggaaactc aaattagtaa taaatagcat ttactctttc tagaatatgc aaataaggat 240

aatacaacat taaacaaacc tgctttggtc tcctgctagg cctgggtcca tgatacttaa 300

caaccccagt ccaagatgca acaaagaaac tgcacatcat ctctaccaaa gacctctgaa 360

ggaaatgaac aatntacaac acacattgat gaacaaaagg agaatgtgcc aaagttaata 420

ttagaaacca agaattgata tgagatagaa aagaaagaac tttactgaat ag 472

<210> 1786
<211> 446
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1786

ctacgctcgc tacccatgga gttcctaata tctccacact tttgggtggg ccattcttgg 60

atggccttga ttttctcagg gtccacttgg acctgatttc taccaactac aaaccctaag 120

aaaactatat tatctacact aaaagtacac ttgtctatat ttgcatagag ggtgtttttc 180

ctaagaactg aaagaacttg cctgatgttt agccttccat agacatcaca aatagaagaa 240

caaacaaaat tgcacatgag agagaagaac atacttgaag atatgaatta tatacaaaga 300

acaagtaaga gaaaacgaga gagaagagnt tgatctaaaa cttgcactag aagtttctaa 360

aaatgggttc tttttacaca aatgactgta actaactaac taactaacta actctgaana 420

tatactcagt agaaaacatt atactc 446

<210> 1787
<211> 364
<212> DNA
<213> Glycine max

<400> 1787

agcttatgca ggcagagttc gagatgagta tgattggaac attgatgcct tacttggact 60

ttaaatcaag caaagcagat gaaggaatat acatacatca aaccacgtat gtgatggaac 120

tgctcatgaa gttcgagatg gacaatacaa tgtcaatgaa gacctctact catccaacca 180

ttgtgcttgg attggacaat gtgtctaagc aggtgagtga aactgcatat ccaggaatga 240

taagatctct tcgatatcta tctacttcca gaactaacat tatgctcatc gtatgagagg 300

caacctaact gctccatggc atttgataga agactccaag acgattatgc catagatgca 360

tgag 364

<210> 1788
<211> 476
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1788

agcttggctt taaaaagttc accttaagat ccgtaacaac ttcaaagcac ctcataattg 60

cctttaatgt gaggacgttc attaaagttg gttttcctag gaagagggta tcatccgcaa 120

attgaaggat agataaagaa aagtcccctt ctcctaaggg aataccttca aaaaagatat 180

tgtttcaccg cttctcacat caagtcacca agaccctctg ccaccatgat gaaaaagaag 240

agggctatgg aatccccttg gtagagacct cttttaccct taaattcttc cgtaggactt 300

ccatttatca aaatagactt ataagtgaat ttcacgcaac atctaaccca cttaatccat 360

attncactaa agtttattct attcataata tagttaaaaa aacgtcacct agtgggcgct 420

tctcacctaa tccactctca ataagatgtc ctgactattt tcatacactc tatcaa 476

<210> 1789
<211> 438
<212> DNA

<213> Glycine max

<400> 1789

gcatctgtgt gcaatacata attcttggta caccacaaca caatggtgta tcataaaggc 60

gtaatataac tttaatggat atggttatga gtatgttaat caattagact ttacctgtat 120

ctttatggat gtatgccttg aaaactgcca tgtattttgt gaagagggat gctagttaga 180

cagcttctaa gacgacttat gaactgtgga caaataggat acctagtata aggcatcttc 240

atgtttgggg ttgccatgca gaaataatga tttataatcc acaagagaga aaattggatg 300

caagaacaat cagtggatat ttcattggtt atacagaaca gtttaaaggg tatatgttct 360

attgttataa tcatagtatg agaattgcaa aactggaaat gcaaggttca ttggaaatga 420

tgaaatcaga gggagtac 438

<210> 1790
<211> 456
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1790

tataganatc aaacacgata ataaattatc ctcacattat aatagaaaca tatgtgcata 60

aataacaaat aagtcataag tcatcaaaac acaaatcatt tgtctaagta acttgcatct 120

agaagttcta attctcttct aatggtgtag aaagagtctt tggttagtgg ttttgtaaag 180

atgtctgcaa gttggttttt agtgtctata aatttttaa aacacaatca ccttttcct 240

aagactaagc gctaattgac tatcaacact taccaagatg agtttttatt atcataaaag 300

gttntatcat atcaaaataa ttntgtttga aatacaatat aataattttg aaaagcataa 360

aaaatatttt gaacaatcaa tcaagtaatt caaacatatc anacaagaat tatacaagga 420

ttgaaggata tagatcacag gcattatcaa acattc 456

<210> 1791
<211> 375
<212> DNA
<213> Glycine max

<400> 1791

gtatatggac gaaagtgcaa tactcctatc tgttggtacg atgatggaga agcactactt 60

cttggacctg aaatgctaca acagattaac gaacaagtga agttgattcg agagaagata 120

aaagcatctc acgataggca gaagagctat tatgatagaa ggaggaagcc actagattct 180

catgaaggag aacatgtgtt tttgaaggtt tctcccatca ccggggtctg aagagctctc 240

acatctatga agttgacgcc caagtatcta ggtccatatc aaatcttgaa gaaggttggg 300

cctgtagctt atcatatcgc cttacctccg agtgtatcaa attcgcatca tgtgtttcat 360

gtctctcaac tgaga 375

<210> 1792
<211> 433
<212> DNA
<213> Glycine max

<400> 1792

atatataggt tccttccaaa ctcttagttc gtagtagttg aaaatttaaa atgagaatga 60

actaaacaaa tattatatta atttttaaag ttttagtata cattaatttg atacaatctt 120

ctataatttg ttggtgaagc aaacaaagta ctaaaaaaag aaatcaatgt tttattagaa 180

atattaaaat tagatttttt acatgcatgc aatgcaatgt ttacataata ttattaataa 240

tactagtaat tgttttcatt cttaaaagaa aattaaaatt atttttaat taaactaact 300

tgagataaat tatattgcaa agatattggt taaattactt attgttgaat gaggtgttta 360

aattgatcga acgagatgtg tgaattattt tattattaaa ttctaactta taaatttaa 420

atataaaatt gtt 433

<210> 1793
<211> 444
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1793

taagcttcct gctatggatg tgttcatatg cactgctgat gcaactaatg aaccaactat 60

ggatgtgatg aacacagtta tatcagccat ggcactggat taccctcctc agaaacttca 120

tgtgtatgtn tcggatgatg gagggtctcc attgattctt catggagtga gggaggcttg 180

taagtttgct atgtggtggc ttccattttg tagaaggcac aaaataaaga acaggtgccc 240

taacgctttt ttttttatt cacaaatgtt agtagttcat attctttgtt agcagaggat 300

caaccccatg aacttttttct ccttctcttc tcccttaacc attcaaccca tcttatatta 360

tcatgtgtcc caaggcttac ttctctgctt tgaatgataa tgatgatggt gatcttgcaa 420

cgagtatgtg ttgtcatgga agat 444

<210> 1794
<211> 471
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1794

agctngcatg aattcacatt ctccccttttc tcaagcaaat tcttcttgac atgatcaaga 60

tcttcatgat ttacattctc ccccgttttg atgatgacaa ccacctgtag gttaggagca 120

aaaacaaaga aaaatatctg aaattctgat accaatgcca gatgtcgtac aggatgtcac 180

gacatcacgc ttcagaacat gcagattata tttgagagta tgaacagatt aaacaggtaa 240

ataacacaag agaattgtta acccagttcg gtgcaatgtc acctacatct gggggctacc 300

aagccaggga ggaaatccac taaaatagtg ttagttcgaa gatctaacag ccactgttta 360

caaccttctc acctaaccac tacccgtgca atctctacct aagagccact cttagatatg 420

agaacccctc tcactccctc tcaatcactc ttccgtgttt acaaataaat c 471

<210> 1795
<211> 361
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1795

ntagatcaat tcaaatggtc ataagctttc actcggaggt tcgattcagg cgcataatat 60

atcgaggctc tcgaaatata gcaacggaag ctctcgagaa atttaaatgg tcataactnt 120

tcactcagag gtgcgattca tgtgcataat atatcgagac gctcgaaatt gaacaacgga 180

agctctctag aaattcaaat ggtcataact tctcactcag aggtccgatt caggcgcata 240

atatatcgag acgctcgaaa ttgaacaacg gaagctctcg agacaatcaa atggacataa 300

ctcttcactc ggaggtgcga ttcatgcgca atatatatag aggcgctcga aattgaacaa 360

c 361

<210> 1796
<211> 364
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1796

agcttgcaaa gatattntat gggccctacc aaatcgtgga acacatgggc aaaactgctt 60

acaaactcca ngttgtgaaa gatgctcgca ttcatccagt tttccactgc tcattactta 120

agccctntca tcactccacc atagagccca tcacccattt acctctgcct gtcaattgca 180

tgaactgcca acctctgatt gctcccttgg taattctggg ttgtcgctgt aacacggaaa 240

attcaggtgt tggtgctgtg ggacgacctt ctacctgaag agacatcgtg ggaagattga 300

gagccattga aagctacctt ccaccttaag gacaaggtgc ttttccaagc catgaggaat 360

gata 364

<210> 1797
<211> 445
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1797

agcttcttat ctaaggcact cttttggtgg tgaatcttct tcttccatgg cttattctct 60

agtggatggt gcctcctctc acctcttctc ctttatcttt cgctataact ccatggctga 120

aaatcaccat tgaaggacct tattgaagct caaagatcaa gcctccatag aagcttctca 180

accaagcttc catcactcat gattgtcatg tatgaatgca aaaactatnt actgtagcaa 240

ttcgtggtat ctttcctgac aaagttaggg ttgccataac tcgtctatgc tttctttnta 300

atgctatcta tagcaaagtc attgacccta gaaaattgga tgaattggag aatgtggctt 360

ccattgtcct ttatcaaatg gagatgtatt ntcctccatc attntttgac ataatggttc 420

acttaattgt tcatctggcg aggga 445

<210> 1798
<211> 443
<212> DNA

<213> Glycine max

<400> 1798

agcttacggt ccatgacctc atacattcgc tcttattggg tatatcccac tagttttctt 60

cttaaaagct tgctaatttt atgccatgca gataggctat atggaagtat ccacatacaa 120

cagagggaag ttgaaagggc gtagaaacta aacatatttc aagcgtttca ctttaacgca 180

caattgtcta atgaacagag ttgcactcat ctacaatttc aagctgacgt acagcataag 240

tatccatttc cctcgacatt aactcaaatt ttgtgtacag aacataaaaa tatttgttac 300

taaatactga ttctgactag gacaggatag ccatgacatc tgaggccctc aaggcaatgt 360

agacagaacc atctctgccc ttgaagtcat tcgctgcata tctggagtac agaactgtat 420

tcccaggcat gacggacaat ggc 443

<210> 1799
<211> 449
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1799

agcttctggt gggacatctt gacttgcttt ccattctgac attcaccaca gattctgcct 60

tcttctattt tcagattgag gatgccttta acagcacctt tgtcaatgat tttcttcatg 120

cctcttaagt gcagatgtcc aaatctttga tgccatattc tgacttcatc ttctttggag 180

gatagacatg tggaggagta gctggtttct tggggtgtcc ataggtaaca attgtccttt 240

gatctgctgc ccttcattag aacttcactc ttctcatttg tcaccaagca ttctgacttt 300

gtgaagttta cattgaaccc ttcatcacac acccgaccga cgctgatcaa gtttgcagtn 360

agtnccttta ccagcagtac tttgttcaga ctaggaagtc catcatgagc tagctttccc 420

attccaatga tctttccttt agagccatc 449

<210> 1800
<211> 350
<212> DNA
<213> Glycine max

<400> 1800

aaagcatttc tttcaaggat aaaaacaagg tccatgtaaa ttaagaatag ctatccacaa 60

tcactaaggc ataatagttc cctcctatac tcatagttct aaaaggacca aacaagtcta 120

aatctaagag ttcaagcaat ctagaggttg aaatcatatt tttagattta aaagaaattc 180

tagattgctt tccctttga catgcatcac acaagtcatc cttcccaaac ttaaacttag 240

gaagtccctt aaccaactta ttgcctctaa gaaactctga gatcaataca tttatcttcc 300

cgtgtttgat taccactaag cattgatata aaactaagtc taaaacaaaa 350

<210> 1801
<211> 470
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1801

tgaccaggaa ttatntgtat gggttggatg ttgaattctg gttgttcctg gtgcggagat 60

gatggtacag agggtgaacc angagctgaa gtttcttttg gtgaggtagc catggaaaag 120

caaagcgttt ggaatgattt cgtaaatttc tgagagctgt tggggaatgc agaaaacgag 180

attaacacga gaatataagt ttgaatgagg aatgtagagg gacgtgtgaa gcaacggtcg 240

aatttgcttt ggttcagtag tgaacgtgct attaatgtta agtgattcgt ttgggcacgt 300

tcagatatca gtagttgcta caattcctct agcagacaaa tgcccagctt gcccctcagt 360

ttttcaaact gttttgcatc caatgccttt gtgaaaatat ctgctatttg ttcctcagtg 420

tcaacatgct ccagtgtgat aactttatca tcaacaagct ctctaatata 470

<210> 1802
<211> 425
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1802

agctngccaa aggtcgaana ggagcttgtc cgatcaattg agcaagacca aagaaaacat 60

gtgggccatc atcgaccaat acaaggaaaa gttaagccta gcggtaactc acaaacaaag 120

gctagaggac gagtacgtga aggtataagt cctgcaagtg gaaagggaag caagggaaag 180

ggtgatcgat tcattacaca gagaagcaat gatgtggatg gataggttct cctttactga 240

aattctgata ctggggacag atgtcgtaca ggatgtcacg acatcgcgct tcagaacatg 300

cagcttgtat atgaccgtat gaacagatta nacaagtaaa taacacaaga gaattgtaac 360

ccagttcggt gcaacgtcac ctacatctgg gggctaccaa gccagagagg aaatccacta 420

aaata 425

<210> 1803
<211> 470
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1803

tcaagatgta gttaagatac ctgacaactt ctgttcgtgt ntgttgcttg atagaaacac 60

agatgctaga tataataata tgaggaaggc tgcttctcgg gcagattccg gtgacaacta 120

tttatactgt ccaagggttg tagatctaca ggatgaggat ntaaggcact ttcagtggca 180

ttgggaaaag ggggagcctg tcattgtcag caatgtgctn gcaaaaacat ctggtttaag 240

ctgggaacca cttgtcatgt ggcgtgcatt ccgtcagatg actaagacca agcatgaaca 300

acatttggat gtgaaggcaa ttgattgctt agattggtgt gaggtttgtt taatttctca 360

atcttgaact tcgagggaat tttgcacaaa ttccattgct catgttcatt ctcatgaagc 420

ttatgtttaa attgtgtaat gttggtactt attttaactg gaaccactga 470

<210> 1804
<211> 473
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1804

agcttaacta actccaaggc atcacctgct gctttatact ccgaatcggt agttctcacc 60

taccagaagt tccagaatcc agtacagact tctatttcag cttatgtgtg agtaaaatat 120

tgctcaaata ataaatcatg ttgatgttgc tattcaggaa aaataacaaa ataccaataa 180

attatgttaa taataaaggg gttggtatgt gttgatggta aattatggag ctacttattt 240

acctgcaaca actccccgca ccctaagctc ttttgataac ttttcaacaa attgtcgggg 300

attgagatgt cgaacgcttg aaaattcaac ctcaaactct tctgggacca tgttacagca 360

ataaggaacc caagatgaaa gaattcgctt tcggtcacat ttagcaacta taggagccct 420

gttagggaaa catttaacaa aatagacgtt attntacaca tggagataac aat 473

<210> 1805
<211> 451
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1805

ntaagaagtt gtcaaacatt aatgaataga aaacaacata ttgtagttgc tactgacaag 60

aaatcaaact tggtgaaaag agaatatagg attcatttga tggcaacaat tgattgtatt 120

catttctatt gaagcaaaga ttgacatttc gtggtcatga tgaatcaatt tattcacaaa 180

atcaagataa ttctattgag cttctacata ttcttgacaa tcataatgaa gatattgata 240

acgttctaaa aaatgctcgt ggaaatctca aaccagtggc acctaatatt aaaaggatat 300

tgtgatagct gccgcttgtg agaccaccaa aattattgtt gatgatgtta gagatgattn 360

ttttgccatt ctaattgatg aatctcgaga tatatcaatt aaggagcaaa tattggttgt 420

ttttgttatg cagataanaa tggaagtgtc a 451

<210> 1806
<211> 436
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1806

tactatgtcc caacaatcct actagtagtt cctgtggact cttgttgcat aaacattctt 60

gccaatccaa aatcagaaat tnttgggttc atattctcat caagtagtat gttactagct 120

ttcaagtctc tgtgaatgat ttttagtctt gagtacttat gaagatagag tattccttga 180

gaaatccctt ctattatgtt gaagcgcttc ttccagtcta gtaacatgct tctagtgcaa 240

tcttgtcaat taaaacaagg cagtatgtgt tagaatatat actatacaag agtaatacac 300

tgcaagacat acatagttat gcttaagata ggaaagcata agtaaaggat taaaggaatc 360

atccgtaaca attattgaaa aattcagtca gaanacttga aatttcctca taagagcatc 420

gatggtatat ataatt 436

<210> 1807
<211> 381
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1807

taaatcttaa taattagtag gatgttcttg gcacttctca tgttaaattg ttcacattat 60

cttaatattt ttaaactttc tttcacaaaa gtaacaaaat aaattatttt ctataaaata 120

cactgaacta catctaagct taatcaactt tagcaaagta tcattaaatt ttctcataga 180

tgtatntatt ttataattaa tttatagaaa taactaattt tcaaaaaaaa aatcatgaaa 240

ttaacaaaat aaactatttn tacaaaatac accgaactaa atatgaattt aataaacttt 300

agcaagctat catttaatct ttttcatana tggatttatc ttatgatatc atctactcat 360

gtatcaaaat taatttcatg a 381

<210> 1808
<211> 450
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1808

tgtgggtgga ggacgcatga acgaaaacac aatttatggg tcttcgtaaa agggttgagg 60

atggagaatt gcactaagca atcactacgc acggttccaa gctccagggt ggaggacgca 120

tgaacgaaaa agcaattcat ggggctccga aaaagggttg aggatggaga attgcactaa 180

gcaatcacta caaacggctc caaactcgtg ggtgaaggac gcatgaacca aaacgccatt 240

catggggctc agaaaaaggg ttgaggatgg agaattgcac taagcaatca ctacgcatgg 300

ctccaagctc ctgtgtggag gacgcatgaa cgaaaatgca attcatgggg ctccgaanaa 360

gggttgagga tggagaattg cactaagcaa tcactatgca tggctccaaa ctcgtgggtg 420

aaggacgcat gaacgaaaac cccattcatg 450

<210> 1809
<211> 456
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 1809

cgtcttgctg gatatttata tgcatatttt tctgatgatc accgaggaac aattagggat 60

caacttgaaa cttatgtgcn ttaagtgaga cgcacatgct tctttttttca nttgtgaaga 120

tgttcaaagt ttggctatga agatggttca cactgagaaa catttggtat ttccattggt 180

ttataaactt attgagctag ctntgatatt gccggtgtcg acaacatccg ttgaaagagc 240

tttttcagca atgaagaata tcaagtctaa attgcgcaat aagatcaacg atgtgtggtt 300

caatgacttg atggtatgtt acaccgagcg ggagatattc aagtcacttg atgatattga 360

tattattcga acatctaccg caaagaagtc tcggaaagga cacttgcctc gtaatttatt 420

taacccgctt tgtaaattat gttatctctt tattta 456

<210> 1810
<211> 426
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1810

agctagagcg taaactanat gccttggttt acctgttaac ctaactggcc atgggataaa 60

aatctgcacc tttcgccaca ctctgtggtt tatgctcctc taccgaccac catacagacc 120

tttgcccttc tatgcaacaa tctgaagcaa ttgaacaacc tgaagtttat gctgaaaaca 180

tctacaatag acctcctcaa cctcagcaac aaaatcagcc acaacagaac aactatgacc 240

tctccagcaa taggtacaat ctcgggtgga ggaatcatcc cgaccttaga tggtcgaatt 300

cttcacaata gcaacaacaa caacaacagc cttattatta aaatgctact gggccaagca 360

gaccatacgt tcctccacca atccagcgac agctacaaca acgacacatc ggacccgaaa 420

tagcaa 426

<210> 1811
<211> 409
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1811

agctagctaa cccatggaag ctcctaatat ctctcactct ttntgnggtg ggccatcctt 60

ggatggcctt gattttctca gggtccactt ggaccccatt tctaccaact acaaaaccta 120

agaagactat attatctaca caaaaggtac acttctctat attttcatag agggtgtttt 180

cctaaggact ggaagaactt gcctgagatg tcctaagtga tcatctaggc tcctattgtc 240

cactaaaata tcatcaaaat aaacaactac aaatctacct atgaaatccc ttaagacatg 300

atgcataagc ctcataaagg tgcttggtgc attagtgagc ccaaaaggca tcactagcca 360

ttcatacaaa ccaaacttgg tcttgaaagc ggttttccac tcatcaccc 409

<210> 1812
<211> 446
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1812

agctntacgc ggacaagcat cgtagggaag tctttttgtt tttgggactg ggctctggct 60

cgacttcgtt cttacaggca gccctctgcc aaaggggatc actcaaccaa tgtgaagtta 120

gctcgttgtt attatggccc atttcaggtc acagttaagc tcgggcccgt agcttatcgc 180

gtggattttt cggcaggcgt ttgcatccac ctggtgtttc attgctcgaa cctcaaacct 240

tttcggggcg agacagactc caattcctca attcctttgc cacccaattt tcacgagaat 300

caaccactca tatcccctct tgccattctg gngtctcgtc gtgcaacctc tgatcctcat 360

agttcttggc aggttttggt gcagtggcag ggtctcccac cggaggagac gtcgtgggaa 420

gattgtgacc agtctttgca ggacta 446

<210> 1813
<211> 441
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1813

tatggtcgtn ntgaattgct tagaccttat gttttcaatt tctagcgcca ctatatagta 60

cgggacacaa tcggacatcc gagtaaaaag gtatagtttt ttgaatttac tgagagcttc 120

agttttcaat ttcgagtgtc tcgatatatt acaggactca atcagacatc cgagttaaaa 180

gttatggtcg tttgaatatg ctacgagctt ctgttttcaa ttgcgagcgt ctagatatac 240

taagggacac aatcgcacat ccgagaaaaa agttaatgtc gtttgaattt gcacagagct 300

tctgttttca attttgagcg tctcgatata ctacgggact caatcggaca tccgagttaa 360

aagttattat ggtttgaatt ngctaggagc tactattttc aanttggagc atttcgatta 420

taacgggact caatcggaca t 441

<210> 1814
<211> 424
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1814

ggatcttaag cactgagctg cagcttgagc aattaaacga tgataacttt tttctcggat 60

gtcggattga gtcccgtaat atatcgagac gctcgacatt gataataaaa actctgtgaa 120

aattcaaaca acgataactt tttactcaga tgtccgattg cgttccgcaa tatatcgaga 180

tgctcgaaat tgaaaatgga agctcgtagc acatgcaaac cacaataact ttttactcgg 240

atggccaatt gtgtcccgta atatatcgcg atgctcaaaa ttgaatacaa aagctgtgag 300

cacatacaga cgatagtaac tntntactcg aatgtccgat tgcgtcccga agtatatcga 360

gacgctcaaa attcagagta gatgttgtga ccacaatcta acgacaataa ctctttactc 420

ggat 424

<210> 1815
<211> 423
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1815

gcttctacat cctatgacag tgttgcctca cttttgcttt tttgactcta gcaatagaga 60

cactatatag tggtacctgc actccaagaa ctttggatac aatcgcctta ctgattcaaa 120

ctcggcaatc ctntaaagca gctagatgag ttttgggtca atggtctatg ggttgaataa 180

tgtgataaaa ataacgcttc aatagtgtga tacatataca taagattatt aacatataat 240

gtataaaata aaaacacagc ttatataagc ctacatattc taatgtatgt gaaaaaagga 300

tttaatctta tatattatat cttagaagat aatctctaag agtataaaac tatcgtaaag 360

ttaaaaggaa taaaagttat attttgaaat atgttcgcat aagacttata ttaatattat 420

att 423

<210> 1816
<211> 352
<212> DNA
<213> Glycine max

<400> 1816

cttgagcttc gctcattacc tgtcataagc tatttttaca aagctcggct cggcttatat 60

aaaagtgtgg ctcggcccac gagcctattt aaaagtctgc ctaacatcgc ccttgattaa 120

ccaattatct taaaacctag cgaacaacga actataagaa gaaccttagt caaattcgtg 180

tcagtactgt acaaatccaa aaataatgga ctaacataat catagtgaat tcaagcggca 240

caacacagcg tacatcatga gaaaataaaa agaacgtcat tttatgagac gtatgaatta 300

gacatggttt gcacaacatg aattttatct tacgtgcaca gtgtgtatga ac 352

<210> 1817
<211> 403
<212> DNA
<213> Glycine max

<400> 1817

cttgaatgct ctattcaatg gagttgacaa gaatatcttc agactaatca acacatgcac 60

agtggccaaa gatgcatggg agatcctgaa aaccactcat gaaggaacct ccaaagtgaa 120

gatgtccagg ttgcaactat tggctacaaa attcgaaaat ctgaagatga aggaggaaga 180

gtgtattcat gacttccaca tgaacattct tgaaattgcc aatgcttgca ctgccttggg 240

agagaggata acagatgaaa agctggtgag aaagatcctc agatccttgc ctaagagatt 300

tgacatgaaa gtcactgcaa tagaggaggc ccaagacatt tgcaacatga gagtggatga 360

actcattggt tcccttcaaa cctttgagct aggactctcg gat 403

<210> 1818
<211> 455
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1818

ctaagctcgg agatttatca ttggttctac tcgatgacac cagaatatat agttggaatc 60

atcaagcttn tctgaaatcg aaggaaaaga ttgatgtgaa tgatgagagg aagtggacac 120

agcaaaattg ttttctgcca ttgatgaatc cttctaagag attggacatt agatcctcca 180

agttctgagt ctgtacgaaa tgctgttgga gttcttcaag agattggggc attgtcagtt 240

gatgaacaac tcactcagct agggcagaag cttggctgtc ttcctattca tccatcaaca 300

ggcagaatgc ttatttttc catatagatg atatgtcttg atccagctct aactcttgct 360

tgtgcattcg agtttaatga tccatntgtg catcccactt tacctgatga atagaagaga 420

gcttcagctg ctagatctga gcttggctct ttgta 455

<210> 1819
<211> 481
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1819

ntaatatatc aaccaccaat attagataca attaactaat tatgtgttta cttcatctng 60

tttgaattcc aataagatac atatgtacag cttatgcact ttgatttttg ttatcgacat 120

ttatagtttg aaacaaaaat gcaaattgga ataataaatc atggtagcta gacaaataca 180

attttggtta attttttaa gagataaaac tagtttatat tcatatgggc cgtcttgatt 240

aatttgaatt tgaatttcaa gcgagatttg tgtatttgtt aattntggtc aaaaaaatta 300

ttggttgacg aaattaattg atttaaaatt taaacaaaag ttaaatatgt tatgaacgaa 360

aataaatata taagcacaat tagaaacgct aaattaatct actgtcttag ttaaaatcat 420

gctggtgaac acaatctaga ggttagtgac atataacgag tggagatcct cttgagtgca 480

g 481

<210> 1820
<211> 465
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1820

ngaaggacat acacaaagtg tgactatatg atgtgacaat cggttgtagc tagcatatac 60

tcacctcccc ctctaaaatn taattggatt gggcttcccc caattcaatt aaatttattt 120

cccaatacat acatcaaata ttcacttaat gcatgtgaaa ttacaaagca acccataata 180

caaaaattag tctaggtatc ctaaaatata aaggctgaaa aatcctatat ttctagggta 240

ccctacctac attatgaaac cctaaataca aggcccanaa aaaaatgaaa ccttaatata 300

atatgtacaa agataagtgg gctcatactt agtccatggg cccaaaatct accctaaggc 360

cgatgagaac cctagagcct tctcttgcat ctctggtcta atcttcttgg agtcatctat 420

ccaatggcct tggagggtag gaatgcatca ttcccttccc cttga 465

<210> 1821
<211> 424
<212> DNA
<213> Glycine max

<400> 1821

tctcgatata tgatgcgcct gaatcggacg tccatttgat aagttatgac tctttgaatt 60

tcctgagagc ttgcgttgtt caatttcgag cgtctcggta tattatgcgt cagaatcgga 120

cttccgtgtg acaagttatg accattttaa tttctcaaga gcattcgttg ttcaatttcg 180

agcgtctcca tatattatgc gcctgaatcg gacttccgtg tgataagtta tgaccatttg 240

aatttctcga gagcttgccg tgttcaattc caagcgtctc gatatattat gcacctgaat 300

cagactttcg tatgacaagt tatgaccgat tgaatttctc gagaggcttc gctgttcaat 360

ttcaagcgtc tcgatatatt acgcgcctga attgacttcc gtgtgaaagt tatgacaatt 420

taat 424

<210> 1822
<211> 382
<212> DNA
<213> Glycine max

<400> 1822

cgcctgaatc ggacttttct ttgtaaagtt atgaccattt gaatttctcc agagctttcg 60

ttgttcaatt tcgagcgtcc caatatatta tgcgcctgaa tcggacttcc gtctgacaag 120

ttattaccat ttgaatttct cgagagcata tggtgttcaa tttcgagcgt ctcgatatat 180

tatacacctg aatcgggcat ccgtgtgaca agttatgacc atttgaattt cttcagagcc 240

ttcgttgttc aatttcgagc gtcccaatat attatgcgcc tgaatcggac ttccgtgtga 300

caaagtatta ccatttgaat atctcgagag cactcgctgt tcaatttaga gcgtttcgat 360

atattatgcg cctgaatcgg ac 382

<210> 1823
<211> 428
<212> DNA
<213> Glycine max

<400> 1823

actatgaata ctaagcttca tggtctctgg tataggctct gggactttcc attgcaactt 60

atgtggaggg caaagaaggc cttcttctgg gggccagagc cataagtgag acaccactct 120

agaagagtta gacttctaac cttgtgtcag gacctatggg ccaaggaata gtctcaggta 180

ctcaattttt acggaacgtc tgttttgatt tagctgtttg tagcacgtct caatgcgctg 240

gttgaacgac atgcaatttt tacccttaca ttgaaagggt ttcgcattga ggggttttcc 300

acttcaaatt gtgtctctgt tttctttcat ttctattatg tgctctatac tttattggta 360

ctcctgacag gtactcgcaa gggtgggaaa atatatgtac gttatctcgt cttactctgt 420

tatagatt 428

<210> 1824
<211> 487
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1824

ngcttatctc ttcaggatgc tcaacacagt actgcatgtg ctccttcaac ttagacctac 60

aacaagcaaa tagacaagag catataaatc ttctcacaaa tcacaacaaa ttcagcatta 120

gcaagttcac atgtcacaaa ttcaataccc gaattccttg ttcaggctgt tcgcagccac 180

ggttgctgcc tttccgccgc cgtatttggc cacaaagtca tccttcacac gctccagaaa 240

agccacaggc acctgtctcc caatcgattc atccgcaaca acacaataag ctacaaaaaa 300

caagtgtgtg agtcagacat tcatttccaa aaacacagca ccgaacttca gataagccta 360

taaacaaata ataacaacac gaatttcatt tcagttcatt ttcaaacaca tcaccgaact 420

tcanaatagc ctctaaacag atcagaacaa cacgaaattc atttcatttt caacacaaca 480

ccgaact 487

<210> 1825
<211> 375
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1825

tattgtcgtt nngaattgct tagaccttat gttntcaatt tctagcgctt cgatatagta 60

cgggacacaa tcggacatcc gagtaaaaag gtatagtttt ttgaatttac tgagagcttc 120

agttttcaat ttcgagtgtc tcgatatatt acaggactca atcagacatt cgagttaaaa 180

gttatggtcc gttgaatatg ctacgagctt ctgttttcaa ttgcgagcgt ctagatatac 240

taaggcacac aatcgatcat ccgagaaaaa agttaatgtc gtttgaattt gctcagagct 300

tcggttctca attttgagcg tctcgatatc ctacgggact caatcggaca tccgagtcaa 360

aagttattat ggttt 375

<210> 1826
<211> 462
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1826

agctntgagc aaattcaaac gatgataact nttactctct gatgtcggat tgagtcccgt 60

aatatatcga gacgctcgac attgataata aaaactctgt gaaaattcaa acaacgataa 120

ctttttactc agatgtccga ttgtgttccg taatatatcg agatgctcga aattgaaaat 180

ggaagctcgt agcaaatgca aaccacaata acttttttact cggatgtcca attgtgtccc 240

gtaatatatc gagatgctca aaattgaata caaaagctct gagcaaattc aaacgataat 300

aacttttttac tcgaatgtcc gattgcgtcc cgaagtatat cgagacgctc aaaattcaga 360

ataaatgttc tgaccaaaat ctaacgacaa taacttttta ctcggatgtc tgaatgaatc 420

ccgtaatata tcgagacact cgtaatctaa aactaaagct ct 462

<210> 1827

<211> 436
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1827

gcttggagtt tccagtgcca attcgtcttc ttctttagtc cagtcttctt ctggcttcag 60

ttcattagag ggctttcctt ctgtgtccag catcttggga tgttcccagc ctttgatgac 120

agctttccag gttctgctat ctagtgattt gaggaaggcc accattcttg ctttccagta 180

ttcatagttg gttccatcaa gaaatggtgg tctgttcact ggtcctnctt ctntctncat 240

gttcatcaga aattatcntc ctagatctca ctcagtgatt tcgagtgcct gctctganta 300

ccaatgaaat tcttgatact gggacagatg tcgtaccgga tgtcacgaca tcatgcttca 360

gaacatgcag atngtatgtg tccgtatgaa cagatttaaa caagttaata acacaagaga 420

attgttaacc cagttc 436

<210> 1828
<211> 473
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1828

tattaatata tgattaatat aattaannaa tatttgtaaa attagctgat aaattagttt 60

ataaatgtta atagcataaa aatacatatt taattattta attatatatg tatgtattta 120

atttgtttcc aataacgtgt catcataaaa actagggcaa tatttttttt aaaaaaaatt 180

gtattataaa actataaaat gtttgagttg tataaagcat taattttcta ctaatttttc 240

tctttttga acccaatttt tttttttgat atttttgtaa aagttaggga gctacatact 300

nttaattgta tttccttctt aacatggcat tccttcttaa cgtgaattat ctttatataa 360

atggcttntt tttttcattg actgaaaant ttaaagatcc gagtgcacaa atgacatata 420

tgatagtaag ttactgagct tttgttaaat ttatacctga atntcatact taa 473

<210> 1829
<211> 364
<212> DNA
<213> Glycine max

<400> 1829

tcctagacat aagaatgcgc atcacgtaac aacttcttct gatgatgcca gataaggtca 60

tgagggataa tctcagctac cttgaagtta gcagatggct aagtaaactc tctgtttagg 120

tggtagcaaa gctcatatgt gcatcattta ggactttact ggcatagtaa atagagcgaa 180

gcatcttata cgcctctgtc ctagcactgc accaacaacg tagtcactag caccacacat 240

catttcagac tctaggctgc aatttggggc cacaatcact ggagctgaca ccagcctccc 300

tttcatggtg tgaaatgcta gcatacattc ttcatcgcac ttatacacag catctttgtt 360

cgat 364

<210> 1830
<211> 419
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1830

tctcccanaa aatggtgtcg tcagcaaatg ggaggatatt cactagaact cttgttcttc 60

cctaccaaga agctntggaa gcaatctttt attgttgctt ccctcatcat tcctgtcaag 120

ccttcaacaa ccaagtcaaa caatagaggg gccaaaggat ccccttngtc tcaaatctct 180

tgaggcttaa attcagaggt tgagcttcca ttcactagaa tagatataga ggctgatgtg 240

aggcacccct taatccatcc aatccatctg tcatggaacc tcattcttct catcatatga 300

naaaggaatt gccaagacac taaatcatag gctntttcga aatccacttt aaacaccatg 360

caggacctca tagacctcct angcctctca agtacctcat tagcaaccan aacaccatg 419

<210> 1831
<211> 454
<212> DNA
<213> Glycine max

<400> 1831

agcttcatgc tgaagtatgt atgacaaaac tttattactg ttattcaaca catacaagtg 60

agcttgtaac aaatcttcta cacttggagt gataacatgc agtccttttg aacccttacc 120

gcccactctg tcgtcatggc gagactcagg aaggccaata ggtttagcct tttcaatgta 180

ctctgaataa aattcaatgg cttcttctgc aatgtacctt tcaacaatag atgcttccag 240

acgatgtaga ttcttggtat acccttttaa gatcttcatg tattgctcaa ccaggtacat 300

ctaacgcaaa taaataggac cacaacattt aatttctctg acctgatgaa caattaagtg 360

aatcatggtg tcaaagaaag taggaggaaa atacatctcc agttgacaca gtataattgt 420

ggcctcattt tccaggccat caaacttgac agga 454

<210> 1832
<211> 381
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1832

tcaaaggtcg agatgttaga caagtggcct cagatatctt attattaggg ggttgaatta 60

agatattcca aactacttcc ccaattaaaa atctatttca ctttcttttt aagttataaa 120

ttcccttaac aatgaacttc ttaaatatta attcaaataa aaaaattgag tatgaatata 180

aagcaataat aaacaaagga gattaacgga agagaaagtg caaactcaga attatacttg 240

gtccgccaca cccttgtgcc tacgtncagt cctcagcaac ccgcttgaga gttcactatc 300

ttgtagatcc ttttacaagt tctaacacac aaggacaatc ctntctttgt gttagaattc 360

cttacaacaa gagaccacag t 381

<210> 1833
<211> 447
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1833

ctgatatgga tattagatta aaggtaaaag ctggcacata ttatacattg tgtagggtaa 60

tgagtgcaga aagttgtact atgcctaagt gggtagcatt aacaagatgg ccatttggta 120

gcttaacact aatgggacta atttgacgat atgaataaaa atttgttaaa gaagaagaaa 180

catggtcagt ggctcctgaa tctaagatcc aagaggtaga gttggattta ttcgtaagac 240

aaaaccatac ctgttggatc gttattggtg caagacgaaa tagaggcaac ctgtggttta 300

atggacgctg aggttccggc cgacggctgt tgtattaaag ctagaagtgc tatgtactgc 360

tctgatgaan aacgaacctg ttcttgtgat tcttggggat agtattggtc atctgtggcc 420

ttcccttcag ttgccactac actatta 447

<210> 1834
<211> 457
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1834

caagcttgag atattnttaa gccatacaat gtctttntaa tttgtacact ntgtcttcct 60

ggccatcaac ttgaaaacct agaggctgat caaaaaacac atcttcttca agaggaccat 120

ttagaaaagc agacttgaca tccaattgat gcattggcca ccttctcaaa cttgcaatta 180

caactacaag ccttattgta tcaatccttg ctactggagc aaaaatttca ccataatcca 240

caccttctct ttgcaagaaa ccctatgcta ctagtcttgc cttgtgcttg accacctctc 300

ctttgggatt cttcttcact ttaaagaccc atttaactac aatagctctt ttccctttcg 360

ggagagtcac aagatcccag gtatggttct tcttaattga gcttaattcc tccttcattg 420

cttgaatcca ttgaggttct tgcaatgttt cctctac 457

<210> 1835
<211> 370
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1835

agcttggact tnctgtgttc tgggaacctc tttttcttta agtgtaccca aacccaatca 60

cctggttcag gcacgactat ctttctgctt ttgttggctt gccttgcata gctcgcattt 120

ttcttttcaa tttgagcctt cacttgctca tgcagcttct tcacatactt agctttagtc 180

tatacgtcct tatgcttaac cataacaatg ttaggcatag gcaacaaatc aagaggagtn 240

taaggattac ccccatacac tatctcaaat ggtgaacaat tacttgtgct atggataagc 300

cgattataag caaactcaac atgaggcaaa catgcttccc aagatttaag atttttnttc 360

aaacaatcct 370

<210> 1836
<211> 464

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1836

ggctaagtcn tatttgatga tgccaaagac tcaagtcaag aatcaagagt cataacagtt 60

tcaagaatca aagagtcctt caatcaagaa tcaagattca agtgaagatt caagagaaga 120

ctcaagatat gcaagaactt caagaaaagc atcaagataa gtataaaaag attctttcaa 180

atgaaaagat tgaatagcat aaacagaagc acaaacaatt ttataactgt ttcacaaagt 240

agtaattgat taccatgggc atgtaatcga ttaccaatgt ttttgaatgt tggatttcaa 300

atttcaagag tcacaacttg tgataaaaca ttttcatatt tgtgtaatcg attacacaac 360

atttgaaatc gattaccagt gtttctaaac attggtattc anatctaaac atgaagagtc 420

acatctattg atgtgtaann tgatacacta aatggaaatc aata 464

<210> 1837
<211> 466
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1837

tatagcttac ttattatcca caaaaagctt cactccatca ctttccttga ttnttaattc 60

ttgtaataat gtgtccaacg agacagcttg gcaagcactc attgtagctg gaacatactt 120

agcttcacat gttgataaag ccactatgga ttgcttctta gaactccatg atattggtgt 180

tgcaccatac atgaatatgt aacctatagt actctttctg tcatctctgt ctcctcccca 240

atccgcatca gtatatccca ctaattcctc tgagttgttg ttgtctttat ttggaaatag 300

aattccagta ttgatggtcc cttttatgaa ccttagaatc ctcttagcag ttaggagatg 360

aggaattctg ggtcttttcg tatatgtact taccagtcca atagcaaatt ccaaatcagg 420

tctttgatga cacaagtacc tgagagaacc aacaatatgt ttgaac 466

<210> 1838
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 1838

ctgcaataga tgccactnnt actcaatttt taaatgatat gttgacaagg aaacacaagt 60

atattcacaa ggagaatatt gttatggaag gaaattgcag tgctatgata caaaaagatc 120

cttccaccta accataaaga ccctggaagt gtaaccattg cttgttcaat tggtgaagcc 180

acccggggaa aggctttcat tgatttggga gccagtatta acttaatgcc actctccatg 240

tgaagaacat tgggagagtt ggagatcatg cccactagaa tgactttaca acttggtgac 300

cggctcatta ccagaccata tggagtggat gaagatgtgt tggttcgagt aaaacattnt 360

atcttcccag caaactctat ggtaatggat atctatgaag ataatgac 408

<210> 1839
<211> 423
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1839

gcaattaaac gaaataattt tacgcacatg tcatattgag tcccgtatat atcgagacgc 60

tcgtattgaa aacgggagct cgttgcaatg gcaaccgaaa taacctttaa ctcggatgtn 120

cgatttgagt ccgtaatata tcgagacgct tcaaattgaa aacagaagcc ttgagaaaat 180

tctaacgaga attatttttt actcggatgt ccgatggagt tccgtaacat atcaagacnc 240

tcnaaattga aaacggaagc tcatagcaaa ttgaaacgaa agtaactttt aactcggatg 300

gtccgattga gtccgtaata tatcgacacg atcgtaattg aaacaaaagc tcgtagcana 360

cgcanacgac aataacattt tgactcggat gtccgactgg agtcccgtat atatcgagac 420

gct 423

<210> 1840
<211> 328
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1840

gggggggttg aattaaagat attccaaact tttctcctaa taaaaatcta tcttactttt 60

acttaagtat gaatcccttt atgacagtct tcttanatat taattcaaat gaagcaactt 120

gaatatgaat ataaagcaat aataaataaa ggagattaag ggaagagaaa atgcaaactt 180

cagtttatac tggttcggcc acacccttgt gcctacgtcc agtccccaag caacccgctt 240

gagagttcca ctaacttgta aatttctttt acaagttcta aacacacaag gacaaccctt 300

cctttgtgtt tagagattct ttacaaca 328

<210> 1841
<211> 439
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1841

agcttcggtg ggctgccaaa ttcctcanaa ccttttgttc tcgaaatgaa cactttaggg 60

gtcgacatgg gcgccgtcct tgtccaatat ggacatccaa tagccttctt tagcaagacg 120

ttctgtctga aactccaaaa ctcgtcgacc tacattaggg agctcgttgc cattaccacg 180

acagtcaaaa agtggtgcca ttacttattg ggccatcact tcacgattct aacggatcat 240

agaagtctta aagagctaat gactcaggtt gttcaaacac ctgaacaaca gatgtattta 300

gctcgtctat tgnngtacaa ctattcaatc cagtatcggt caggcaagac caacactgcc 360

gctgacgccc tatccagaat cacggaacta gtagcgggac aatntctaat gctaacaata 420

ccctaacctt tgtttttt 439

<210> 1842
<211> 459
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1842

agcttcccaa ccaatcttcg atatctttca ggatcagaat aaggctcccc atgattgggt 60

agcaattttt gatttggatc cataggagta tcaattggtc tacaatctga cataccagtt 120

tctttaagta tgtctaacgc atacttcctt agtctaaaaa tgactaaata aatgttcttt 180

tagttgagca atttttcctt ggtcatttct tatgatgact atatcatcta tatagaccac 240

caagtaaaaa catctactcg atgaggtatg acaataaaaa actgaatggt ctgcttcact 300

tcgttttatc ccaaaagcct gaacaactga gctgaatttt ccaaaccaag cacgtgggga 360

ttgtttgagt ccataaagag acctncaaaa tttgcaaacc aagctagact tcctctgagc 420

aacaaatccc ggtggttgct catataaatc tctattcta 459

<210> 1843
<211> 470
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1843

agcttcctta atcacctcat taaggactag aacaccatgt aggatgtgtc tgttntttat 60

gaaagttgtc tgcctctcat caataagacc agatatcact tgtctcaatc tatntgctaa 120

taacttagct atcaccttgt acatacatcc aatcaaggag atgggtctgt agtcatcaaa 180

tgactgggga tgtttaattt tgggaatgag agctatgaag gaagcattac tgcctctagg 240

gaaactgcca tgtacatgga attcatcaac aaatcttctg aagtcagctt tcagcatatc 300

ccanaattct ttaatgaatt tgaagttgaa accatcangt ccaggacatt tgtccncatc 360

acaactccat actgcttctn tgatctccaa atctgaaaaa ggaacaacca aagactccct 420

ctgctcctgg gttagtgaag agaaatgcac tccatcaaga gtgggtctac 470

<210> 1844
<211> 458
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1844

tggagaggat gcttaatgga ggaaaagaaa gacggagaga attagagagg ggggagcacg 60

aaattgaagg aataaaagag gtagagaagt ggaactttga agtatgtctc acaagactct 120

cattcatcaa agttacaata agtgttacac atgcttctat ttatagacta ggtagcttcc 180

ttgagaagct ttcttgagaa aacttccttg agaagctttc ttgagaaaac tttcttgaga 240

agcttctttg agaaaacttn cttgagaagc tagagcttat ctacacatac ccctctcata 300

actaagctca ccttcttgag aagcttcctt aagaagattc cttgaaattc tgatactggg 360

gacagatgtc gtacacgatg tcacgacatc acgctttaga acatgcagat tatatttgac 420

agtgtggtcc gtttaaacaa atagataaca caagagaa 458

<210> 1845
<211> 409
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1845

agcttgttgc attntagtga aagaacaccg agtactattt agtctcacaa atgcaagaac 60

tacgtaggtc tgagttcctc atcacaaatt gaggatacgt aggagcaaaa gccccgcttt 120

tgtcgaccac ctcgcctttt gctatcgtga cctgtgagtc cggtggcacg cggaaacacc 180

cgatggttat ccgcgcacac tntttgctat cccatgacct atgagtccgg tggcacgcgg 240

agacacccga tggttatccg cgcacactct ttgctatcca atgacccaag ggtccggtag 300

catgcagaga taccttcggg ttatccgcac ctttcgccag ctagaggcaa gcgagcccgt 360

tgacatgcag agatcaacgt ggtcatctgc acctttcctg gagatgtca 409

<210> 1846
<211> 354
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1846

agcttatgct gcanacatct acaatagacc tnctcaacct cagcagcaaa atcaaccaca 60

gcaaaacaat tatgacctct tcaacaacag atacaatccc ggatggagga atcaccctaa 120

tctcagatgg tctagccctc aacaacaaca acaacagcct gctccttcct tcaaaatgtt 180

gctggtccaa gtagaccata cgttcctnct tcagtgcaac aacaacaaca gcaacagcaa 240

catcaataga gacaacaatc cactactaag gcccctcctc aaccttcatt ggaagaatta 300

gtgaggcaaa tgacaataca gaacatgcag tttcagcagg agacaacctc aatt 354

<210> 1847
<211> 484
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1847

agcttgttgg tggcaaagtc aaaatctaat agaatgtata cttgaatcaa cctgtagcta 60

gctatttttg tattcattgt aactaacgga gattctaaat ttccacttaa tatgtgaaga 120

tgtacctttt ctgagacctt attgctacta ccatttagta gctctggtgc catccaaggt 180

agagttccac gaacaccacc agacaccaag gtatttcgct taatctttga taggccaaaa 240

tcaccaacct ggtgaaaagc aagtttctta gctttatcac aatgaagaca atgtaataga 300

atgaataatc cacagcttga aaagatacct tgcatattgg ccgcatatga tccttcaagt 360

tcacgagcan atngtcacat ttcaagtcan aatgcacaat atttttcgag tgtaaatatt 420

ccactccaaa agcagcattc atgggcaata tcagtctctt gcggcgtcaa gatacctgga 480

ataa 484

<210> 1848
<211> 428
<212> DNA
<213> Glycine max

<400> 1848

ctaagctaga catacatatc tcttcttgat acactaattc aaataatcta tttcatggtc 60

tacccaatga agacccttat gctcacttgg ccatctatat agagatatgc aatattatca 120

ggttggtggg tgtgcctgcg gatgcaatca ggttgagtct gttctcattt tctttatctg 180

gagaagctaa gagatggctt cattctttta aaggaaacaa tctgaagtca tgggatgaag 240

tagtagaaaa gttcttaaag aagtacttcc ttgaatcgaa gactacagaa ggcaaagctg 300

ccatatcttt tttccaccag ttaccagatg aattgttgag tgatgcactt gaaagattag 360

aggtttattg agaagactcc actcaaggtt tttagaccaa tacagctcaa catattatag 420

atgggtga 428

<210> 1849
<211> 430
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1849

agcttgcttc tacaaaaaga atacacacac atgacctcta tttatagcct aagtgtcaca 60

ganaattgga ggggaaattg aatnttctat tcaaatttca cttgaattag aaattgaatt 120

tatggagcca aatttcggag ccaaaatttc actaattatg attcgtgaat tttagctatg 180

gttcaaccca ctagtccaag atcaagtcca agattctcca ctaagtgtgc ttaggtgtca 240

taagacatgt aaagcatgaa gtatatgcac aaagtgtgac tatatgatgt ggcaatggag 300

tgtagcanac aaatgctcac ctccccgtct aanattaatt agattgggct tcncaaattc 360

aattaattta tttccaacaa cacataaata ttcattaatg atgtganata caaactaccc 420

taaacaaact 430

<210> 1850
<211> 250
<212> DNA
<213> Glycine max

<400> 1850

actagtactt tggtttctag ccgtgtattt ggctatatta tgacatttga accatttaat 60

gatgcaatcc ttcctaggaa gggaccaatc actagaacca tgagccagag gctccaagaa 120

gattgggcta gagctgctga agaaggccct atggttctca tgaaccttat gatagatttc 180

tgagcccatg ggccaaggtt gggtccaatt atctttgtac atattagact aggatgtcat 240

tatatttggt 250

<210> 1851
<211> 467
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1851

gcttaagctc cttcaactgc acaaggctct taatatttga agagtattct tgtggaacct 60

tcacctgacg aagacacttg acaaaactta tctnctcctt cttggacaaa gtatggcaag 120

ctgggggcaa gtaacttttc ttcccatcag accttggatg caactgtgat cttataccca 180

tatcagctag atcttgacgg gtattcaagc catccttcgt cttgccttga atggtaagga 240

gcgtcccaat cacactgtca caaacatttt tctccacatg cataacatca atacaatgtc 300

taacgtcaag atcacaccag tacggaagat caaagaaaat ggacctcttc ttccatatgc 360

aactctgact tttatccttc ttttgggtct tcccaaatac agtgttcagg tgttgaaccc 420

gctgatatac ctgctcacca gtcaacggta tcgacgcaat atcatgc 467

<210> 1852
<211> 417
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1852

ttctaacgac aataactgtn tactcggatg tnctgattga gtctagtaat atatcgactc 60

gctcgaaatt gaatgttgaa gctctaagcc ctattcaaca acaataacgg tttactcgga 120

tgtccgattc agtgacgtaa tatatcggga tgctcgaaat tgaatgttga accttctgac 180

ccactcaaac gacaataacg ttttactcag atgtctgatt gaatcccgan atatatcgag 240

acgctcgaaa tngaatgttg aagctctgag ccaattcaaa cgacaataac tttttactcc 300

gatgtctgat tgacgtccgc aatatatcga gacgctcgaa attgaatgtt gaacctatga 360

gcctattcaa acgacaataa ctttttactc tgatgtctga ttcgagtccg taatata 417

<210> 1853
<211> 324
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1853

agcttggact ntctgtngtc tgggaacctc tnctttctca ngtgtaccca aacccaatca 60

ccttgttcaa gcacgacttt ctttttgctt ttgttggctt gccttgcata gctcacaatt 120

ttcttttcaa tttgagcctt cacttgctca tgcaacttct tcacatactc agctntagcc 180

tgtgcatcat tatgcttaaa catagcaatg ttaggcatag gcaacanaat caagaggagt 240

caaaggaata aatccatata ctatctcaaa tggtgaacaa ttagttgtgc tatggacagc 300

tcgattataa gcaaactcaa catg 324

<210> 1854
<211> 362
<212> DNA
<213> Glycine max

<400> 1854

tctaaacctt gtacaagaat gaagctctga taccacttgt tatataagtg gcctcaaata 60

tcctaagaac ggcgggggtt gcagtaagat attccaaact gtttccccta atttaaaaat 120

tattttactt tttactcaag gtattaatct cctcaatgac aatcgtctta aatatgaact 180

caaaccaaac caccttgata tgaatatata gcaaacataa ataaacgaga·ttaacggaaa 240

agaaaatgca aacctcagtt tatactggtt cggtcacacc cttgtgccta cgtccagtct 300

ccaatgcaac cgcttgagaa gtccactaac ttgttaattc cttttacaag ttctacacac 360

ac 362

<210> 1855
<211> 463
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1855

taacaatcag tgtcatacta tngatcaaaa canagcaggt attaatatgc catactagac 60

tcaaaatatg ccacaaacac tagacctaaa tcagtgtcac agaaattgga agaaaatatt 120

ttatccaagc acaaacttca agccttattc catgtattgg ggggaagtta tggctggcca 180

tatgggtaga ggtgtcataa aggagcaagt atggaggaag ggaccttgga ctgctgaaga 240

ggacaagttg cttgttgagt atgtcaggtt gcatggtgaa ggcagatgga actctgttgc 300

tangcttgca agtaagaaac accaaacttt tttcactggt ttgtttctta atatatatga 360

ttcggatttg acatttataa gtgacaatat agcacaaaaa caactgaaat ngttttcaac 420

ttctactgtt catngtggct acattcatgt tcacccgaag ctc 463

<210> 1856
<211> 313
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1856

tacacttctt tcagagaaag gagcttaaca ttttcttctc aaaaactgaa aataacacta 60

ctaagtcttc aatctgtact taatgatgct gaggagaaaa aaatcactaa tcctgctatc 120

aaggaatggg tggatgagct cacacacact ctctatgacg ctgatgagtt gttagatgag 180

atcaacaccg agacattgtg atgcaaagtg gaagttgtga cctaaagtca acccattggt 240

gattaggcgc caaacgtgct ttcttattct ttcanaaggg tttatggggt catcaattat 300

gagatacaaa gct 313

<210> 1857
<211> 345
<212> DNA
<213> Glycine max

<400> 1857

agctaactaa tcaaatggga caattggcta ctcagttaaa tcaacagcag ccccagaatt 60

ctgacagatt accttctcaa tctgtctaga atcccaaaaa tgggagttcc attacattga 120

gatcgggaaa gcaatgtcaa agacctcaac cagcaacatc ttcctcatct gcaaatgaac 180

ctgcccaacc tcactctact ccagaaaaag atgatgacaa aaatttaaag agtaagttac 240

ctaacaattt ctatgaaggt gaatcttcca cttgtaattc tgatttacaa aagcagcata 300

tccctcttcc attcccttca agaagcaatt ccaacaaaaa aatgg 345

<210> 1858
<211> 361
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1858

cgaaatgcag atattgtttc atttcggaag agtgcgcaac caaaaagtac agtctttcca 60

tgactattca tacccacaaa aattccaaat ggcacttcat aagaattgac cttgtgtgta 120

gtatcaaata caacaacatc accatattnt tggtgcccat cagagctaga agtatgagac 180

caaaaaatat gctctcacct tctctcttca tcacgtggat atgcatactg gaaattatag 240

ccacttcttt ttgcatcctc accgtacttg agaagatctt ggcatcattt ctttcactta 300

tttttggttt cacaaaaaat acgaatgccc tttcataaat ggaaatacca tgcttacatt 360

t 361

<210> 1859
<211> 423
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1859

agcttattga ttntgataat atcactatag aaaatacaac attaaaagta atttaaacac 60

aaaataatca atctttatat tgtgtntttc ttgtcagatc tcattccaag tgaatttatc 120

catgttatta cggatgcaca tgtttaccac aatcatgtga ggccttngca ggagaagctc 180

cataaccagc caaaaccttt tccagtatgt gtaatgttta gcacttcttt tactttatat 240

tgtgactctt ttacttgttg acccccctaat ctacttcttg tagactttgg agatcaatcc 300

caaaatgaga gatatagatt cttttgtggc tgttgatttc aagctcatag gctatgatcc 360

tcaccagaag attgacatga agctggctgt ctaaaatctg gggattctca ctccttcgaa 420

ctg 423

<210> 1860
<211> 409
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1860

tncgctnttg gtgaataata agaaaaaagt catctatcca aaattatcac actcctttct 60

tcatccaaca atgaattggt ctatttaagg aagatgatac acagcattat tgcacatctc 120

tgtagaagca gccactatag taaacaatct tctctatcta aaatggagtt tgttctaaat 180

tacctaaatg ccactgccat tggagttctt tctataaccc tcttcttttt gtttttgtat 240

aatcccttca aatttgcatt atgtaaaaaa gaggctccca aagttgcagg tgcatggcca 300

atacttggtc acctaccact attgagtggt tcagagacac ctgatagggt tttgggtgct 360

ttggctgata agtatggacc catattcacc atcaactatg gtgtcaaaa 409

<210> 1861
<211> 386
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1861

ctctaggatc ttcttgactt ctcttgataa aacttcaact tgcccattgg tctggggatg 60

gtaagggaag ctaccttgtg tctgacacta tagtgctgga ggactntctt gagttggatg 120

ttacagaaat gagatcctnc atcacttatc agtacccttg gtgtgccaaa ccttgagaag 180

atgtttttct tgaggaagcg aataatagtc tctgcatttg catggttcac aactatttct 240

tccacccatc ttgttacata gtccacaacc aatataatgt attcatttga gtaaaatgat 300

tgcaatggac caatgaaatc catcccccag cagtcaaaag cttcaaccct cagaatgttc 360

tatagtggcg attcattcct tctgga 386

<210> 1862
<211> 224
<212> DNA
<213> Glycine max

<400> 1862

cactgcctca agtagttcac gatctgcttc cataggataa cacgttgcct aacagttact 60

atcaggtcaa gagatcttac gcttgcacta gccagtgatg gaatgaatcc acatggcaat 120

ttaagcactc aaaacagctc atggccagat ctactattaa tttacaatct tgctcctgag 180

ttgtgcatga agagaaaata catgacgtta tcgatgatga tatc 224

<210> 1863
<211> 457
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1863

tatctaanac tgcgattgtg agattgatgc ttattcggaa aacctctaat cctgcccatt 60

tttagtctaa tattagttca cacttgtaat tctaaatcta atatggctga aaaatagaga 120

acattggttt ccttttctta tacgtatttt tcaatttttg ttcctacttt attatgtgtt 180

tatagacttg agtgaaatga atacaaactc aacttttgga tcatattatg aatcctagat 240

caattgtgct tcgtctatat atttcgtggc atcataaatt atcttgtaaa gcctttcatt 300

tgtctatatt tataaatcat aaatataaac aatatcatag atattctttg tgaaattcaa 360

tattaaatct tatatattca ttgtttttct ttctcaacaa ctctcatatc tccatctatc 420

tagnttatct atngactntt atgcggatct acatata 457

<210> 1864

<211> 404
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1864

cccatggaag ctcctaatat ctcccacact atntgggatg ggccattctt ggatggcctt 60

gattntctca aggtccactt ggaccccatt tctgccaact acaaacccta agaaaactat 120

attatctaca caaaaagtac acttctctat atttgcatag agggtgtttt tcctaaagac 180

tgaaagaact tgcctgagat gtcctaagtg ataatctagg ctcctactgt acactaaaat 240

atcatcaaaa taaacaacta caaatctacc tatgaaatcc cttaagacat tatgcataag 300

cctcataaag gtgcttggtg cattagtgag cccaaaaggc atcactagcc attcatacaa 360

accagacttg gtcttgaaag cgggtttcca ctcatcaccc tttt 404

<210> 1865
<211> 447
<212> DNA
<213> Glycine max

<400> 1865

tgtagagtct ttcgtcagga ctcgggcttg tgccctgttg gtgccatgga gatgatccaa 60

aagtctctac ctgaatctct aagaaagagt gtaaacaagt gtgacctcgc acaatccaac 120

aagagcatat aatggattcc acacaacttt acttttcgat atctcatacc taaggagctt 180

gtaaaataat tgcttggtag ccctttttttc ttactatggg agacaatcta cttcaagttt 240

taaacaacag ttcacaactt caattgtagc tgcattagtc gtatctgtct gcaattttcc 300

aatcgagaca aaactgctac tacaattgct actgcagttt ataaccttga tgtgcgttgc 360

ttgctctatg atgtattatt cttctgtaca aagatgacag ggtagcacca acagagaaat 420

ctaatattgc aatgtgtagc attgagt 447

<210> 1866
<211> 471
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1866

catgcangct ttctgctcga tactcatctg ggttgtgcga ctaccatttc catcaacaga 60

caactgatcg tagttgctca aggaaacaca caaaatggcc aattcaacat tctcaaacat 120

ttctagccac ttgcaatttt ctgctagccc tctagcatgt attggaatta gttgatacct 180

gcaatcaatg agaacaaagc atatgacaca gatcagcaac tttttatagc agctctggca 240

atcggatcaa tcatgactac ctataaaatt tctcacatga aacaataggc gcaaatattt 300

tcacccacct aactaaagaa tcatgtagat cggcagtgtc gacagtttcc tcacgagctg 360

gccgaggaaa tgaaaactct accagaagcc atcccattgt atgaagtaac tccttcagca 420

tagaggatat ctaaatccga gggttcataa tcagtcctca atatctcaac a 471

<210> 1867
<211> 305
<212> DNA
<213> Glycine max

<400> 1867

aagatacatt gatcattcgt ttgtgttgaa gctgctttac ctttttgact cagaagacca 60

aagagagagg gattacctga agactatcct ccaccgtatt tatggaaagt tcatggtgca 120

tcggccattc attacaaaag ccatcaacaa tatcttttac aggttcatat ttgagacaga 180

gaaacacagt gggattgcag agttgcttga aatattgggc agcataatta atggtcttgc 240

tttgcctttg aaggaagacc ataagctgtt tcttgcccgt gcgttgatcc cgcttcacaa 300

gccta 305

<210> 1868
<211> 440
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1868

agcttatatt aaatagagta taaggagtac tctaatgtat atgtaaagtg atatccgnta 60

atttgaataa atatatatga tctaataaga tgaacaaaat taatataaaa tatgtttagt 120

ctgttagatt gtaaaatgaa cacaatttga aagacaaata agaggaagat acatgttttt 180

gtctaaatat gattggatat ttttctcttt atagcgcttt tctctctgag gtcttttact 240

gagtttcata aaatgttgta ttggaggatg aaatacctac aaagatactg tgacgcttaa 300

ataagattnt ggcctagagt aataaataaa catgttgtac taacctcaag tccacaagca 360

tcgttataat cctcgtatcc gagatattat gcacttatat gcctggtggc catcacggtt 420

ttatccttgt aaatacaact 440

<210> 1869
<211> 189
<212> DNA
<213> Glycine max

<400> 1869

tgttagacag acggcctcag ttctcttaag aaggggggtgg ttgttttacg ataacaagaa 60

ctctcgcgca attcgccttt cactctctgc tcttacatga acgatgcacc ctcaacatga 120

attactctaa agacaattct ccatagactg ctttaatgga agagagaact gcacactaga 180

ttcatgctg 189

<210> 1870
<211> 404
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1870

tattacgtgt tgatgattat atgtatatca attgttaaaa tatattagaa attaatagtt 60

caaataagaa aattaaattg aaggaaatta atatattaag attcaacgat aaatactttc 120

aatgcanttt tagtttaatt atttattaga ctcttttaat tgaaaataat atagttcgat 180

ttaatatgta catgttttgt gccatgtaaa tattaatatt gtgtgatgtc tatatgattc 240

atgagatgtg ataacatgtt tcattgagat tataacattg tgattgaaaa taaatataaa 300

tgtttgatta atacttgatg tgatattact tgtgttgtga cttatgaatt ggtgaatata 360

caataattcg actggtgttt actttgagaa aaatgtttat gtgc 404

<210> 1871
<211> 459
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1871

tcttagttnt agatgatgca gatgagtntg tagatacctc atgcactcct ctaatgacta 60

tagcatcatt tctggtgcta aactgttggg agttggaagc catcttctca attaaatttt 120

tggcttcagt aggagtcatg tctctaaggg ctccaccact ggcagcatct atcatacttc 180

tctccatatt actgagtcct tcataaaaat attggagaag aagctgctcc gaaatctgat 240

ggtgagggca actggcacat agtttttaa atctctccca gtattcgtat aggctctctc 300

cactgagttg tctaatactt gagatatcct tcctgatggt cgtggtccag gaagcaggan 360

attnttttc taagaatact ttcttaaggt catcccagct cgtgatggac cttggagcaa 420

ggtaatacag ccagtccttt gccactctct ctaaagaat 459

<210> 1872
<211> 474
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1872

taattcttag agggngaagg ccctttcang ggcggtgcat gatgtgtttt taaaagttgt 60

agctaaaaca gttccaaatt attgtatgag catttatcat tttccaaaat ctttagctaa 120

tgaacttcat aagatgatga gctccttttg ttggggtgcc aaaaggagtg gtcatagagg 180

gattcactgg atggattggc acaagctggg cagttcacaa ggaacatggc ggaataggtt 240

ttaaagacat atatggattt aacctcgctt tacaagggaa acaagggtgg aatctattga 300

aaaacccaac tgctttggtt tcaaagattt tcaaagctag atattatcct aaagcggatt 360

tcttggtggc cattgagcat aaataatcct tcatactctt ggagaagcat atgcaattct 420

tgggttctat taagggaaga ctatagatgg aaagttggaa atgggtcatc aatc 474

<210> 1873
<211> 417
<212> DNA
<213> Glycine max

<400> 1873

agcttgaagg taaactagat gccatggtta acctgttaac ccaactggcc atgaatcaaa 60

aatctgcacc tgtcgccaga ctatgtggtt tatgctcctc tgtcgaccac cacacagacc 120

tttgcccttc tgtgcaacaa tctgaagaaa ttgaatagcc tgaagcttat gctgcagaca 180

tccacaacag acctcctcaa cctcaacagc aaaatcagcc acaacagaat aattatgacc 240

tctccaacaa caggtacaat cccggatgga ggaatcatcc caaccttaga tggtcgaatc 300

cttcacaaca gcaacagcaa caacaacaga cttattttca aaatgctgct ggcccaagca 360

gaccatacgt tgctccacca atccagcagc aacagcaaca acagccccag aaataac 417

<210> 1874
<211> 410
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1874

agcttcttga tgtagaaaag acaaaagtta tattctttaa atatttaatt tctcaaatag 60

aactttgggt ttcctatgta tttcatctca aattatttct tcaatcaatc tatagctttt 120

ggaagctctt caaaagttcc aataatatat acgtcatcta cataagcaat gattatgaaa 180

atatattttt agattttcct gaaaaatgac aaataagatc attttaatat ccttccttta 240

acaagtactc actaagtcta ttatacaaca tgcgacttga tggctttagt ccatacaaag 300

tattcttctt gagaatatgc attattggac aaactatttc ctttaaggag ttntatgcan 360

atgccattat aaatagagtt atataagtaa gatgtaacaa tatccattat 410

<210> 1875
<211> 457
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1875

gagctngctt ctacaaccaa ttgaatagga acatttgcct ttggaggcat gggtaaggga 60

aagattacta gtataggtaa aatccgtgtt cctttcttag cctccataga caacgtctta 120

tatgttgaag gtttgaagta taacttattg agcaaagtta agtttgcgac aatggttata 180

ttgtgtcctt caacaaagac caatgtatag tcaagataca agatgacaag tncttattta 240

ctactaaatg acacaacaat ctgtatgaga ttgatctgat aggtctaagt aaacaaaata 300

taatgtgtct gctttgtaga gaatatgaga gatggatttg gcacaaaata tttgggcatg 360

tgaatctgan acatatctca caactttctt aaaaaggaat tagtgaacag acttcctaag 420

atttgttgaa actctcatct tctctgtgaa gcatgtc 457

<210> 1876
<211> 320
<212> DNA
<213> Glycine max

<400> 1876

tatgaccatt cgaatatctc aagagcttcc gctggtctat gtctagcgtg tagatgaggt 60

atgtccccga ctctgacatg agcgtgaaaa gatgtgacca ttctattgtg tcgagagctt 120

atgatgttca gtttagaacg tctcgatata ttatgagacg cgcatctgac gtgaagtgag 180

acaatccctg atctcttgga tattttccag agcttccgga gattactttc aagcgtatag 240

atgagctatg gacacgaacc gcacattcca gtgaaaactt gtgacggttc gaatttctcg 300

agagctttcg gtggccaatt 320

<210> 1877
<211> 475
<212> DNA
<213> Glycine max

<400> 1877

actaagctta caagggaaga taacacctca ttcatatttg gtcgatgttc aagatctggg 60

agggtgcagc acaatgataa cttaatgagc tctggcaaca cttcgtcatg gtcaacatcc 120

caggtaaaca aagggtctac aatattggca agttgtttta ttccattttt aagggctttt 180

gtcactactt cacgcaaagt gattggcaaa ccatcctctt tttagagtcc tgtcggcctt 240

ctttttgtta gaaactccat tactatgaca ccgaagctga acacatctgc tttagtggtt 300

actttcctca tgtaggcaaa ttctgaaaat tacacagcat aaatatcttg tttagagagt 360

gaaacttata aaaactctcg ggtatacaat gttaataaga taagaggatt cgaaacatag 420

tgacaaaata agacgttgtg taattgtgcc agtcttggtc atgctacctt ctctg 475

<210> 1878
<211> 459
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1878

ntgtaataca ccaaattctt ttctttgttt atttgcggcc acttgaatta tttatttcaa 60

tttctatcct tatacccata gtaagtattg acatttatcc atattttatt tttccattat 120

cagctgacaa ggttgaagct attctatcta atttttttata gataattttc acacatcaat 180

gaaaactcac ataaaaataa ataaaaccca tgcacaatac aaaaccttat atttcttttg 240

tattatatta attatataaa aataaatttg aattataatt gaatatgttt gctgttttga 300

gaacccccttg aatcactatt aagatacttg attgaaaagt ttaaatatat caataaatat 360

atgttttaac atatagtatg acacacattt attatctctc tatacattaa taatatatta 420

cattagaatg gataaatgca tatgtatata tatatatat 459

<210> 1879
<211> 464
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1879

cgtcactcan aacaactcat tgtgcatgaa cctattgaat ctagctntca acattgaaat 60

aaagatataa caattgaaat tgtaacatct cattttctta aaactaattt taagaaaatg 120

ttatttataa ataaatagag ttttagaaaa atgatgagat ttttgtaatt aaatgaataa 180

gaagaaataa ttgtattaaa ataatggttt gagagaaaat aaaaaggata catttgatag 240

gaaataaaat agagtgtttg tttataaagt aataaaaaaa tagagtagac aatagactaa 300

gagtatctaa ctatgaatag agacatgcta ggtcatttnt aactntctct ccctctcagt 360

ttgcgtntct ttctcctcct ctaaacctnt ctattccgca tccaccaatt tatcccagaa 420

aatgtgatct cgactcattc atcgtggatc gcataatatt aaca 464

<210> 1880
<211> 367
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1880

actatgaatg acaaattcct tgggataaag gtagtggtgc catgttttca aagcccgtac 60

taaggcatac aactccttat cataagttga atagttaagg gtaggaccac ttaacttttc 120

actgaaataa gcaattggat ggccttcttg caacaacaca gccccaatcc caacatttaa 180

agcatcacac tcgatttcaa aagatttttg aaagtttgca acgcaagtat ggnggcatta 240

gttagctttt gcttaagaat attgaaatct tcttcttgtt tctctcccca ttagaaacca 300

acatttttct tgggcacttc attgagaggt gctgtcaatg tgctaaaatc attcacaaat 360

cgtctat 367

<210> 1881
<211> 369
<212> DNA
<213> Glycine max

<400> 1881

gcttaagctc cttcaactgc acaaggctct taatatttta agagtatcct tgtggaacct 60

tgacccgacg aagacactga cagaaactta tcttctcctt cttggacaaa gtatgagatg 120

ctgggggcaa gtaaattctc ttcccatcag accttggatg cgactgtgat cttataccta 180

tatcagctag atcttgacgg gtattcaagc catccttcgt cttgccgtga atgttaagga 240

gcgtcccaat cacactgtca caaacattgt tctccacatg cataacatca atacaatgtc 300

taacgtctag atcacaccag tacggaagat caacgaaaat ggacctcttc ttccatatgc 360

aactctgac 369

<210> 1882
<211> 486
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1882

agcttctaca ttcaatttcg agctnttcga tatattactg gactcaatcg gacatccgag 60

taaaaagtta ttgtagtttg aatttgctca gggcttcggt attccatttc gagcgtctcg 120

atatattacg ggactcaatc ggacatcaga gtaaaaagtt attgttgttt gaatttgctc 180

agagcttcgg tattccattt cgagcatctc gatatattac gggactcaat cagacatccg 240

agtaaaaagt tattgtagtt tgaatttgct cagggcttct gtattccatt tcgagcgtct 300

cgatgtatta cgggactcaa tcagacatcc gagtaaaaag ttattgtcgt ttgaatttgc 360

tcagagcttc tacattcaat ttcgagctgt tcgatatatt acgggactca atcagacatc 420

cgagtaaaaa gttattgtcg tctgaatttg tcagagcttc atattccatt tcagcgtttg 480

attata 486

<210> 1883
<211> 484
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1883

agcttgcttc tacaatatcc nnctttttgat gatgacatct tctgaaatca agaagcacac 60

acacactttt tcctagtcga tcactcatat aaattctcct cctttgtttt tgaatttatg 120

tttatcttaa aaataagttg attactcatg tgaattcttg atttaatccc atttctctcc 180

ccctttggca tcaacaaaaa gccaaagtgc gtatcaaact taaggtatac aaatataact 240

taaacatcta tacttaatat tcatgaaaaa aatatcaacc aaatcatgaa gcaagaagca 300

agaaccatga aaaccatgaa gcaacaacca tgaatagatt aattttaaac tccacatagt 360

caaataacat acttaatatt ggtccaaaca taccatgcaa ataaggaaat agtatattgt 420

tcaaatatca taataataat agagaaatta tttgataagt cactaacatc tattagtcct 480

aact 484

<210> 1884
<211> 393
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1884

ggccgccacg gagttntccg actatgctct tgtgtggtgg aacaagctac aaaaggagag 60

agcacgaaat gaagagccaa tggttgatac atggacggag atgaaaaaga tcatgaggaa 120

gcggtatgtg ccggctagtt actcaaggga cttgaaattc aagctccaaa aactaaccca 180

aggcaacaag ggggttgagg agtatttcaa ggaaatggat gtgctcatga ttcaagcaaa 240

tattgaagaa gatgaggagg taactatggc tcgatttctt aatggtttga ctaatgatat 300

ccgtgatatt gttgagttgc acgagttngt tgaaatggat gatttgcttc acaaagcaat 360

ccaagtggag caacaattaa naaggaacgg agt 393

<210> 1885
<211> 447
<212> DNA
<213> Glycine max

<400> 1885

tgcaggtgct gctactggtg gaggcacttg aatttgcttg ccagaccaca aggtgatggc 60

actcacattt ttcggattct gcacagtttg tgaaggcaat ttgtcaaaaa tttgggactg 120

agcttggttc aactgagtag ccatctgccc catctgattt gttagactct gaatagaggc 180

tcttgtctct tgctgaaatt gcatattctg gatagtcatt tgcctcacta actcttctaa 240

ggaaggttga ggaggggcct cagttgcttg ttgtctttgc tgttgctact gctgtattgg 300

aggaggaaca tgtggcttgc ttggaccatc aacattctgg aagggaggga caagctgttg 360

ttgttgtgga cgacttgccc atctcaaaat tggatgattc ctccaacctg gattgtatct 420

gttgcttgaa agatcataat tattctg 447

<210> 1886
<211> 465
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1886

gcttcaacat cagaccactt ccagggtgct ggtactactt cacatggact tgatggggcc 60

tatgcaagtt gaaagccttg gaggaaacac gcctgcctat gttgttgtgg atgatttctc 120

cagatttacc tgtgtcaact ttatcagaga gaaatcagaa acctttgaag tattcaaaga 180

gttgagtcta agacttcaaa gagaatagga ttgtgtcatc tagagaatca ggagtgacca 240

tggcagagaa tttgaaaaca gcaggttcac tgaattctgc acatctgaag gcatcactca 300

tgagttctct gcagccatta caccacaaca gaatggcata gttgaaagga aaaacaggac 360

tctgcaagag gctgctangg tcatgcttca tgccaaagaa cttacctata atctctgggc 420

tgaagccatg aacacagtat gctacattct acacagagtc acact 465

<210> 1887
<211> 431
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1887

agctcatgct ttttccccaa gctgtacagt ttattatttt aaggactgtt ggcaagtgat 60

agtatgatgt agtaaagaaa catgcataat gagattaaag tagtggttac tagtggtaat 120

tacagtatat atggttgata actggagagt aataaaccta gcgaggtgta atatatcaag 180

tgtgatagaa aatgtgttac tagcatttca catatactaa ttacagaaaa ctacttatgt 240

ttttattcaa gttaattagc tattactttg tatgtggcag ttctttcttc tgtgtatgtt 300

gagtggctgt agcatatgtt ggttcaacac agtatgttnt gttctctgca ttaggaattt 360

cccagttaac agacccctg cattatcact cactgtgagt gtcaatggtg tgagtgcagc 420

actctacaca c 431

<210> 1888
<211> 460
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1888

tgccnanata aagaaaggga atagattgaa tctagtaaga tgcattaagg atgaagaagg 60

aaaagtattg gtcagagatc aagatatcaa agaaagatgg gagaaacatt ttataagctt 120

ttcaattatg gacaaaggat cagcttggaa gtgaagacag agcatatgca ttgcaatttt 180

agcaagaggc aagaggagta tgacttggaa gtgaagatgg gagaagatgt cataccacat 240

gttactaagt ttaaatatat gggatcaata atataataca atatcatgag gaaattaatg 300

aggatgtcac acatagaata caagcaaggt ggttaaaatg gagaaaggcg tcaagggtta 360

tttgtgattg caaaatacca actttaaatg caagttttgt tgtacagcaa tagtttgact 420

atactctatg gtagtgaatg gttggtttag agggacaata 460

<210> 1889
<211> 335
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1889

agcttcacat cataccactt ccagcgtgct ggatctactt cacatggact tgatggggcc 60

tatgcaagtt gaaagccttg gaggatagag gtatgcctat gttgttgtgg atgatttctc 120

cacatctacc tgtgtnaact ttatcagaga gaaatcagat acctttgaag tattcaaaga 180

gttgagtctt agacttcaaa gagaaaagga ttgcgtcatc aagagaatca tgagtgacca 240

tggcagacaa tgtgaaaaca gccgggtcac tgaattctgc acatctgaag gcatcactca 300

tgagttctct gcagtcatta caccacaaca gaatg 335

<210> 1890
<211> 433
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1890

agcttaagct ccttcaactg cacaaggctc ttaatatttg aagagtatcc ttgtggaacc 60

ttcacccgac gaagacactg acaaaaaatt atcttctcct tcttggacaa agtatggcag 120

gctgggggca agtaaatttt cttcccatca gaccttggat gcaactgtgc tcttataccc 180

atatcaacta gatcttgacg ggtattcaag ccatccttcg tcttgccttg aatgttaagg 240

agcgtcccaa tcacactgtc acaaacattt ttctccacat gcataacatc aatacaatgt 300

ctaatgtcaa gatcacacca gtacggaaga tcaaagaana tggacctctt cttccatatg 360

caactctgac ttttatcctt cttttgggtc ttcccaaata cagtggtcag ggtgtgaacc 420

cgctgatata cct 433

<210> 1891
<211> 467
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1891

agctngagca ggttggaatt ggaaagcaac aaattaactg gagaaatacc ctcctccctt 60

ggtaatctta aaaggcttca attcttgtaa gtatggcatt ctgtttgcta ggctctacat 120

atatataatg agtcttaggc cttagcatgt atttttgtg caatgtttaa aagtgtctgt 180

ttcttgtcct gctaccagaa cattgagcca aaacaatctc agtgggacta ttcctgaatc 240

acttgccagt cttccaatct taatcaatgt gtatgtaaaa taatggtttc tagaactctg 300

ccattntttt aaagtatatt tcattaattt agtatctgat tgattattca aacttctctt 360

ttgcagtctg ctagattcaa ataatctgag tggccaaatc ccagagcagt tatttaaggt 420

tcctatatac aagtatggat ggtacaacca taaaattagt atatgat 467

<210> 1892
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1892

tctcgtagta gaacataggc aacgtatcta ccataatcgt gatcatctcc ctctcagtca 60

tgggcgggat gacttgggct gctaggtctc tccacctttg agcatattct ttaatggact 120

catgttctcg cttggtcatg ctctgaagat ggttccgatc aggagccata tccgcgttgt 180

attggtactg cctaatgaag gcagtttcca agtctttcca tgaccggatc tgagaagctt 240

ccagattggt ataccacgcc actgctgctc cggctaagct gtcttgaaag aagtgcgtca 300

acagctcttt gtccagagaa tatgccccca tccttcggca atacatccaa agatgacctc 360

ttggacacgt cttccctttg atntatcaaa atctggtatt ttaaacttt 408

<210> 1893
<211> 464
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1893

taagctcctt caactgcaca aggctcttaa tatttgaaga gtatccttgt ggaaccttca 60

cctgacgaag acactgacaa aaacttatct tctccttctt ggacaaagta tggcaggctg 120

ggggcaagta aattttcttc ccatcagacc ttggatgcaa ctatgctctt atacccatat 180

cagctagatc ttgacgggta ttcaagccat ccttcgtctt gccttgaatg ttaaggagca 240

tcccaatcac actgtcacaa acatttttct ccacatgcat aacatcaata taatgtctaa 300

cgtcaagatc acaccagtac ggaagatcaa agagaatgga cctcttcttc catatgcaac 360

tctaactgnt atccttcttt tgggtattcc caaatacagt gttcaggtgt tgaacccgct 420

gatatacctg ctcaccagtc aacggtatcg gcgcaatatc atgc 464

<210> 1894
<211> 374
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1894

agcttgccct tgttcttcac cctaaagtgt atataaatta ggaacaaacc ttttgtagaa 60

gcttgctcac ccctagaagc tcctaatatc tcctatactt tntggggagg gccattcttg 120

gatggccttg attttcttag ggctcacttg gaccccattt ctaccaacta caaattctaa 180

gaaactatat tatctacata aaaggtacac ttctctatat tagcatagag agtatttttc 240

ctaagaactg aaagaacttt ccttagatgt cctaagtgat catttaggct cttactgtac 300

actaaaattt catcaaaata aatgactacg aatctaccta tgaaatccct taagacatga 360

tgcataagcc tcat 374

<210> 1895
<211> 406
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1895

catgcaagct tcttaatgtt atagaattca atagctcaag gaagcgaatg tcagtgatag 60

tgaaagatga agaagggaaa anttttctac tctgtaaagg tgctgacagg tctgtgataa 120

aataatttat agccttcaac ttctagcctg cgcatttaac ctatggactt gcctaactta 180

ttttttcatg cagtgtcatg ttggaaaggc ttgcaaacaa ttggaggaag tttgaaagga 240

aaactgtgga acatgtgcgt gaatatgctg acacaggtct aaggacccta gtacttgcct 300

attgcgaact tgatgaacaa gaatacaagg agttcgatga taaattctct gaagtaaaaa 360

attctgtccg cgcagatcag gaaactctga ttgaagaagt atcgga 406

<210> 1896

<211> 452
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1896

agctngttac tatgataaga gcatacctgt tgtttcctga agtccaagta caagactttn 60

tgtcaataat atcaccaaaa actatcacat taacaaaatc acagcctcta agatttcgac 120

aaattattag gtagccttga agcattatgt ttttatgatt ctaatctacc attctcttta 180

tatataatac ataactatat tttttaattt gtaattaatt ataatanntc aatatgttat 240

gtaaaaaaat agttaaaata attaacatta taatgattnt agactatcta ataatttcta 300

gtaagaattt aatgtataac aaacctggaa gcacagaagg ctaccacata atccgtccca 360

gaacaagtga aaatactatg tggatcatca taagcatagc tgtaagaaag tggacatgcc 420

tncttaaact tcttcgaata aaacgtggga tt 452

<210> 1897
<211> 164
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1897

agcttataca tggagcaagg taaattctca ttatatcata ttgcttaagc acaagaaaca 60

tcatattgcg aggtaaatgt taaggcagat aaacaatcaa aactcctatc taatatctac 120

cactctatgt ctcttctatn tgcagggnaa agcaatcctt gcta 164

<210> 1898
<211> 466
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1898

tgttccgtct aaaactcaga ttaaacgagg anttttctgc aaaatacctc tntgatcaac 60

attctgaata caaaccattt tgtaattctt ttgcgaagtt aatggtttgc atagcaaaac 120

ttgacggagt ctttatagta actaataatc attcactcag tcctcacttt cctctggttt 180

cacaaagaat tcaatatgag ctattctact tggttgctga tagccaaccg aatcagcata 240

tgggtgtgac acagatggtt tggcaattga aaccagatgc tggactttta acattccacc 300

tctcccaatg cttaacttac ttcctctatt ttctttaata acactgctag gcatattaga 360

acgtgttgct ctgaggaact tatatttgta cctgttaaca acaagcatag taatgacaaa 420

taaatcgctg gcaaggaaat gacaactaac acataaataa tagttt 466

<210> 1899
<211> 415
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1899

ctttgaatcg gtggtctgat tgtgttccaa aggatatcga gatgctcgta attgaaaacg 60

gaagttctga gaaaaatcaa acgacaataa cttttaactc ggatgtccta ttgagccctg 120

taatatgtcg agacgctcaa aattgaaaac ggaagctcta agaaaagtga aacgacaata 180

acttttgact cggatgtncg atatagtctc gtaatatatc gagacgctcg gaattgaaaa 240

cagaagctct tagcaaattc aaacgacaat aacttttgac acggatgtct gattgagtct 300

cgtaggatat ctagacgctc ataattgaaa acggaagctc tacgaacaat caaacgacaa 360

taacctctaa ctcggatgtc tgatcgagcc ctgtaatata tcgagacgct cgaaa 415

<210> 1900
<211> 192
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1900

agcttaacat cagaccactt ccagggtgct ggatactact tcacatggac ttgatggngc 60

ctatgcaagt tgaaagcctt ggaggaaaga ggtatgccta tgttgctgtg gatgatttct 120

ccagatttac ctgngtcaac tttatcagag agaaatcaga aacctttgaa gtatttaaag 180

agttgagtct aa 192

<210> 1901
<211> 469
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1901

ggaggatatc tatgtttatt gtaacattca tcaatattgt gatttgtgaa tccataatgt 60

gtacaaacct tgcttgcttt cctatcaaaa ctccctttat caaagcttca ttggctactt 120

cctcctcctc tagaagtata acttggagga aaaccatttt tcctataaca tctgtccact 180

atgtgattat ccttaccaca gtatgtacat gatttcgatg aaagtgagcc tgttgcattg 240

atgagactag tgtntcccat cagatcacta ttattgatct gcctttcttg ctgaacaaca 300

tatgagaaga cctttgctat gctaggtaat ggatccatca tcactacatt ggatcagaca 360

atgccaaaat gataatttaa acctctaaga aactgcataa cttgatcttg tttcttcctt 420

tctataacac taccaagagc atcacatata cactttnggt cacatatac 469

<210> 1902
<211> 480
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1902

actataaaac taagctacca cgacatctga attcatgtac gacaaatctc tatgcggtct 60

tagttggaac atggacgcta gagtggcaag ggcgtcggcc atctgatntt cctctctagg 120

aatgtgatga aaggatatgt catcaaagaa ttctatcaac ttccttatgt aagcctcgta 180

aggcaccaat ttatggtccc tggtctccca ttcacctttc aattggtgaa ttaccaatgc 240

caagtcccca taaactttga gcaacttgac cttgatgtca atcgccactt ggatcccaaa 300

ggcacacgcc ttatactcac ctatgttgtt tgtgcagtcg aaacccaacc tagccatgaa 360

aggtatatac tattcatcca gngaaaccaa tactgcgcca actccatggc ctagtgcatt 420

agatgcgcca tcaaaccaca cgaatccatt gtccctgtct tcatcctcta ctttctcctc 480

<210> 1903
<211> 428
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1903

agctttcaac actggcaact gcaagatant tgtaagttct ggcatatatg ggattaggcc 60

aaatggaaaa attacaaatg tcaaaagact aaccggtagg gccatgacta acacaaggcc 120

aataaagcaa cggccttaag cctcttttca attattgaaa ttntatatat ttttaaaata 180

cttctaaatt aatagataat aaatttttatt atattatttg tatttaactt gtttctaaaa 240

taattagtaa aatttattct ctctaaatat aaaatagaat aactatattg aatgagaata 300

tttttaagaa ttattgtgtt tgataagaac aagtaaaaaa attctctana aaaaatatct 360

ttggattctt tttgctaata ttttctctta ctatattttt cataatgcac aatgaacaag 420

atagattc 428

<210> 1904
<211> 448
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1904

gtacaagacc gnggaattag ccattagtgt gtggcctgga tcttctgttg gactagtttg 60

acccctgtgc ttgacaccat gtggcccaag tactccacct gggtttgggc gaaggaacat 120

ttcgagagct taatgaagaa ctggccctgc gacaaaaccg tgaaagccaa ttgcaaatga 180

agtaaatggt cattgaagga gctactataa attagtatgt cgagatgtgg acatcaaagc 240

ccaagcccat gacaaccacc agccccaggc ccatgactag atggaagccc aagacccaat 300

acaaggcata ggaagaccca tgacaagagc aagagctaaa aaggcacaag atgctttgga 360

acatatggtg attattctga gggtagttca aatgcaagga gaggcccaac acttggagtc 420

tcaaaaggga atgttgctag tcctatgt 448

<210> 1905
<211> 380
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1905

agcttcaagg ttcanagttg gatcaaaagc ggcttgaggg acttttccat ttcccgagca 60

tcagttgagt ggcgcattcc tgttcctgat gacaagaccc agactatata tgtatggttt 120

gatgctttac tagggtaagg atatgtatct tatagcttgt gcgtgctcct ctagcttccc 180

ttgactctat tctataatct tataggtcct gtctatcata ctcaccgact atcatcttgt 240

ttattgttcg aaatacatag ctaaatgcat gaaagttcac attatgcatg atcatttgta 300

cagaatcacg ataaagaaca gcttggactt ctgctatttt gctgaatatt ctctattaca 360

tgtgtcgcta atcaccttcc 380

<210> 1906
<211> 426
<212> DNA
<213> Glycine max

<400> 1906

taagctcttc aatgcttcct ctttcttgct gggagaagtt cttatcattt tgacatgcat 60

accaaaagcc ttagcaaact tgacagccac atgacctatg cctccgaggc ccaccacacc 120

caagtgcaac ccaggctgag caagcctata atatttcatt gggctgcata ctgtgattcc 180

agcacatagc aacggggcgt gcaccatcta acggaagaga ttttgggatt agcacgacaa 240

agttctgatc aaccactatg atatctgagt ctccaccttg agttattgcc ccatcataat 300

agcgtgcact gtaggttaca tgtatttttg gacaatatac atagaagccg atgctgtcgg 360

tccaacatga gccacacgaa cctacagagc cacccacacc acgcatgcac catcactgca 420

ctttgg 426

<210> 1907
<211> 396
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1907

tgagcccact tatctntgta catattagat taaggtttca ttattttctg gccttgtatt 60

tagggctcta taatgtaggt agggtaccct agaaatgtag gatttttcag cccttgtatt 120

ttagggcacc tagactagtt tttgtattac gggtatgttt gtaatttcac atgcattaag 180

tgaatatttg atgtgtgtgt tggaaaataa atctaattgt attgggagaa gctcaatcca 240

atttaattct agaggggggag gtgagcattt gcttgctaca ccccattgtc acatcatata 300

gtcgcacttt gtgcatatcc ttcatgctct acatgcctca tgccacgtta gcatatttag 360

tggataattt tgaacttgat cttggttagt gggctg 396

<210> 1908
<211> 421
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1908

agctggcttc ctttgattnt cggcatgtct cgggacttca catatcgngc aacaaagggt 60

gccaagtatc tcgaagcggc caatcaaagg ttgtatatca tcaaataata atccccggac 120

gaaattaggg tatgacaggg tcgaagcggc ttcctatacc aatgtcacga ggagtgtggt 180

ggtcagattc ataaagaggg agttgnattg tcagtacgaa ctccctagga agatcattac 240

tgacaatggc acanatctga ataacaaaat gatgcaggat atgtgcatgg atttcaaaat 300

ctagcatcac aattccacgc cctaccgacc aaagatgaac ggagccgtgg aagcagccaa 360

taagaatatt aagaatatta ttcagaagat gacagtgtcg cacaaagatt ggcatgagat 420

g 421

<210> 1909
<211> 453
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1909

ngaaggagtt tattgcatca gggaacaatt tcactttaaa agtgtgtcct aattggattc 60

ctaattntca acttacctat ttggatgtga catcatggca gataggtccc aactttccat 120

cgtggattca atcacaaaac aaacttcaat atattggact gtctaacacg gtgattttag 180

attctattcc cacttggttc tgggaaccac actctcaggt tgtgcattta aacctctctc 240

ataatcatat ccatggtgag cttgtgacta cattacaaaa tccaatatct atccaaactg 300

ttgatctaag cacaaatcac ttatgtggta aattacccta tctttcanat gatgtgtatg 360

agttagacct ttcaaccaat tcattctctg aatccatgca agaatnctta tgtaacaatc 420

acgacaaggc aatgcaatta gaatttctca atc 453

<210> 1910
<211> 340
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1910

tctaattgat taacggaagc tcttgagana ctcaaatggt catatcttat cacacggacg 60

tncgattcag gtgcataata tatcgagacg ctggaaattg aacaacgtat ggccttgaga 120

tattcaaatg gtcataacta gtcacacgga tgtccgattc atgcacataa tatatcgaga 180

tgctcaaaat cgaacatcgg aagctctcga gaaattccaa aggtcataac tcttcacacg 240

gaagtccgat tctggcgcat cacttcataa gatgctctga attgaacacc ggatgctctc 300

gagaaattca aacggtcata acttgttaca cggaagttcg 340

<210> 1911
<211> 469
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1911

tctanactnt atacaagaat gaagctctga taccacttgt tagacaagtg gcctcagata 60

tcttaagaag ggggggttga attaagatat tccaaactac ttccccaatt aaaaatctat 120

ttcacttttt ttaagttatg aattccctta atgacaatct tcttaaatat tgattcagat 180

aaaacaattt gaatatgaga ataaagcagt aataaataaa ggagattaat ggaagagaga 240

gtgcaaactc agatttatac tggttcggcc acacccttgt gcctacgtcc agtccccaag 300

caacccgctt gagagttcca ctatcttgta aattccttct acaagttcta aacacacaag 360

gacaatcctt cctttgtgct tagaattcct ttacaacaag agactcacgg tctcttaatc 420

ccttagagaa tgaggagaag tagaagaata aatctctcta gaaagagat 469

<210> 1912
<211> 432
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1912

agcttcaaga aaaagatggc ctcagtatat tccttatttc cagaagggaa ttccatcaat 60

agacctccaa tctttaatgg agagggttac cactactgga aaacccgaat gcaaattttt 120

attgaggcaa tagatctaca tatttgggaa gccatagaaa tagggcctta tatacccacc 180

acaggagaaa gagttacaat agatggtagt tcatcaagtg aaagcataac tatagagaaa 240

cctatagata gatggtctga agaggataga aaacgagtac aatacaactt aaaagccaaa 300

aacataataa catctgccct gtgaatggat gagtatttca cggcttcaaa ttggaagagt 360

gctaaggaaa tgtgggacac tnttcgatta acacatgaag gaactacaga tgttaaaaga 420

tctatgataa at 432

<210> 1913
<211> 493
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1913

acactcagat actaagctgt tcgccatcgt tcgcgtgtat gacatccact ccacaaggtt 60

tgaagttgag gagaccttca atcctattac acaacgtggc cgacaaaagt gggcagttaa 120

cttgaatggt cattattgtc aatgcagaag gtattctgcg cttcactatc catgttcaca 180

tattattgca gcttgtggtt acgtgagcct gaactactac caatatatag atgttgttta 240

tacaaatgag cacatcgtaa aagcttactc cgcacaatgg tggcctcttg ggaatgaagc 300

gactattcct ccttctaatg acgcatggac acttatccct gacccaacag caattcgtgc 360

gaaaggtcgg cctaaatcaa caaggataag gaatgagatg gattgtgtcg aaccctctga 420

gcaccgacaa aaatgcagta gatgtggagc cgaagcgcat aacangcgtc gatgtccaat 480

gcaatctgag cgt 493

<210> 1914
<211> 464
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1914

agctnntgga aatgatntct atacaaaagt tagtcgtata aagtgactaa cacacttagg 60

ctataaatag aggtcatgtg tgtgcatttc ttcaactttg atcattttag aattacgctt 120

caaagttcag acctcttttg aggcacaaat tttcgtgctc cttctcctac cttcaggctc 180

ttatccatgg attcctatgg tggtgagctt cttcttgact catcttctcc ttgaagtggt 240

gtctctaatc aactttcttc cttattcatt tcgctaccat taaacttcaa gaagaaaagc 300

actccattgt tgaagaagat ccaaggccta caagttccac atggagctac attagtattg 360

ccctttctcc tacgtatcct tagatgcgat gaggaactta gacctacgta gttctttaag 420

tctgaatggt tgttgtgcta catngatttt atcttaattt taaa 464

<210> 1915
<211> 395
<212> DNA
<213> Glycine max

<400> 1915

ataccttcat ctgacttatt atcattattt cctaagctat cttttccatt attcaataca 60

aaacatttac gaccaaagat atgaagatgt gagatgtttg gttttctgcc attgaacaat 120

tcatatggag tattctttaa aatgggtgtt attaaagccc tatttaaaat gtagcatgct 180

gcgttaacgg ctttagcccc tatagttgtt ggaagaggag tatcatttag gtcagtccta 240

tctatctcgt tcaaagatct atttatactt tctacaacac cataatgtcg aggggatctt 300

ggtgttgaaa agctatgctc aattccatgc ttatcacaca ataattgaca ttcttcactt 360

gcacactgac gcgcatgatc actcctaata gatat 395

<210> 1916
<211> 409
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1916

ggaagganaa cttgatgcct tggtcaacct agtaactcag ctttccatga ataagaaatc 60

tacacttgtt gcaggagtct gtggtctatg ttcttctgca gatcaccata cagaaatctg 120

tccttttttg cagcaatctg gagtcaatga gcaacctgaa gcttatgctg caaacattta 180

taatagacct catcatcagc aaaacccaca acaccagaat aattattgac ctttaagcaa 240

tagatacaat ccatgctgga ggaatcatcc atatctgaga tggacaagcc cttcacaaca 300

acaacaacct gtccctccct ttcagaatga tgttggtcca agcaagccat atgttcctcc 360

tttcatacaa cagcagtcac aacaaagaca acaagcatct gaggctcct 409

<210> 1917
<211> 484
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1917

tctntgagaa aacttccttg agaagctaga gcttagctac acatacctct ctaatagcta 60

agcttacctc cttgagatga gaagctagag cttagctata cacaccctat aatagctaag 120

ctcaccccca tgacaaaaaa catgaaaata caaaaaaaag tccttactac aaagactact 180

caaaatgccc cgaaatacaa ggctaaaacc ctatactact agaatggcca aaatacaagg 240

cccagacgaa ggaaaaatct attctaatat ttacaaagat aaatgggctc atacttagcc 300

catgggctcg aaatctaccc taaggctcat gagaacccta gggccttccc ttggatctct 360

agcccaatct acatggagtc ttctacccaa tgcccttgca gagtaggatt gcatcattga 420

gttatgtgga gttntattga cctaagttga aattatgaga tttcaaatct tacctaaacc 480

tact 484

<210> 1918
<211> 475
<212> DNA
<213> Glycine max

<400> 1918

agcttgtagg cctaggatct tcttcatcaa tggattcctt tgcttcttgg aaaatgaatg 60

gcagcggaat ggagaaggaa gagagagaga gagaggagac gccacttcaa ggagaagatg 120

agtctagaag aagctcacca ccataagagg ccatggataa gagcttgggg gaagaaggag 180

atgaatgaag ggagagggag agaagagcac tgaaatttgt gctccaaatg agctttgaaa 240

tctgaatttt aatattcaaa tgatcaaagt tgaaaaaaat gcacacacat gacctctatt 300

tatagcctaa gtgtcacaca aaattggagg gaaattcaaa tttcacttga attggtggag 360

ccaaactttg gagccaaaat ttcactaatt atgattagtg aattctagtt atggttcagc 420

ccactaatcc aagatcaatt ccaagattct ccactaagtg tgcttaggtg tcatg 475

<210> 1919
<211> 325
<212> DNA
<213> Glycine max

<400> 1919

cccgttgttc aatttcttac gtctatatat gtgatgcgcc tgttatcgac cttcaagaga 60

aaagtaatga ccatctgaaa ttctcgagag cttccgctgc tcaatttcaa gcgtctcgat 120

ctgttatacg cctgaatcgg acctccgagt gacatcttat gaccatatga atatttcgag 180

agcttccgcc gatcaacgtc tagcctcatg acatattatg cgcctgactc ggacctacta 240

gtgagaagct cagaccatta gagttggtca cgagcttcca acgatcaata cccagcgtct 300

cggcatgtga tgcgcctgaa ttgga 325

<210> 1920
<211> 344
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1920

agctctaaca tcagaccact tccattgtgc tggatctact tcacatggac tcgaaggggc 60

ctatgccagt tgaaagccat ggaggaaaga ggcatgccta tgctgatgtg gatgattcct 120

cgagatatac ctgggtcaac tgtatcagat aaaaatcaca catcctngaa gtattcaatg 180

agctgagtct aagacttcac ctagacatag actgtgtcat caagagactc atgagtgacc 240

atggcaaaga gtacgaaaac agattgttta ctgaattctg ctcatttgaa cgcatcactc 300

atgagttgta tgagccatta caccacatca gagcgacata tatg 344

<210> 1921
<211> 425
<212> DNA
<213> Glycine max

<400> 1921

ttatgctatt acctaaactt atgagctcta gctaggttgt agcttcctat aataggtata 60

agaataggat caaagcttct actttgacaa tcacagtgtc aaggacttaa ctgatgacat 120

tattgcaaat tcaatgtttt gacattcctt aattttgtag gtactaccaa tgggaaacgg 180

gcaaccccaa atccagaaat gggttctaca tctcaagggg aacggaagag gaagcggtta 240

gcaaccgacg gagaggagga aactttgcaa agccaattaa ttgatgtctt agaaaagaat 300

ggcaaaatgc tacatgatca acttgaagct cagaacctga atttccagtt ggatcgccaa 360

cagcagaaag acactgcaag taacatagtt gctgtacttg ataagcttgc agatgctcta 420

cggag 425

<210> 1922
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1922

agctgcatac tgttntcatt atgacaataa aatatttttg caggctatac agctggatcc 60

agaatntgct aacaacattg ggcagattgt tcttcttggt ggtgcttttg cagtaaatgg 120

caatgtgaat cccgctgctg aagccaacgt gagtatttca atcctgtatt caaattctta 180

atataacttc cataaaaata ttgtatcatc cacaagtcaa tctgtctaac tcttcggttg 240

gatttgttcc agacatttgg tgatccagat gctgcagatg ttgtatttac aagtggggca 300

gatgtacttg cagtggggat aaatgttacc caccaagttg tactgacagg taccccttg 360

acaaattctt tggctccttt gtatacttga gtcatttttg taaaattc 408

<210> 1923
<211> 437
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1923

agcttctggt ttaattacgt gcgtctcgat atctctactg tgacacaatc agacatccga 60

gtgaaaatnt attgtgcttt anatgtgctc agagcttcag ttttcaatta ggagcgtctc 120

gatatattac gggtctgaat cggacatccg agttaaaaat tattgtcgtt tgaattttgc 180

cagagctttc gttatcaatt acgagcgcct cgatatccta cggtgctcaa tcggacatcc 240

gaggtaaaag ttatagtcga tagatttttc ccagagcttc cgttttcaat taagagcgtc 300

tcgatatcct acgggacaca atcggacatc cgagtcacaa gttattgtcg tttgactctt 360

cttagagctt cctgtttaaa tttcgagcgt cttgatatat tacagggcgc aatcggacat 420

ccgagttgaa agttatt 437

<210> 1924
<211> 495
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1924

agcttagcta actctatagg agacatccta taatgagcta tggatatggg tccagtacca 60

ggtactaagt ctatggaaaa ctctatctct ctctcaggtg gcagatcaga tatatcctca 120

ggaaacactt caagaaactc tctaacaaca gggaggtcac acatagaaac ctttgtctct 180

acttctaggc tagacaagat catgtacact tgagcatctt cctttanaga tgtcacaact 240

tggttggcag agataaacat catatcctta ctcactctag aatcatcaaa caccacactn 300

ttatcaaaac agttcaacaa gacatggttg gaagataacc agtccatacc aagaataaca 360

tcaatctgac tcataggcaa acaaatcaca tcaattaaga atgttctacc agaaatctcc 420

acagaacaat tcacacacac ataagaaagt aacatagaac cactagtagg ggtctctacc 480

actagatctt tatta 495

<210> 1925
<211> 375
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1925

agcttctaca ttcaatttcg tgctnttcga tatattacgg gactcaatcg gacatccgag 60

taaaaagtta ttgtcgtttg aatttgctca cggcttcggt attccatttc gagcgtctcg 120

atatattacg ggactcaatc ggacatcaga gtaaacagtt attgttgttt gaatctgctc 180

agagcttcgg tattccattt cgagcatctc gatatattac gggactcaat cagacatccg 240

agtaaaaagt tattgtagtt tgaatttgct cagggcttcg gtattccatt tcgagcgtct 300

cgatgtatta cgggactcaa tcagacatcc gagtaaaaag ctattgtcgt ttgaatctgc 360

tcagagcttc tacat 375

<210> 1926
<211> 480
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1926

agcttcttct tgtnntttcg ccccattgan aacaacattt ttcttaatta cctcattcaa 60

aggtgctgcc aaggtactaa aatccttcac aaatcgtcta taaaaacttg ctaggccatg 120

aaaacttctc acctctgtca cacttttagg tgtaggccac tcttgaatag ccttgacctt 180

ttcttcatca acttaaaccc ctttggaact caatacaaaa ccaagaaaca caacatggtc 240

tttgcaaaaa atacattntt caaggttagc atacaattgt tctttcctaa gcacacacaa 300

caccgattnt aagtgtacaa catgcaaatc aagggttatg ctataaacaa ggatatcatc 360

aaagtacacc accacaaatn taccaatgaa ttctctcaaa acatggttca ttaatctcat 420

gaaagtgctt ggtccattag tcaaaccgaa aggcataacc aaccattcat ataatccata 480

<210> 1927
<211> 469
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1927

agcttaacag gttcaggtgc tggtgttgct actggtggag gcactttgaa ttggttgcca 60

gacctcanag tgatgacact cacattnttc agattctgca cagtttgtga agacaatttg 120

tcagaattnt ggggctgagc ttggttcaac tgagtagcca tctaccctat ctgatttgtc 180

agactctgaa tggaggctct tgtcttttgc tgaaattgca tattctggat ggtcatttgc 240

ctcactaact cttctatgaa aggttgagga ggagcctcag ttgcttgttg tctttgttgt 300

gactgctgct gctatatcgg aggaggaaca tatggcttgc ttggaccagt agcattctgg 360

aaaggaggga cagactgttg ttgttgtgga ggacttgtcc atttcagatt tggagattcc 420

tccaacctgg attgtatctg ttacttaaaa gggcataatt attctgatg 469

<210> 1928
<211> 391
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1928

agctnttgga aggatcaaaa agtgccttat gaattctccc gtgcttatgc caccagtacc 60

tggaaggcct ctcattntgt acatgaccat gttggacgag tcaatgcggt gtatgctggg 120

gcaacatgac gaatccggga agaaagagcg cgttgtttac tacctaagta agaagttcac 180

gacctgtgag atgaattact ccttgctcga aagaacatgt tgtgctttag tatgggcatc 240

ccatcgccta aggcagtaca tgcagagcca tactacctgg ttgatatcca aaatggaccc 300

ggttaagtac atctttgaaa agccagctct cacgggacga atcgcccggt ggcaagtcct 360

gctatccgag tttgatatag tctccgtcac c 391

<210> 1929
<211> 484
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1929

agcttgctaa cccatggaag ctcctaatat ctcttacact ttntggggtg ggccattctt 60

ggatggcctt gattttctca aggtccactt ggaccccatt tctaccaact acaaacccta 120

agaaaactat attatctaca caaaaggtac acttctctat atttgtagag agggtgtttt 180

tcctaaggac tgaaagaact tgcctgagat gtccttagtg atcatctagg ctcctactat 240

acactaaaat atcatcaaaa taaacaacta caaatctacc tatgaaatcc cttaagacat 300

gatgcataag cctcataaag gtgtttggtg cattagtgag cccaaaaggc atcactagcc 360

attcatacaa accaaacttg gtcttgaaat cggntntcca ctcatcaccc tttttcatcc 420

tgatntggtg ataaccactt ttaagatcaa tctttgaaaa gatattggca ccatgcaact 480

catc 484

<210> 1930
<211> 455
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1930

tactcaagct tgtccaanat gcaaacaata ataattgtca aacggatatc ctattgagta 60

ttgtaatata tcgagacgct tgtaatggaa aacagaagct cgtagaaaat gcaaatcgca 120

ataactttta actcggatga tcgattgagt cccgtaatat atcgagacac tcgaaattga 180

aagcagaagc tctgagcaaa ttctaacgac aataactttt gactcggata tccgattgag 240

tcatttaata attcgagacg ctcaaaattg aatacagaag ctctatgcaa attcaaatga 300

cagtaacttt cgactcggat gtccgattga gtcattttat gaattgagac gctcaaaatt 360

gaatgcacga gctcttacca gatccaaatg acaataactt tntactcgga tgtacgattg 420

agtgccgtaa tatatctaga cgctcaatat tgaaa 455

<210> 1931
<211> 479
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1931

tactcaagct cttatccatg gcttcctatg gtggtgagct tcttctttac tttcttctcc 60

ttaaagtggc gtctccaatc atcattcttc catctccatt ccgctgtcat taatcttcaa 120

gaagcaaagg actccattga tgaagaagat ccaaggccta caagctccac aaggagctac 180

atcattttgg gtttgatatc tagactttta gtccactatt actattgtgt agggtacatt 240

tgtcctttgc aacaattaat aagtataaat taacataaat atctcatcat caatataata 300

ttctcaacaa caacatgata aattacaaac aaaaaattat agaccaaccc acccatcata 360

aatatgtatg actttaccat tataacaatt ntatacttca tgtttaaggg tatcaaaacc 420

cctcataagt ctttgggtac tatctccttc atcttttatt atgtgcatat gaccttcat 479

<210> 1932
<211> 399
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1932

cggattcttt ttactctgga aacctcttct ttctatgtga acctcaaccc aatctctggg 60

ttggtaaaca acctttttgc gacccttgtt tgcttatcta gcatagctct cattcctctt 120

ttcaatttgg gccttgactc tttcatggag ctttttctca cagtccgctt tggcttgtac 180

ttcctcatgc ttaaaaactg aaatattagg cattggcaac aaatcaagag gagttagtgg 240

attgaaacca taaataacct caaaaggaga acaactagtg gtgctatgta tagccctatt 300

ataagaaaat tcaatatgag gtaagcaaac ttcctaattn ttaagattct ttttcaaaat 360

ggtccttagc aagataccca aagtcctatt catgacctc 399

<210> 1933
<211> 408
<212> DNA
<213> Glycine max

<400> 1933

aacacgacat ggagactatc tagcatagct aatagggaag acaacaacta aacattccca 60

gatggtaagc gtgcaattat aaatcccaat tccactgcag tacatgatca caattcctat 120

taactgctat tggcagtaac caagttcata aagaacagtc cacaactcaa tgcggccgga 180

tctgcccgca atatccctaa atcgacagcc atgcgaccac aatctaaaac cttggtagta 240

acataagcat ggggccaaat acatgaataa gagaggctag ttttacttta cccctgagca 300

aatatgcgac cagcctcaag agcattgtga ccaacttcac tattacccat gtcatcttct 360

gttggaaagt ctacagcggt accatgagcc ctaaccaatc tccatcgt 408

<210> 1934
<211> 470
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1934

tactcaagct tctcatgctg agtaggaccc cagtagtacc ctntcaatcc cactacattg 60

ggatgcctga tgtttgcaat ttttttagcc tctttggtaa attcttttct ctttgttgcc 120

attccttctc ttagccactt cactctcaat aacaaaccat gctccagagt tgccttgtaa 180

gatgtaccat gactgcttct ccccaaaact tcagctgggg ctccagacag ctcctcatgt 240

gtcaatgtta ttgcatcatc aagaaaataa agttctccag tcaatttatc tgctgatctt 300

gcatatagtc ttgcatgatt tcctacagaa actgaatcac tagatcctgg tgatgaaaag 360

tggctatttt ttgatgggga gaaccttgtt gcagctgcca ttttttcatc atggctgata 420

atctcagatg acgaaccttt ctgtgaggtc acaaaatcct cggctgatac 470

<210> 1935
<211> 437
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1935

tactcaagct tgtatctgtg gattcacttt cgatctcaac tataccataa ggtataacat 60

tattcaccac aaaaggacca atccactttg acctcaactt accactcatg agtccgagcc 120

tagagttata caataaattt ttttgtccaa ccacaaagtt cttcttagct atcaagctgt 180

catggaactt cttggtcttc tcctagtaga atttggaatt ctcataggct tctaaacgga 240

tctcatctag ctcacttagt tgcaacttcc tttcctctcc agcctggtcc ataaagaagt 300

tgcaagtctt tacagcccag taggctttgt actctatctc tacaggaaga tggcatgtct 360

tgccaaagac aacccgataa ggagacgttc ctatgggtgc tntgtacgca gtcctatgcg 420

cccaanaagc atcatct 437

<210> 1936
<211> 477
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1936

agctagaaat ccaatgcaat ccaagttatg atctaatcat ttatctattc catatccaat 60

tgactaaatt aattaacata agtgcataac ataaccacca catatctaat caactggatt 120

taaagttgca accgtgccaa ttcgacgata atataaaacg aagtaaactc acgaacctat 180

catcatcatt attggtgtat tgaactaatt aaatttttttt ctatcgtcaa acaaacatat 240

tattattata gtaacaggta ccagnggcac cacatatcat acatatatat ataactaatt 300

aattagtgca acatatacac aataaaaccc aactgtctag ccaaacgctc taataacaaa 360

aataaataaa ctatatattc ttataatgaa gactatcaag aaaggaataa gaaacaatgg 420

agattatatt ccacggcacc accatgcact attagtatat tactaatcat ccatgga 477

<210> 1937
<211> 390
<212> DNA
<213> Glycine max

<400> 1937

gaaagaaggt tgtcttcgaa cccggagatt gggtttgggt gcacatgaga aaagaaaggt 60

ttccggaaca gaggaaatca aagcttcaac aatggggaga tggaccattt caagtgcttg 120

aaagaatcaa tgacaatgct tacaaagttg agctgcccgg tgagtataat gttagttcca 180

ccttcaatgt ctttgattta cctctttttg atgcagatgt agaatccgat ttgaggacaa 240

atccttctca agagggagag aatgatgagg acatgaccaa gagcaagggc aaggatccac 300

ttgaaggact tggaggacct atgacaaggg ctagagcaag gaaagccaag gaagctcttc 360

aacaagtgct gtccatacta tttgaataca 390

<210> 1938
<211> 448
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1938

agcttgaaat tgaacaacgg aagctctcga gattatcgag tggtcatata atttcacaca 60

gatgtccgat tcggggaaat aatatatcga gacgcacgan attgaacaac ggaagctctc 120

gagaaatttg aatggtcata acatttcact cggatgttcg atccggggac ataatttatc 180

gagacgctcg aaattgaaca accgaagctc tcgacaaatt agaatggtcg taacttttca 240

cgcgaatgtt cgattcgggg acataactca tctagacgct cgaaattgaa caacggaagc 300

tctcgagaaa ttcgaatggt cataagtttt cacacggatg tccgattcgg ggacataata 360

tatcaagaca ctcgaaattg aacaacggaa gctctcgaga aaatcgaatg gtcataacgt 420

ttcacacaga tgtncgattc ggggacat 448

<210> 1939
<211> 409
<212> DNA

<213> Glycine max

<400> 1939

tgagcgcttg ccatagcttc taactcaagc cttctggcct catatacttg ggaagcctct 60

tctgcagtgt tgaaagtgcc taaccatata cgattgttct gaaatgggtt atagatctca 120

gaagcccatt taccccattt tctctgcctg acacctctat atttaccagg agtcttcctc 180

ctcgctgatg gggtatgagt caaaaccctc ttcttacttt ggggttgacc tttagtgcta 240

accctcattg tatttatttt gttattcaac tcacaagaac tagtttcaag agtggtgaat 300

gtgtgaagaa gacggagaag agagatctca cacatacttc ttttaactat tctcgggttc 360

tgaatcctct tggagtcatc atcggatgaa tcagtagcat caggatcgt 409

<210> 1940
<211> 478
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1940

agctngcatt acaatagatg tttttaaaga taaattaaat aaattattat tattatataa 60

tagcataccc aaagcgaatc atttcttgat taggtaaaat gttcactaac ttttgcttag 120

attcctaagt agaagcatcc tttctaattc atttttttttc tctcttcttt tttataatta 180

tttaggtggt aagtcctact ctactaggtg actatgatta ttaaagaatt tggccatcaa 240

cattagtatt atttttttaa taaacgtgtt catattttaa aggatataaa atgctcagat 300

tcaagtgcaa gaacagaatg tattacaatg ataaaaatta ataaaaacaa attatttata 360

aaatttaaga ctggataagt tctcattaat aattatgtat actctattcc tataaaatat 420

aagaatggtg gcttaattat gtattctcta cttgccatgc aacatnttta tgggtcat 478

<210> 1941
<211> 489
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1941

ctcacttgat gcatagagaa gagtaacacc accacctgca caaagcacaa cacantcaaa 60

ttgattgaac aacatagaat tagaactaag catacaactg ccagtgctaa taatctacct 120

ggtactatgc cctcctctac agctgccttg gttgcattta aggcatctgt cactctatcc 180

ttcttctcac caacttcagc ctcactggct cctccaatct gcanaagtaa ggtttcagat 240

gttaatttta tcatgacaaa accatatgat gaagcaccag ataagactta acagcaagca 300

aggtaaactc aaataaacaa accttcagta ctgcaacacc cncagaaagc ttggctaatc 360

tttcctgtaa cttttccttg tcataatctg aagtgctatt ntcaattgct gatctaatct 420

gcttgttaaa attcatcaca agacacaagt aaaacacatc aataagtatc agtacatgaa 480

acagaatac 489

<210> 1942
<211> 377
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1942

tcagtgtcat actatngatc aaaacaaagc aggtataaat atgcaatact agactcaaaa 60

tatgcaacaa acactagacc taaatcagtg tcacagaaat tggaagaaaa tattttatcc 120

aagcacaaac ttcaagcctt attccatgta ttgggggggaa gttatggctg gccatatggg 180

tagaggtgtc atagaggagc aggtatggag gaagggacct tggactgctg aagaggacan 240

gttgcttgtt gagtatgtca ggttgcatgg tgaacgtaga tggaactctg ttgctaggct 300

tgcaagtaag aaacaccaaa ctgttatcac tgtttcgcta ctaaaatata tgatcggatt 360

ttcacattta caaccga 377

<210> 1943
<211> 491
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1943

gcttacanag agaatcatct agatataaca actgtggaag ttctcttacg aggctatgct 60

tttcaagctt taagattaac ctcaagctag catgaccaag cttctcatgc catgcccaat 120

gatgctcttt gactgagagt aagcatgaca ctttttttact ggatagatca ccaagtctaa 180

tcttatagag atttccttgt ctcttagcag agaagagtga agacctatcc ttgttttgga 240

ctatacacat atccttaata aaggtgacat tatatccact atcacataat taacttatgc 300

ttagtagatt atgcttcaat cctttaacaa gcaacacatt ntcaatagga ggatagagag 360

ggatacaaat cttactgaca ctagttatca aatctttttg attccctcca aaagtgatcg 420

ccccatcaga catagggctt aggaattaga acatagactn tnttcctgtc atgtgtcgtg 480

agcagccact g 491

<210> 1944
<211> 137
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1944

gtctcacatt atctgcctca attcttggag tgcagcttat gtatctattg ngtaacttca 60

ctcagtgtca attgatttta agatgaaatc taacatggta tcagaaccca taatctatct 120

tggttctcgc ctattct 137

<210> 1945
<211> 468
<212> DNA
<213> Glycine max

<400> 1945

tactcaagct tgtagattat tgatttaaac attatttagt ttattctttc ttttatacat 60

aatatacatt tatgtaaagt ttactttcac catttagttt gtcaaattat atcaaattca 120

agttagacaa cattattttc aatatttgac tcattgtatt aagttgaata tgacaattct 180

attattattt gtatctaaag ataattatta taaaattcaa taaatttaca ttacattccc 240

taaaaaaatt ataatacata atattttata atattttata atttgatgac aataataatg 300

ataaaatgca ttaggctagt taactcaact gaaacctttt caatgaaatt tatgtcttta 360

aaatataata tcatattaaa tatgaataac tttagtctca tgtaagtatg atataatatg 420

gacttaactc ataaaattct gacttttaca ttactcaagc tttattaa 468

<210> 1946
<211> 313

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1946

agctntactg taacaatgaa gaatgcttct atgaattact tcatcccccct gaagattgca 60

atgtgaactc atccttgtca ttcacacttc aggtactttg taaagtattg gcggtgtggt 120

acctttagtt ctactaatat ccgcccttct aatagttgaa acttgaattt ctgtatgttg 180

cctttctaga tctgcagagt cgatgacatc ctttgtgaaa gccttataaa aggttctgtc 240

gatcatttcc acagggcgag gaccataagt gttgaatctt ctggaacaat atctgcctct 300

ggaatgggta tgc 313

<210> 1947
<211> 454
<212> DNA
<213> Glycine max

<400> 1947

tactcaagct ctgatggtgt tgagaagaca tcacatgttt gtcatcatca attatgggga 60

gaatgtgaat gtatgtatac atgattttga tgatgtcaaa agaagaatca aacaagactc 120

attttgcttc aagattaata caagattgtt tcaacaaaca aagccttgat tcaagatttc 180

ttcaagatca agccttgtct cacaatgaaa ggtttcaagt cattcaaggc acatgtaatc 240

gattaccaat acatgtaatc gattaccaat ggtttgaaat tgtgtaatcg attacacatc 300

atatgtaatc gattaccaga gactctgaat gttgggaatt caaattttaa atgaagggtc 360

acaactgttc aagaaaaaca actatgtaat cgattacact aattctgtaa tcaattacca 420

gagaggattt taaggaatat cgccacagtc acat 454

<210> 1948
<211> 390
<212> DNA
<213> Glycine max

<400> 1948

ttaacacctg agctgcagct tgatgcaaca tttgggaggt attgattctt cgagatgatg 60

cgctccatga gaggttggat caaatggaga atagagatca taatgaagaa gataggagga 120

gacaacggaa tgatggtgtt tctagacaaa accgaattga tggtattaaa ctcaacattc 180

ctccatttaa aggaaagaat gatccggacg cctacgtcga gtgggagatg aagatagagc 240

atgtcttctc atgcaccatc tatgaggagg accagaatgt gaagcttgcc gtcacggagc 300

attccgacta tgctcttgag tggtggaaca acctgcataa cgagagagca agagatgaag 360

agccaatggt tgatgcatgg acggagatga 390

<210> 1949
<211> 462
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1949

agcttctttg agnaaacttc cttgagaagc tactgcttag ctacacacac ccctctcata 60

actaagctca cctccttgag aagcttcctt aagaagattc ctaaagaagc tagagattag 120

ctacacatac ctctctaata gctaagctca cctccttgag atgaaaagct agagcttagc 180

tacacacccc ctataatagc taagctcacc cccatgacaa aaaaaaaaaa aacatgaaaa 240

tacaaaaaaa gtccttacta caaaaactac tcaaaatgcc ccgaaataca aggctaaaac 300

cctatactac tagaatggcc aaaatacaag gcccaaacga aggaaaaacc tattctaata 360

tttacaaata taagcgggct catacttagc ccatgggctc aaaatatacc ctaaggctca 420

tgagaaccct atggccgttc cttggatctc tagcccaatc ta 462

<210> 1950
<211> 490
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1950

agcttcttag tctcggctaa tgaagatgaa ttctttgcta cttcatgcac tcctctaatg 60

acaatagcat catttctggc actaatttgc tgggagttgg aagccatctt ctcaattaaa 120

tttctggctt cagcaggggt catgtctcca agggctccac cactggtagc atctatcata 180

cttctctcca tgttactgag tctttcataa aaatattgga gaagaagcta ctcaaaaatc 240

tggtggtgag ggcaactggc acatagtttt ttaaatctct cccagtattc atataggctc 300

tctccactga gttgcctaat gcctaaaata tccttttga tggccatggt cctgcgaagc 360

agggaaattt tttctaagaa tactctcttg aggtcatccc agctcgtgat ggaccttgng 420

gcaaggtaat atagccagtc cttctccact ccctctaaag aatgaagaaa agccttcaga 480

aatatgtgat 490

<210> 1951
<211> 364
<212> DNA
<213> Glycine max

<400> 1951

agcttgtcag ggaacaatta tgcatgtatt catagatgag agctttcttg cgtccttcca 60

aacagaatca aagaagtatg acaacattaa catgagaagt tctactgata cactattaga 120

aaatatgttt tctacatcgg ttatttatga ctttcaacat cggtttttca accgatgttg 180

aaagtaccga cgttgatagt attatcgtta acatcgggtt ttgaaaaacc gatgttaacg 240

taaaattacc aacatcggtt atataaataa ccgatgctgc taatatgaat tacacccaca 300

caatgtatat taatgctgaa agttaacatc tgtttttaca tagaaccgat gttgtgttca 360

gaat 364

<210> 1952
<211> 442
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1952

agcttattgg agatggagct tcggtggaga gataagtcct tgtttggctg atttaaagca 60

tttgaattac ttggacttga gcggcaatta tttacttgga gcaggtatgt caattccttc 120

tttccttggg acaatgactt ccttgactca cctcgacctc tctgatactg gattctatgg 180

gtagattcca tctcagatnt ggaatctctc aaatttggtg tatcttgacc tggcgtatgc 240

cgccaatgaa acaattccat ctcagattgg gaatctctcc acattggtgt atcttggcct 300

tggaggtcat tctgttgtcg aacctctgtt agctgaacat gtataatggg tatcaagtat 360

gtggaagctt gaatatcgtt atttgagtaa tgcanaccta tccaaagcat ttcattggct 420

acacactctc caatctcttc ct 442

<210> 1953
<211> 446
<212> DNA
<213> Glycine max

<400> 1953

agctttctct cacaattaat gtgtctactg actaacaatt ctaaatgcaa gttcacattc 60

ttgtgccttc tttgtctaac atacacactt gctcaaactc atgaaaagag acacaaattc 120

catcaaaatc atgcactcaa ttcaaaataa agacatacac ccatttttca caaaaagata 180

aaagtacttc actgccatat cattaaaact aagttaaact gttcaaaatg cttcataata 240

agcaaacaaa ctacccataa acaaaactaa caaaaaggaa ttaatgtact aaaaccatga 300

ccataataat aataataatc taaaaggcaa caacaaaaga aacacaaaat catcaggaat 360

atcaacattc ttgtcagtgt gagccacaat ttcctcagca gtccatccag tcagaaaagt 420

cataaccatc atctatgttg caagat 446

<210> 1954
<211> 440
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1954

agctntgaaa tctgaagttt aatattcaca tgatcaaagt tcataaaaaa tgcacacaca 60

tgacctctat ttatagccta agtgtcacac aaaattggag ggtttgaaat tgaatttgtg 120

gagccaaact ttggagccaa aatttcacta attatgatta gtgaatttta gttatggttc 180

agcccactaa tccaagatca aatataatat tctccactaa gtgtgcttaa gtgtcatgag 240

gcatgaaaag catgaaggac atgcacaaag tgtgactata tgatgtggca atgaggtgta 300

gtaagcaaat gctcacctgc ccctctaaaa tttaattgga ttgggcttct accaattcaa 360

ttaaatntat ttccaaccac acacatcaaa tatccactta gtgcatgtga nattacaaaa 420

ctacccctaa tacanaaact 440

<210> 1955
<211> 469
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 1955

agcttcacan aatgtggaga taaggatgtt atagtacaag ttcctttaac tagtacttct 60

acttcaagaa ttgttgttcc ttatactgtt gaaccacaca acaatcaaga agaacaacaa 120

attaatgatc ctgaggttaa caatgaacct atagtagaac aatcacaaga catagtatta 180

agaagatctc atagagaaaa ggagatctgc tatttcgaat gattatgtga tttatctaca 240

aaagtcggaa aatgacttaa gcattgataa tgatccatca gtttcatttt caaaagccat 300

taatggtgat gattctggac aatgattaca tgctatgaaa gatgagctta aatcaatggc 360

acanaatggt gtatgggacc ttgtggaatt gcctgaagga tgcaagagag ttgggtgtaa 420

ataggtctnt aagactaagc gtgactctca tggaaatatt gaatgacac 469

<210> 1956
<211> 302
<212> DNA
<213> Glycine max

<400> 1956

aaactaagct tgtaaagtgc tggatgggct tttccttcgc aagttgactt gaagatgtac 60

aacagttacc ctgagctctc tgatgccttg tgcaagatgt ataactcctt caccattggt 120

aactataatt aatccataat ttaccataca tcaacttttt tttatataga atttaatgac 180

tgatcataac tcttacgtat cagtatctag attgttttct gtttaatata actacccaaa 240

agatatggat cttaaatttg atcatgttga aagctcacta atggtgtatg tgaatattaa 300

at 302

<210> 1957
<211> 432
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1957

agcttgaacc tgctaatcaa aagcccttct tctgttccca aaatcaagtc tttaatttat 60

ctgatatttt ggaaacacgt caatttctga aatatatact ttatganaaa cgattcttaa 120

aattaattag attgatctca ataatgcaga ttttaatcta atgcccttg tttgagttta 180

tcttttaaat attaaaagat atgtttaaca aatgttgcaa taattgtgaa taatataaat 240

aacttaaaag acgtctccaa tgctntttcc atatttgata acgcacattt aaaatagttt 300

gtaacaaagc tgcataaaga aatacttaat ttttaataat gaataaacaa gcagatctca 360

aatctatcag cgactggtat agacatcata cataaagagc acacatacta tgaaggcttg 420

tcattgtgaa tc 432

<210> 1958
<211> 475
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1958

gaagttagat atatgtgatt atctattcgt tatatatata tatatatata tatatatata 60

tatatatttt gcagtttgtt aattaagact taaaggccca tgtcagtgtt atatatttat 120

tgttttgaat tggttagtgc atgtatatta catagatttt atactattat taattaattg 180

atgttgaaga tgttataatg ttgttatgat atgatttttg aaaattagtt gattcagtgt 240

atgtgtatat aggttgtgtc ttgtaaatat tgctatgaat gtataatatg atatatgagt 300

ataagtgaag tatgcgtgct tatgaatata tgtgaagaca atgtgtcatg gtatgtgtgt 360

gtgctgcgaa aaaatgtgag aagaatctac tcccccggga taggaatctn caagagatnt 420

tgaaattaaa ccatgtgcat attgtgtgtg aaccatgaat catgttgtgc atatg 475

<210> 1959
<211> 481
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1959

ctcgacccgg atccttaagt cactgcggct gcagcttggt cctgattana agaaatcttc 60

tttaataaag ccaatctagt tcgacaattg gtgaagttgg agtataatga tggtcatagt 120

atgattgagc acttgaataa ttctaaaggg ctcgtaaatc aattaaccaa aattgagatg 180

aagattgatg atgagttgca agcccttcta ctccttagtt ccttgctgga aagctgggac 240

acactcgtgg ttacacttag taactcagct ccagaaggaa agctcaccat ggatacagtc 300

agtgacagcc ctctcggtga agaagcaaga agaatggaac gaggtgagtc tatccatccc 360

gaggctaatg ttattgagaa tcggggtagg aatgagactc gtggatgtaa taagagccga 420

gatctgagtt ttcccaacac tattcaacac tatggatgta atgttattga gactcgttca 480

c 481

<210> 1960
<211> 397
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1960

agcttgaagg anaacttgat gcctttgtca acctagtaac tcagcttgcc atgaatcaga 60

natctacacg tgttgagaga gtttatgatc tatgttcttc tgcagatcac catacagatc 120

tttgtccttc tgtgcaacaa tctaaagcaa ttgaacagcc tgaagcttat gctgcaaaca 180

tctacaacaa acctcctcaa cctcaacagc aaaatcagcc agaacagaac aattatgacc 240

tctccagcaa caggtacaat cccgggtgga ggaatcatcc caaccttaga tggtcgaatc 300

cttcacaaca gcagcaacaa caacctctat ttcaaaatgc tgctggccta agcagaccat 360

acgttccttc accaatccag caacaacaac agcaaca 397

<210> 1961
<211> 398
<212> DNA
<213> Glycine max

<400> 1961

agcttgcata caagattctt cttgcctggc acttcaaaac cttctggttg ggtcatatag 60

atgtcttcct ctagatcccc atgcaagaat gcagctttaa catctaactg ctccaagtga 120

agattctctg cagctactat gctcagaata actctgatgg tagtcatctc tacaactgga 180

gagaagatct ctgtgaaatc aattccttgt ttctgctgaa acccttcac cacaagtctc 240

gccttgtatc ttcttctacc gccagattct tcctttagcc tatagaccca cctattctgt 300

aatgccttct ttccttctgg caatctactt aaagaccacg tcttattctt ctgaagggat 360

gacatctcat ctttcatcgc tagctcccac tcaatagt 398

<210> 1962
<211> 334
<212> DNA
<213> Glycine max

<400> 1962

cactattgat gctgcaattg agtgaagaga tctggctatt gcaagaacga gtttcgttat 60

tacagagagc tatcacgata cacaacgagc ccacgctgtt gtttgttact tatatttaat 120

atgttaaatt acttatttat tcttataatt tcgttctttg tatttttaa tttcaatagt 180

taataatgta attttcttaa atacttatag tttaaaaata tttttctaat tctgaccatc 240

tgcattctaa ttctttttcta cctcatatcg cttaaaatta atctttttaa ttcatataat 300

ttcgatttta atcatcttta atccctgtcc aaaa 334

<210> 1963
<211> 269
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1963

ctgcangcat gcaagcttgc ttctacaatc aagaatgata tgaatgttct aattctgata 60

ataacaatca ctgagtggat aatgttattg attagaggaa gctaattgaa gccaccagga 120

aagaccatta cccgcttccc ttcatggatc aaatgcttga gagacttgca gggcaatctt 180

tctattattt tttagatgga tattcgggct ataatcaaat tgcagtggat ccttaggacc 240

aagataagat agctntcaca tgccccttc 269

<210> 1964
<211> 284
<212> DNA
<213> Glycine max

<400> 1964

tgaatggttc gttcagtctg accatctgtt tgaggatgat aagctgaact aagcttcaac 60

tttgtcccca aggcttcatg tagactcgtc caaaatcgcg aagtgaacct cggatccctg 120

tcagatacaa tactagaagg aattccatgc aaccttacta cttccttgat gtacaactcc 180

atgagtttct ccattctata cttcatattc actgggataa aatgagcaga tttggcgagt 240

cgatctacta tgacccacac tgcatcatgt ccacgactag tctt 284

<210> 1965
<211> 287
<212> DNA
<213> Glycine max

<400> 1965

tcaagagaca gtgcctgagc tgcttaaaaa ctccttgctt gttatgaaga tgaggggtat 60

actggcccag aggagtgcct tgggtggtga tagtctgtgg gaacttacat ggctacacgt 120

gaataacatt tcaccatcat tgcaacttga ggtattccct gagcaggatt ctgagcattt 180

gcagcacaaa cagggtgaat caataagttt gctgcctgat gaaaagggtt tcgtgccttc 240

aagtgaaaca acaatctgcg aacatgctgg cattcgttgg taactat 287

<210> 1966
<211> 380
<212> DNA
<213> Glycine max

<400> 1966

caggcatgca agcttcattc ctttctcact catgtgtcca agtttttgat gccacatggt 60

cgaattattg atagcttcag taactgctac cttatcctca tctgcaagca tgtaaagaag 120

accttgcatt tttccacgag ccacaacgag attgcctttt gttaccttcc aagctccatc 180

accaaaagtg gtgtgatgtc cctcattatc caactgctct atagatatta aatttatctt 240

taaggcggga atatgtctga cattgtgcaa tgtccatagg gattcactgg aggtcttgat 300

gttgatatca cctcttccga caatgtcaag agactttcca tctgcaaggt aaactttccc 360

aaatcttcca gaaatatagc 380

<210> 1967
<211> 346
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1967

agcttagatg cagaacaaga gaggttacat ggatatataa gagatctcga gcaaaatagg 60

tcgcgtatga tataatttaa aatgtaagtc caacattggt tttcaataca aaaccgatgt 120

taacagaatg atgttaacgt taacatcggt tttcttcaag aaaccaatgt taactggtca 180

tacgttaaca tcgattntca gaaaatcgat gttaacgaac ataggttaac atcggttttc 240

ttcaaacccg atgttaacga agagatatta acatcggntt tggaaaaacc gatgttaaca 300

aattaatgtt aacataggtt ttacaagaac cgatgtaaac gtcact 346

<210> 1968
<211> 460
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1968

cgaaggcaca ctggatgtgt tggtcaactc ggtaacccag ctgttcttga atcagaaatc 60

tgtacctgtc gcaagggtta ggggatagtg ctgctctgct gaccacgata cagacctttg 120

cccttccatg cagcaaccta gagcaattga gcagcctgaa gcttatgcag gacatatata 180

caatagacct cctcaacctc agcagcanaa tcaaccacag cagagcaatt atgacctttc 240

cagcaacaga tacaactctg gatggaggaa ttaccctaac ctcagatggt ccagccctca 300

gcaacaacaa caacagcctg ctccttcctt ccaaaatgct tctggcccaa gcagaccata 360

cattcctcca ccaatacaac aacagcaaca acctcagaga cagccaacag ttgaggcccc 420

ttcacaacct tncctcgaag aacttgtgag gccaatgact 460

<210> 1969
<211> 429
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1969

caggcatgca agcttctagt ctcaattnta gcgtctcgat atattaccca attcaatcgg 60

acatccgagt aaaaagttat tgtcngttga atttcctacg agcttctgtt ttcaatttgg 120

agcgtctcga tatattaaag gactcaaccg gacatccatg tataaagtta ttgtcaattc 180

atatttctta gagcttcgga ttaaaatttt gagcgtctcg atatattacg ggactcaatc 240

agacatccga gcaaaatgtt attgtcgttt caatttgata cgagcttcta ttttcaattt 300

ggagaatctc tccatatatt acaacactct gtcgggcatc cgagtaaaaa gttattgtcg 360

tttgaattct ctaagagttt ccgttttcaa tttggagcgt ctcgatatat tacgggactc 420

aaccggaca 429

<210> 1970
<211> 348
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1970

cgctacattg atgcatcttg gctacggaat cttcgaattg ggcacttann atttggaggc 60

ttaagtctgc tatcaaagga gaagatggta agaggactac cctatattaa tcaccctgat 120

caactctgtt aaggatgttt acttggcaag aaatttagaa tgatttttcc aaaggagtca 180

aactcaagag ctaagaagcc acccgagcta atacatgtta acgtctgtgg gccaatcaag 240

ccccaagctc actacgtaaa aataaatatt tcctctttct cattgattat ntttcaagac 300

aaacatgcgt ctatttctta aagcacaaat cataagtctt ttccacct 348

<210> 1971
<211> 400
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1971

atcttaagtc gactgcagct gcagctatta tttcanaacg agttttgata atttatcatt 60

ataagaacaa aatatatgca tgttgaaatt tataagaatg aaatctaaca ttatatgata 120

taaacatatc tttaaggttt gatataatat tcataataac ctacttaaaa atatattttg 180

aaataataca tttaaataag acataagctt atttttaat aaacttaact ataaaattta 240

gtctaccgct ttatataaat caacatgatt aacattttaa aaaataaata catgtaagat 300

tttaatgtat tatatcaaat ttaatataat aataacacta ataatgaata tttatttatg 360

aacttttaaa taaatgatct tggtaagtct aaaaaagttt 400

<210> 1972
<211> 395

<212> DNA
<213> Glycine max

<400> 1972

agcttcatgc ttaagtatgt atggttaaac ttcattacta ttgttcaaga catactagtg 60

agcttgtaat aaatcttcta gacttggagt gatcacatgc agtcctcttg aacccttacc 120

acccactctg tcatcatgcc gagactcagg aaggccaata ggtttagcct tctcaatgta 180

ttctgaacaa aatttaatgg cttcttctgc aatgtacctc tcaataatag atgcttctgg 240

acgataaaga ttctttatat acccttttaa gatcttcatg tatcgctcaa ccgggtacat 300

ccacctcaaa taaacaggac cataacattt gatttctctg accagatgca caatcaagtg 360

aatcatgatg tcaaagaaag caaggggaaa ataca 395

<210> 1973
<211> 177
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1973

tgcaatgtat tgctcgacaa ggacatgaat gctngttggt tatcttgggc ttgcaaggct 60

gcatcaccat gaacatgtgg ctgacacaac aagagtgata gggactctgg ggtacatggc 120

acctgaactt gtccgaatcg ggcgaccatc agctgcatgt gatgtgtata gtttcgg 177

<210> 1974
<211> 158
<212> DNA
<213> Glycine max

<400> 1974

gcttcttccc gttcgtcgtc atgcaggttg tcaacatctt cattaagcct ctgtctcatg 60

ctctatcttc aggctgatat tccaagctgt gaatgatgaa catgcagtcc cagcttgcgg 120

cggctctcag tcgaagccta cgtacgctgg ataatcaa 158

<210> 1975
<211> 389
<212> DNA
<213> Glycine max

<400> 1975

agctttgatg caacatttgg agagtgttaa tgaatcaacg agatgatgcg ctccatgata 60

ggttggatca aatggagaat agagatcata atgaagaaga aaggaggaga agagggaatg 120

atggtgttcc tagacaaaac cgaattgatg gtattaaact caacattcct ccatttaaag 180

gaaagaatga tccggaggcc tacttggaga gggagatgaa aatagagcat gttttctcat 240

gcaacaacta tgaggaggac caaaaggtga agcttgccgc cacggagttt tccgactatg 300

ctcttgtgtg gtggaacaag ctacaaaagg agagagcaag aaatgaagag ccaatggttg 360

atacatggac ggagatgaaa aagatcatg 389

<210> 1976
<211> 415
<212> DNA
<213> Glycine max

<400> 1976

ccaatatgaa taacatcttc caacaatcaa aataaatatt tattctataa tgataaaatc 60

attttcaatt ctttttaaaa aaaattaccc tgtatgaaat tgaaaaagtc aaatctttta 120

ctttacgtgt tatttcaaaa atctaatatt tctatttttc ttttgcagaa atgaaatgac 180

agctatacat aaataggaat gacaatgatc aagatttaca tagggtccta tagtattcct 240

tatataactt ttaaaatatt tattataaaa attaataaat ttatggtttg atttataaat 300

aaatgacata ttggaaagtg aaaaagatct ttacactatc aatagatata ttactttcta 360

tatttctcag aaaaggctat atatatatct atattatcac ttaatagtct ctata 415

<210> 1977
<211> 298
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1977

aattaataat actaaaatta gatagacttg tttgaacttt aaattggtct gatatctagt 60

ttggatatag tttatcaaat tgcatttctt actacaccgc gataacatat attgtagtaa 120

ttacaatgtt tgcattatta cattaattat actcgtcatt tgtgtaatat ttttttataa 180

tgtcaaattt taccaatcta aattntatta agcagataat atttatataa aaaacagaga 240

caatatgtag ataattagat taatttctta agcatgttat taagagggtc ttattctg 298

<210> 1978
<211> 331
<212> DNA
<213> Glycine max

<400> 1978

tggacattac ttcttctatg gacgctatat ctacgcgcat aatatatcgt tacgctcaaa 60

atcgaacaac ggaagctctt gagaaattca aatggtcata acccttttcac tcggaggtcc 120

gattcatgcg cataatatat cgagacactc gaaactgaac aacggaagct ctcgagaaat 180

tcaaatggtc attacttttc actcggaggt tcgactcaag cgcataatac atcgatacgc 240

tctacattga acaattgatg ctctttagcc aatcaaatgg gcataacttt tccctcggag 300

gtctaattca ggcgcattat atatctacac g 331

<210> 1979
<211> 401
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1979

cttaacanaa ggcattcaaa gtgggtggaa tttctagagc atttcccttа tgttatcaaa 60

cataaaaggg aaaaggtaat attgtagccg atgctcttcc tcggcgtcat gcattgcttt 120

ctatgcttga aacaaaattg attggtcttg aatgtttgaa aagcatgtat gaaaatgatg 180

aaacttttgg agaaaatttt aaaaattgtg aaatttttttc agaaaatggt ttctttagac 240

atgaaggctt tctttttaaa gaaaacaaat tgtgtgtgcc taaatgttct actagaaatt 300

ngcttgtttg tgaagcacat gaaggagggt taatggggca ttttgggtcc aaaagactct 360

agaaacatta caagaacnat tttattggcc tcatatgaaa a 401

<210> 1980
<211> 389
<212> DNA
<213> Glycine max

<400> 1980

tacacattca acttcgagcg tctcgatata ttacgagtct ctatcaaaca tccgagaaaa 60

aagttattgt cgtttgaatt tgctcagagg ttcaacatta aatcttgagc gtctcgatat 120

atgacgggac tcaatcagac atccgagtag aaagttattg tcgtttgaat tagctcagag 180

cttcaacatt caatttcgag cgtctcgata tgtgacggga ctgaatcaga catccgagta 240

taaagttatt gtcgtttgaa tttgctcaga acttcaacat tcaatttcga gcgtctcgat 300

atatgaccgg actccatctt acatccgagt aaaaagttat ctgccgtttg aattggctca 360

gagcttcaac attcaatttc gagcgtctc 389

<210> 1981
<211> 357
<212> DNA
<213> Glycine max

<400> 1981

aggcatgcaa gcttagagcc aattcaaacg acattaactc ttttctcgga tgtctgattg 60

agacttttta tataacgaga tgctcgaagt taaatgttta agctctgagc caattcaaac 120

gacaataact ttttactcgg atgtttgatt gaggcctgtc atatatcgag acactcgaaa 180

ttgaatgttg aagctctgag ccaattcaaa cgacaataac tttttactcg gatgtctgat 240

tgagtcccgc catatatcga gacgctcaaa attgaatgtt gaagctctga accaattcat 300

acgacaataa ctttttactc ggatgtctga ttgagtcctg taatatatcg agacgct 357

<210> 1982
<211> 227
<212> DNA
<213> Glycine max

<400> 1982

ggacaagtac ctaagaatat ctgttccatg agattctgaa gtttttttcaa gggtcttctc 60

actctaactt aggcgtctaa cttcaccgcc tgttttcaat ttatccttca ggcaaccctc 120

gagtttcgta ttatggatag tgattatgtg cttgtaatca ggtgaacaca cctgatatgg 180

tttgcgggca catctacatg cactttcatt tccctcatga tgatcac 227

<210> 1983
<211> 432
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 1983

cttgcagctt gtccttatgg ttattaatgt atgaattgtt gcttttgcac ctcttccttg 60

ttttgttata tatctgtttg cattcgggat tccaattttc atcaacagtg gttaccctac 120

tcctcacgtg aagtggaact tgtgggttat ccacaagctg ctgcttaccc tagtttatgg 180

tntcatactg ttcatgtatc attctaggtg gagagaaagg ttacctggtt agtgtcctgg 240

attgttatat tattttatct ttaattagtt ttatgatagc atagtttatc ttcctctttt 300

ngcagcaagg cctgcttact ataagtatgt taccattatg ttcatcttga atgcaattgc 360

gctgtttgct cgcggcatta ctggaaacgg tgctgctttc ggattctggt tagattcttc 420

tattctatat ct 432

<210> 1984
<211> 382
<212> DNA
<213> Glycine max

<400> 1984

acactgtgtt catgctctcc caacagcaca tgtatactca cgatcccaat cagacactat 60

gctagatggc acaccatgta atccgacaat atcactacta tacacggagg ccaacttctc 120

cacggaaaat atgacactaa tgggaataaa gtgagcagac ttggccagcc tgtcaacaat 180

aacctatata aatcaaacct tttgggttta ggtaggccta caacaaaatc catacaaata 240

ttcgccctct tccactgggg tatctacaag ggttgaactt ccctaaagtc tctggcgttt 300

catcttaccc ttctgacaga ctaaacatgc atacataaac tcactaacct ctctcttcat 360

gttaagacct tacaacagga tc 382

<210> 1985
<211> 250
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1985

gcatctatca tacttctctc catattactg agtccttcat aaaaatgttg gagaagaagc 60

tgttctgaaa tctgatggtg agggcaactg gcacatagtt tcttaaatcg ctcccagtac 120

tcatacaggc tctctccact gagttgtcta atacctgaga tatctttcct gatggctgtg 180

gtcctggaac anggaaaaaa ttttctagaa tactctctta aggtcttcca gctcgtgatg 240

gccttggagc 250

<210> 1986
<211> 506
<212> DNA
<213> Glycine max

<400> 1986

tagaatgcag aagaagcaac aacaatcaat ttaataatgt tctataaaca tgcaaggcaa 60

aattgattgc aataacataa atgagataag ggaagagaga atgcaaacac aattttatac 120

tggttcggcc acttcccgtg cctacatcca gtactcaagc aacccacttg agatttccac 180

tatctttgta aaatccatta caaagtctga accacaaagg gacaacccat cccttgtgtt 240

cagatgcttt acaacaagag actcacaatc tcttaaccaa tctcattgaa taagaagaat 300

ggaagaagaa ttatctcttc aagagaagaa tattacaatg aagatccatg gatgaactct 360

taatggatgt gcaagtgctt gcccaagagt tctttgagag agcatttgac aatgaagttc 420

tcttggaatc tctctcattc tcttttgaga ggataagaca ctttggagca gcaaaactct 480

ctctctaaat tcgtgcccag tcacct 506

<210> 1987
<211> 472
<212> DNA
<213> Glycine max

<400> 1987

tgtagggtta aagtctcatg actgtcacgt gctcatgcaa caattgttag ccgtggctat 60

acgagacatc ttgccaaaca aagtcaactt atccataact cgcctgtgct ttttcttcca 120

tgctatatgt agcaaagtca ttgatcctgt caagtttgat gagctggaaa atgaggccgc 180

aattatactg tgccagttgg agatgtattt tccccctgct ttctttgaca tcatgattca 240

cttgattgtg catctggtca gagaaatcaa atgttgtggt cctgtttatc tgtggtggat 300

gtacccgatt gagcgataca tgaagatctt acaaggtata caaataatct atatcattca 360

gaagcatcta ttattgagag gtacattgca gaagaagcca ttgaaatttt ttcacaatac 420

attgagaacg ctaaacctgt tggcctctct gagtctcagc atgatgatag ag 472

<210> 1988
<211> 334
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1988

gaatctttct tagatattgg agaaaaaagt ctctntgtaa tctattcctt ccttttgagt 60

aaatcccttа gcaacaagtc ttgccttgta tctctcaatg ttgcctaatg aatcccgttt 120

ggtcttaaat acccatttac atccaatgtc ctttgcccca ttangcatct ctacaaggtt 180

ccaaaatttg ttactgtaca tggaattcat ctcatccttc atggcatcat accataaatn 240

tgactcttta caactcatgg ctngatcaaa agtntaggat cattttcagt tacaatatat 300

agtcagattc ttacaaatat acaatataat cact 334

<210> 1989
<211> 211
<212> DNA
<213> Glycine max

<400> 1989

aaaatctgaa gatgaaggag gaagagtgta ttcatgactt ccacatgaac attcttgaga 60

ttgccaatgc ttgcactgcc ttgggagaga ggataacaga tgataagctg gtgagaaaga 120

tcctcagatc cttgcctaag agatttgaca tgaaagtcac tgcaatagag gaggcccaag 180

acatttgcaa catgagagtg gatgaactca t 211

<210> 1990
<211> 498
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1990

gtgcatataa cttgaagagg attgatagta ntatactata gttgtactgg gcttaaaagc 60

ccattagtat aagtggtata caaatatatt cttgtactcc tattttcatt agacaaataa 120

aattcaatgt ctatagaacc aataacagcc acaattgtaa ctagtaagaa gagggttcac 180

aaaataacaa aactacagtc tatttaatat cgtaccttcc aatagggtga gtggtaccct 240

tttccattgc tgatacaaca gcaagagctt ctttttcaca ggtgggaatg caacacgaag 300

gaacatttga ttctgtgttt ctaacatgat gaccataaat gggctcaatt gccttgaata 360

cgagtccacc agtggtcaat gtccctgttt tgtcaaatgc aatagtatga caagaagcat 420

gagcatccag aacatgccca cctttgagtt atatgccctg caaattgggc aactgtcaca 480

gccacaatga aagaagca 498

<210> 1991
<211> 328
<212> DNA
<213> Glycine max

<400> 1991

gcttaacatc agaccacttc cagggtgctg gaactacttc acatggtctt gatggggcct 60

atgcaagttg aaagccttgg aggaaagagg tatgcctatg ttgttgtgga tgatttctcc 120

agatttacct gggtcaactt tatcagagag aaatcagaca tctttgaagt attcaaggag 180

ttgagtctaa gacttcaaag agaaaaagac tgtgtcatca agagaatcag gagtgaccat 240

ggcagagagt ttgaaaacag caagtttact gaattctgca catctgaagg catcactcat 300

gagttctctg cagccattac accacagc 328

<210> 1992
<211> 197
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1992

ccattcttgc tttccaggaa ttcatagttg gntccatcta ggattggtgg tctgttcact 60

ggtcctcctt ctttctccat gttcatcaga atttatctcc ctagatctca ctctgtgatt 120

tcgagtgttg gctctgatac caattgaaat tctgatacca ggggacagat gtcgtaccgg 180

atgtcacgac atcacgc 197

<210> 1993
<211> 386

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1993

tcatccaact aatacatgga aagacaactg tatataccag gcatctaaga tttctcanac 60

attatcatcc atatcagnga ttgaaaagag cctttgatgt aagtcaagaa aatgaaagcg 120

cgccccgtcc attagtagga atagatgtct atgatcgggt aaaagatatc ataactatga 180

ttgggaagac acaaaaaaaa ccgtcatctg atgcaaacat atggaagaaa aggtcaatat 240

tctttgatct tccatactgg tccaatcttg atgttagaca ctgtatagac atcatgcatg 300

tagagaaaaa tgtttgtgat cctttaattg gcaccatccg taacatgaaa ggcaagacaa 360

aggatggctc gaagcgtcgt caagac 386

<210> 1994
<211> 297
<212> DNA
<213> Glycine max

<400> 1994

aaagtcacac gactgtcacg tgctcatgca acaattgtta gtcgtggcta tacgagacat 60

cttgccaaac aaagtcaggt tagcgataac tcgcctgtgc tttttcttcc atgctatgtg 120

tagcaaagcc attgatcctg tcaagtttaa tgagttggaa aatgaggccg caattatact 180

gtgccagttg gagatgtatt ttccccctgc ctttttgac atcatgattc acttgattgt 240

gcatctggtc agagaaatca aatgttgtgg tcctgcttat atacggcgga tgtaccc 297

<210> 1995
<211> 420
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1995

tcaaccaagg ggagatggac catttcaagt gctagaatga atctatgaca atgcttacaa 60

agttgagctg cccgatgagt ataatgttag ttccaccttc aatgtctctg atttatctct 120

ttctgatgca gatggagaat ccgatttgag gacaaatcct tctcaagagg gagagaatga 180

tgaggacatg accaagagca agggcaagga tccacttgaa ggacttggag gacctatgac 240

aagggctaga gcacggaaag ccaaggaagc tctttcacaa gtgttgtcca tactatttga 300

atacaagccc aagttttaag gagaaaagtt caaggttgtg agttgtatca tggtccaaat 360

ggaggaggac taaatgacac cactntattt caactttaga gcggttagtt tgctaaataa 420

<210> 1996
<211> 474
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 1996

tgttggtttt tagctagaca actctttatt actattnntt attttctata ttnttcttcc 60

atcttattct tttcttgctc gctctctttn tgctcctttc tttccatgag atattttgct 120

acctaaacat acgtatattt ttgtgaggta ttttgctata tacatgcgtg tccaaggtat 180

cttgctacct aaacatacat atatatgttt tgtgagatat tnttgctata tacatgcata 240

tccaaggtat cttgctacct aaacatacat atatatattt tgtgaagtat tnttcctaca 300

tacatgcata tccaaggtat ctttctacct aaacatacat atatattttg tgaggtatga 360

ctaccttccg agcttgtgct tgttntattt aaattcctag gatcatgagc aactaggtgt 420

gtcctgctat gacttgagaa acaaaggtga tcaaataaca agcagagatt taaa 474

<210> 1997
<211> 276
<212> DNA
<213> Glycine max

<400> 1997

ataaataaga taagggaaga gagaatgcaa acaccaattt atactggttc agccacttcc 60

cgtgcctaca tccagtactc aagcaaccca cttgagattt ccactatctt tgtaaaatcc 120

tttacaaagt ctgaaccaca cagggacaac ccgtctcttg tgttcagatg ctttacaaca 180

agagacttac agtctcttaa ccaatctcat tgaataagaa gaatggaaga agaattctct 240

tcttcagaga agaatattac aatgaagatc atgtaa 276

<210> 1998
<211> 236
<212> DNA

<213> Glycine max

<400> 1998

gtggtttgtg tgacatggga atgcttgatg aggctagtaa gtatgtggag gaaatgttgt 60

ccatagattt ttctcctcat tctgctgttg ttcacgcctt ggtgaagggg ttttgcaatg 120

ttggtagggt agaggatgct tgtggagtcc tcaccaaggc actagagcat ggggaagctc 180

ctcaatcgga tacttggatg gccataatgc ctgtaatatg tgaagaggat gatgat 236

<210> 1999
<211> 258
<212> DNA
<213> Glycine max

<400> 1999

ctgtgatcgt atccccatat tagctagatc ttgacgggta ttcaagtcat ccttcctctt 60

gccttgaatg ttaaggagca tcccaatcac actgtcacaa acatttgtct ccacatgcgt 120

aacattcatt caatgtctaa cgtctagatt agaccagtct ggaagatcaa agaaaatgga 180

cctctgcttc atatgcaact cttactttta tccttctttg ggtctttcca atacagaatc 240

aagtgttgaa ccgctgat 258

<210> 2000
<211> 406
<212> DNA
<213> Glycine max

<400> 2000

tgttgcctta gcacgcaagt tatttgaata aattccagac gatgtctatt tggaccctct 60

aaagacattg cctattgagg aacaacaaag gcataatgct gagaaggcta ccatgatgga 120

gatagatggt gaaccagtga cgatggtggt agcgatgttg gtggtggcac caactgttat 180

tggtgtggtg gtggtagtga caatgatagt ggcagtgaca ttgatggctg tggtggtggt 240

agtaatgtcc actgtgatgg tgatgtctat ggtggtagta atgatggcgg cagcggtagt 300

gatattagtg gtcatggtga tagcaaccaa ttatggcggt gacaattgat aacgatggcg 360

gccgtggcga tcgaagtggt attggtggtg gtggcgatga cagtgg 406

<210> 2001

<211> 367
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2001

cttaacccct ntctaaatga taggctcata atgcagaaga agattaataa gcaatcaatc 60

taataatgtt ctttaaacat gcaagacaca attgattgca ataacataaa tgagataagg 120

gaagagacaa atgcaaactc gatttatact ggttcggcca ctttccgtgc ctacgtcaag 180

ttctcaagca acctacttga gatctttcac tatctttgta aaaatccttt ctacaacttc 240

tgaacgccca agcaatccct ttaccttgtg ttcaggaaac tcatatttca cgggaccact 300

agtctctcga ttacaattga ctntctgaga agaatagaaa gatntctctc ctttagagtg 360

gataata 367

<210> 2002
<211> 492
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2002

ggcattcgac agtggagctc atccaatgga gtaattgatg ctatagaaat tcacgattta 60

aaggagctga atgctttgga ggctggtagt tctgacagaa atctgaatca atcagaagtg 120

gagctcaaga agtctctgca ggagcaattg tggcatgctg ctaatgccta tgaatctttg 180

ctgaggcaaa aggctagagt gaaatggtta aaggaagggg acagaaattc agcttacttc 240

cacaagctga taaatcatag aagaagacat aatgccattc aaggattgat cattgatggg 300

gaatgggttc acgaccctag tatggtcaaa actgaggctt tcaatcattt catagataga 360

ctttctgagc agaattntaa tagaccaacc ctggatggtg tgcagctacc ttccattggt 420

canagcgaga atgaagccct tgtgggcaga ttntctgatg cagaaataac ctcagctgtg 480

tgggactgtc at 492

<210> 2003
<211> 236
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2003

aaactaaccc aaggcaacaa gggggttgag gattatttca aggaaatgga tgtgctcatg 60

attcaagcaa agattgaaga agatgaggag gtaactatgg ctcgatttct taatggtttg 120

actaatgata tccgtgatat tgttgatctg caggagtttg ttgaaatgga ttatntgctt 180

cacaaagcaa tccaagttga gcaacattaa taaggaagga gtggcttaag agttta 236

<210> 2004
<211> 480
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2004

tcataaggtt atatatggcc tcaaataagc tcctaaggct nggtttgata aactaaatga 60

gactctacta atgtttgaat tcaaatccaa caagtttgat ccttcactat ttgtttattt 120

taaggcttca tccataatct acattccggt atatgttgat gacatcataa aaacatgaaa 180

tgatattcct ttattacatc aactcatttc taagctaaat atagtatttt ctctcaaaga 240

tcttggatcc tcagattatt tcttgggaat gaaagtaaag catctatctg atggttccat 300

tgctttaact tanaccaaat atattagaga cttaatgggc aaaaccaaca tgttagatgt 360

caaacctata tcttccncaa tggtaactgg ctataagctc acctacaagt ggtttaatcc 420

tttcttttta tccctatatg tatangtcat ttgtaggaag cacttaatat gctactataa 480

<210> 2005
<211> 181
<212> DNA
<213> Glycine max

<400> 2005

acccgtccta gcttttccta acttttctaa aacgtttgag ctataatgtg atgcctctgg 60

agtgcgagtt ggagctgctt tgttgaaggt gggcacccta ttgcttattt tagtgaaata 120

cttcatggag cgacccttaa ctacccgacc tatgataatg agctctatgc cttaatgaga 180

g 181

<210> 2006

<211> 443
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2006

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cttcatgggc ttcctgtagg aattatagta taacatcatc tgaaatgtag ctacatatag 120

gttcaaacaa tgtaactaaa taaattagta gtgagtacat tataattgta ggaaaatggt 180

tagtatatag atattatatg taccctaaca ggtttttttaa aacctccttg caaactacac 240

tcgtggtaga ggtcaagctt tttttgtctt tatcatgtat taaaaccttt aatccattct 300

ttgatttgac tctcgatagt gcaacatata attgaccatg actaaacaat ggggtttatg 360

caagtaaagt tcaacactat atcatgactg gcctggagac ttattaattg tcattgcata 420

agagagcatt attggaaata gtc 443

<210> 2007
<211> 459
<212> DNA
<213> Glycine max

<400> 2007

tcccgttgcc cgagtcgacc cggcccgagt tgggctggtt gagtgttaac tccagcgttt 60

caagtctcgg gtcgctctgg taagcgaaaa acgggtacgg gttgatcgtg aacggcgatt 120

tgttgtcctt gagtatcgcc agcagctgtt tgagcgtgtc ttgcatcgcc tggttgaaca 180

acccggacga gggcgggtcc gactgagtca acacgggcat ctgagtgcac tgtggagacc 240

ttgatcttgc cgtcgagcga agccgcgccg agggcatttt ggacatttag catcttcggg 300

actagctgcg acttaatacc ctgatcggat aatgtcaaaa tctcttttcc gacggtgatc 360

atagtgatgt tgctcgccag gtagtaaggc aagacgttct cgataaccca ctgtgtggcc 420

gctgtgggat cgcctgcgag actcgctatg tctccgttg 459

<210> 2008
<211> 145
<212> DNA
<213> Glycine max

<400> 2008

tatatcaata cgctcgaaat taacagcgga agctctctcg atattcatat agtcataact 60

attcacacgg atgtccgggt ctggcgctta atatgtcgag aggctcgaaa ttgaacaacg 120

gaagctcttg agaaatgcaa ctggt 145

<210> 2009
<211> 492
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2009

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taatggagag ggttaccact actggaaaac ccgaatgcaa atttttattg aggcaataga 120

tctaaatatc tgggaagcca tagaaatagg gccttatata cccaccacag tagaaagagt 180

ttcaatagat ggtagttcat caagtgaaag cataactata taaaaaccta gagatagatg 240

gtctgaagag gatagaagac gagtacaata caacttataa gccaaaaaca taataacatc 300

tgccctgtga atggatgaat atttcagggt ttcaaattgt aagagtgcta agaaaatgtg 360

ggacactctt cgattaacac atgaaggaac tgcagatgtt aaaagatcta cgataaatgc 420

actaactcat gagtatgaat tatttagaat gaatgcaaat ganaatattc aaagcatgca 480

caagagattt ac 492

<210> 2010
<211> 414
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2010

caattactgt gtaaatttca tagttgccaa tcattgtctt ctctatatct cttatgaaca 60

acacgagtgc accactttta ctctgatatt agacaaccta taacagagac gggtgtttaa 120

tatttctcta tgaatagaga caactattgg acaagtatgg aactggggca acctcaaaga 180

tttcattaat tgcaactttg tcaagatcat cctctccaga gccgtctact cgtagtaaat 240

gatntgctgc attatgaatc atcaatgaat tatacgtgcc acaattatag catacaatgt 300

attaatatgc agcttaagaa acaaaagttc aatctaatac agcgaattac cagaacagaa 360

gaacccacgg tcatcttcac aaatgccacc aagatcattg ccatctggaa ttga 414

<210> 2011
<211> 311
<212> DNA
<213> Glycine max

<400> 2011

agcttgaagg acaaaaggaa ctcatttcac tcatttgctc attacaaaga tagtatggtt 60

aaactttaga gagatctaga gtcgtgctta gacggtagtg acagggagaa gcactttctc 120

accttaagga agatatcaac agctctatag agcccatcac tcacaatacg tgcatgatct 180

ggaagtagtt cagcaaggga tatgaactct gatggcaaca agtttgggtc tagtgccact 240

tcagcaagat agttgcccat taatgtggat acctttagaa tagacctttg tttgggagat 300

ccggggctgt c 311

<210> 2012
<211> 490
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2012

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taaatatctc ttggcaatct ttctaggatc tataacaagt tcacctcgtc caaatacccg 120

agatgaaggc gcaatgtagg cggtgcggaa ttgaaaactt atgcggagga gataaatgaa 180

atcacatatt gttctcattg tgacagcaaa acttgctagg ctgttatcta tggcgaggca 240

aaatgatttg tggttgaaat aaggaaggta aaagaagaag ggatcgcatg ctatagaaac 300

aatgcacaga atctcaaaaa acttgttcca ataaagaagg ttcttatctt gaggatcaaa 360

tactttnttc tcagacactt taagatcttc tgggaacact gcccaagtag tcactccagt 420

ctttagtgat cttccanatg tctttagtcc atctgaactc ttcttcattc ctagcctaaa 480

tgatttcgat 490

<210> 2013
<211> 447
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 2013

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gtaaattaaa agagaagccc catatacttc taaagcggga gaagaaattt tttataattt 120

ataataaaaa gcaaaatcag actgatgcaa agccaggtga ataagaaaaa acatatgaaa 180

taagtacagc ttgatttgat gttaaagaat atagtcataa gcccaagaag tgaagatgat 240

ctttccaaca atagccaata aattcggcaa gagaagcaaa acatacccca gagaccttca 300

cgaattgccc atttttttgca gttctaagct cagagtctgg ataatgagta acaaagccca 360

taatagatct tcttccccaa taagtattcc aagtgaaaga tgcagcaact aagccaaaaa 420

gaatcacaac tacaataagg agaatag 447

<210> 2014
<211> 422
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2014

cggaagctga cgcganacta anatggtcat tacatttcac acggaagtcc gattcaggcg 60

cataatatat cgagacgctc gatattgaac aacgtatggt gtcgataaat tcatatggtc 120

ataacttgtc atacggatgt ccgattcagg cacataatat atccagatgc tctaaactga 180

acatcgacag ctctcgagaa attacaatgg tcataactat tcacacggaa gtccgattca 240

tgcgcataat atatcgagac gctcgaaatt gaacaacgga agctctcgag aaactcatat 300

ggtcataact tatcacacgg acgtccgatt caggcgctta atatatcgag åcgctcgaaa 360

ttgaacaacg tatggtgtcg agaaattcaa atggtcataa cttgtcacac ggatgtccga 420

tt 422

<210> 2015
<211> 175
<212> DNA
<213> Glycine max

<400> 2015

gcttgaaatt gaacaatgga agctgtcgag aaattcaaat ggtcatatct tgtcacacag 60

aagttcgatt tcagcgcaca ctatatcgag acgctcgaaa ttgaacaacg gaagctttcg 120

agaaattcaa atggtcataa cctattaaac ggaagaccga atgccgcgca taata 175

<210> 2016
<211> 456
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2016

agctgttaac tgaatntaca acgttccaat tgatttcaaa atggtgtaat ctgattacaa 60

catattggta atcaattact agtgcatctg aacgatgcac ttcaagacat tgtgaagagt 120

cacatccttt cataaaaagc gttgagtaat tgactacaag gatttggtaa tcgattacta 180

ctgacaagtt ttgaacacaa gatcaaaaca tgacacctct tcaagtggtt tcttgaccag 240

acttgaagag tctatagaag caataccttg attggcattt gaagagcact tacaacactt 300

acaaccttta caaacaacta ctcgacatga tctataacaa ccttcgaatc tcttcgaaca 360

tcttacactt cttcttatta ttcttttgca aaagctatct aaagtattct ggttttccaa 420

accttgaaaa cagaagtgtg ctatatctct tattct 456

<210> 2017
<211> 446
<212> DNA
<213> Glycine max

<400> 2017

agcttaactg gttgaagctt tcagaaacat gtatctcatg aggtgacata aattaaatta 60

tttatatcaa tattattgaa gatacacgtt tatgagcata aacaatcaat ctaaaaatta 120

taataatttt attgaaaaat aaacttatct tatttaaatg acttttgca caattttaat 180

aagttatcaa gaatatcaca gtaaaccttа aaatgttcat tatattatat aaataaatta 240

gattttgttt ttatctctat tttgatatta aaaaaatatc acaagttaag tctttaatct 300

taaaaaaaaa cttttgatga gtaagaccta aattcggtct atttctcctc ctattcacat 360

ctatagaaga tagtggttca aaataatcag aaagatgcta ttcagcttat ttttacctct 420

ttagagtatg tctctatcgt gttagt 446

<210> 2018
<211> 481
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2018

gtgaagctcc tgtttagcta tacccgattn tactcaacca ttcgtagttg aatgtgatgc 60

tagtggagtt ggcattgtgg ctgntttgat acaaaacaaa acgcctatag cttatttctc 120

ggagaaattg ggaggagcca gattgaacta ttgcacctat gacaaagagt tctatgccat 180

tgtaagagct cttgatcatt ggaatcatta tntgcgttct aatcacttta tattgcattc 240

agatcatgag tcattgaagt atatcaatgg gcagcagaag ttgagtccaa ggcatgctaa 300

atgggttgaa tntcttcaat cttttaattt ctcttcaaaa tacaaggatg gtaagagtaa 360

tgtggtggct gatgcacttt caaggaggta tgctttaata tcaattcttg aaactcgttt 420

acttggttat gagactttga tagattatta taaagaagat gttgattctc gtgaaatata 480

c 481

<210> 2019
<211> 453
<212> DNA
<213> Glycine max

<400> 2019

agcttcttag tttcagatga tgcagctgag tctgtagcta cctcatgcac tcctctaatg 60

actatagcat catttctggt gctaaactgt tgggagttgg aagccatctt ctcaattaaa 120

tttctggctt cagcaggagt catgtctcca agggctccac cactggcagc atttatcata 180

cttctctcca tattactgag tccttcataa aaatattgga gaagcagctg ctctgaaatc 240

tgatggtgag ggcaactggc acatagtttt ttaaatctct cccggtattc atacaggctc 300

tctccactga gttgtctaat acctgagata tccttcctga tggctgtggt cctagaagca 360

gggaaatatt tttctaagaa tactctcttc aggtcatcct agctcgtgat ggaccttgga 420

gcaaggtaat acagccagtc ctttgccact ccc 453

<210> 2020

<211> 392
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2020

ntctctntga agttntgtat gatattcctt tcatacaaaa tttcatactt tgcaacggan 60

aaacataatt aatgccaaaa gtatactatc gaaacatgta attgaaaata catgtaatag 120

aaattaaaat ccctaaattt cataattagg atttatacat aattgagaga aattaaatca 180

tccctagatt taataattag ggttcataca taattggaag aaattaaatc attcttggag 240

aatcataaat ttcataacac atgttttgat atcacatgta aaacattaag ggggttctta 300

gactatcaat tataggaaac aacatgatct taaaacatat gattctcaca tacaatcaat 360

aaacaataga taatggtgca tacctttctt ca 392

<210> 2021
<211> 455
<212> DNA
<213> Glycine max

<400> 2021

tgtagttaag accgcagaca acttctgttc atgtttgaag cttgatagaa acacagatgt 60

tagctatagt aatatgagga aggctgcttc tcgagaagat ttgactgaca actatttata 120

ctgtcctaaa gctgtagatc ttcagtacaa ggatttaagg cattttcagt ggcattggga 180

aaaggggggag cctgtcattg tcagcaatgt gcttgaatgt acatctggtt taagctggga 240

accacttgtc atgtggcgtg cattacgtca tgtaactaat accaagcgtg gccaacattt 300

ggctgagaaa acaattgatt gcttagattg gactgagggt tgcttaattt cccaatcttt 360

aactttattg accttggaga gctctttaca caaattttat tcttcacctt cattctcatg 420

aagattatgt ctaattgttt aatgttggta cttat 455

<210> 2022
<211> 462
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2022

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actcttaaag tcatggctcc acttgtgaaa gtgcttcatc ttgtggatgg tgaaaggaaa 120

ctagccatgg gctatattta tgaagcaatg gacaaggcaa aagaaacaat tatcaagtct 180

ttcaacaaca atgaaagcaa gtacaaagat gtgtttgcaa tcattgataa aagatggaat 240

tgtcagcttc atagaccatt gcatgcagct gcccacttct taaatctaga gtgcttttat 300

gacaacactg acttggagtt tgattttgag gtcaccaatg gtttgtttga gtgcattaag 360

aagttttgat ttagaggtca ccaacttggg acaaaataga atgctgacct atctaggagg 420

gcttaatgga atgttaatca caaaatccaa tctagctttt at 462

<210> 2023
<211> 431
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2023

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tgagtaaaaa gttattgtcg nttgaattgg ctcagaggtt caacattcaa ttttgagcat 120

ctcgatatat tacgggactc aatcagacat ccgagtaaaa agttattgtc gtttgaaatg 180

gctcagagct ttaacattca atttcgagcg tctcgatata ttacgggact caatcagaca 240

tccgagtaaa aagatattgt cgttngaatt ggctcagagg ttcaacatat aatttggagc 300

gtctcgatat attacgggac tcaatcagac atccgagtaa aaagttattg tcgtgtgaat 360

tggctcatag gttgaacact tcaattcgag cgtctcgata tattacggga ctcaatcaga 420

catccgagta a 431

<210> 2024
<211> 371
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2024

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ttgagtcccg taatataacg aaacgctcga aattgaatgt tgaagctctg agccaattct 120

aacgacaata acttttttact cggatgtccg attgagtctc gtaatatatc gacacgctcg 180

aaattgaatg ttgaagctct gagcctattc aaacaacaat aacttttttac tctgatgtcc 240

gattgagtga cgtaatatat cgggacgctc gaaattgaat gttgaacctc tgagccaact 300

caaacgacaa taacttttta ctcggatgtt tgagtgagtc ccgtattata tcgagacgct 360

caaaattgat t 371

<210> 2025
<211> 462
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2025

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ttaaaaagtt ttttcaaaaa ctgagtagca catagattct taacaaaacc ttttaccaca 120

gggtttttac tctctggtaa tcgattacca gattattgta atcgattacc agtagcaaaa 180

ttctgttcaa aaagctgtca actgaactta caatgttcca attgatttca aaatgttgta 240

attgattaca atgttctggt aatcgattac cattgtgttt gaacgttgaa attcaaattc 300

gaatgtgaag agtcacatcc tttcacgaaa atgctttgtg taatcgatta cactgatttg 360

gtaatcgatt accagtgata ggttctgagc aaatcagaag atgtaactct tcacatagtt 420

attgactctt tcacattggt ttaagttntt ctaaacgtca ta 462

<210> 2026
<211> 427
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2026

gctctctctg tcaatgttag gttcatatgc tcaactacac cattgagttg aggtgttcct 60

ggcatggtcc tctcccttct aatattgtgc tcatagaaaa actttctaaa tctgtctaca 120

tattcaccac cattgtcagt tctgtgcctt atgatctcca atcctgtctc attttcagcc 180

atggctttcc atatcttaaa agccacaaat acttctaact tgtattttag aaagtaaact 240

cataccttcc tagagtgatc atctataaaa ctcataaagt attgtttgcc accaatggat 300

gacacatatg ttggtgtaca caaacatcag agtgaacaag ctcaagtntt tccttcttta 360

gggttctgct atctgtctaa aagctgactc tnttctgatt gccaaatatg cagtcttcac 420

acatgta 427

<210> 2027
<211> 473
<212> DNA
<213> Glycine max

<400> 2027

cttttcttct tcactggtta agcagtttac aacatttacc aaagctcttt ccagcgaagt 60

ctgtggagtt gcaagagcgc taatgttttc cttgtcaact tcctccacct tgaagcactt 120

cctgttctcc tctagatatt ttattgcttc aaacaggttg aaggtcacct tctgaatgtc 180

aatgctcatc tccagatttc cattccccat gtccaccaca cagttggcag tcaacatgaa 240

gggtctacct aagataaaag gaatctccgt gtcttcttcg atatccatga tgacaaagtc 300

cactaaaaag gtgaagtggc agaccttgac taggacttct tctaccaccc catacggtct 360

tgtgattgag cggtctgcta gctgaagcgt catcctagta gggtctatct tcagattacc 420

aattcttctg cacattgata ggggcatcag gttgatgctc gcccctaagt caa 473

<210> 2028
<211> 346
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2028

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tatctttcat tgaaactcca tgactgaaaa ccaccattga aagagcttat tgaagctcaa 120

agatccaacc tccatagaag cttctcaagc aagcttccat cacttaggct ataaacagag 180

gccttgtgtg tgcaattttt caactttgat catttgagaa attacacttc aaggtttaca 240

actcatatga ggcataaatt gggtgcccct tctatacctg tccatccact cataatctgc 300

ttcctttaag ctcttatcga tggcttacta tggtggtgag cttgta 346

<210> 2029
<211> 459

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2029

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tgtgagagac atttgactta tgtaaggact aataagtaaa taattaacga ttaagagcta 120

aattgtaatt gggcttaata ggagaagttt ctaggattaa ctgctacttg atgggagtag 180

tggttataaa aggggcttaa tacccactaa cgtgaaataa ggtccccttc ctgaccagaa 240

aagtgttctc tctcactcat agccatcact aacggagaga ggcagaaaag aaaggccaaa 300

ggaagtgaaa tcttatttct ctcatctttc aaggaaatca aagtaacgga gagaagttcc 360

tatggagaaa ggtacaagtc ttcctatgga gaaaggtaca catcattatc tattggtgtt 420

tattgattgt ntgtgagaac catatgtttc aagatcctg 459

<210> 2030
<211> 443
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2030

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ccatcacgaa gtacctgcta aggtaaatta gattagatgt caaatgaaat ggaaacaaga 120

cagtataaca aagtcattgg aaaaggaaaa cttaaacatg caatagtgat gtaagtagct 180

actgttaaat cagtgaagag gggaataacc tttgctttgg gggctaatct ggccataagg 240

gcagcagctg cattgccagc attgttttct tctatgaaac tgatggtgga gtttataagt 300

agcaaaagaa ctatgccagc aaaatcttga taatctccac cttcaccctg cagaagtttg 360

agttattata ttaaatataa tggattgtaa attgtaacat cactgttttc agacagtaaa 420

aattgactga ccgataatga aac 443

<210> 2031
<211> 493
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 2031

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tctcataggc ttctaaacga atctcatcta gctcacttag ttacaacttc ctttcctctc 120

tagcctgatc catagagaag ttgtaggttt ttacagccta gtaggctttg tgctctatct 180

ctacaggaag atgacatgcc ttgctaaaga caacccgata aggtgacatt cctatgggtg 240

ctntgtaggc agtcctatgc gcccaaagag catcatccat cctggtgctc caatcatttc 300

tgttcggctg cacaatcttc tccaagatct ttnttatctc cctgtttgaa atctcagcct 360

acccattagt ttgggggtgg taaggtgtgg aaattctgtg cacgacccca tactttntga 420

gcaaggcata catggaccta ttacaaaaat ggtgccttga tcactaacga tggctctcgg 480

gactccaaac ctg 493

<210> 2032
<211> 399
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2032

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gactagagta tcttggccac atcatttgtg gttttggggt ggcagcaaat aaatccaagg 120

tggcagcaat gagttcctgg ccagttccta aagattcgaa gagtttgaac gggttctagt 180

acagatgcaa aaaatatata aggtttattc tagaatgaat aaaagagggc ttggatttac 240

ttagttgagc cggttggtgg ttaacatttt acgcgaatat tacatgatac aacaatattt 300

aacatgcgct atcattaatg tcatatgacg catgcagagt tctgagtgga acaccgagtg 360

taacatataa gatgtggggt atctttaagg ttttaaaaa 399

<210> 2033
<211> 295
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2033

gagtgaagat gagaagaaga agcttgaata gttgaatgta gaagttgaca acctctgcaa 60

ggtgatcaag gatgttttgg gtgacaaggt tgagaaagtt gtggtctctg accgcgttgt 120

aaattcacca tgctgtcttg tgactggcga ataccgctgg accgcacaca tggaaaggat 180

aatgaaggcc caagctctaa tggacaacag catggcaggg tacatgtcaa gcangaagac 240

catggagatc aaccctgaga acccaatcat ggaggagctc acgaagcgtg ctgat 295

<210> 2034
<211> 207
<212> DNA
<213> Glycine max

<400> 2034

ccggatcctt aagtcacctg cggctgcagc ttaacatcag accacttaca gggtgctggt 60

tctacttcac atggacttga tggggcctat gcaagttgaa agccttggag gaaagaggta 120

tgcctatgtg gtggtggttg atttctccag atttacctgt gtcagctgta tcagagagaa 180

aacagacacc tttgaagtat tcaaaga 207

<210> 2035
<211> 509
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2035

tactaagctt gaggtangag aagatgagtg gagggagagg gagagaaggt gtgctcatat 60

ttatgcctta aatgaggtct gaaattcgaa gtctaatttc tcaaatgatt aaaggtgaaa 120

aaatgcacac acaatacctc tatttatagc ctaagtatca cacacaattg gagggaaatt 180

tgaatttgta ttcaaatttc actggaattt gaatatgaat tggtggagcc aaattttcac 240

taattatgat tagtgaattg tggttatggt tcaacccact aatccaagat caagttcaag 300

attctccact aagtgtgctt aggtgtcacg agacatgtta aacatgaagg acatgcacaa 360

agagtgactg tatgatgtga caatgtggtg tatcaagaaa atgctcattt ccccccttata 420

atggtccaaa atttaattgg attgcgcttc tcccaattta attaaatnta tcctccaata 480

cacacacatc agatagtgca cttaatgcg 509

<210> 2036
<211> 459

<212> DNA
<213> Glycine max

<400> 2036

agcttgtcct tgactcatct tttccttgaa gtgacatctc taatgatctt tcttccttct 60

ccattctcct gtcattgatc ttcaagaaac aaaggacttc attgatgaag aagatccaag 120

gcctacaagc tccacatgga gctacatcaa ggaggaagca cactatgata ttgatttaca 180

ttcttataat aatgctatcc cttttaatgt tgccaacaat gcaaagttta agaagatgct 240

tgatacagtt tcctagcatg gtccaggatc tgtcccttta tcatacaatg atattaggat 300

gaaggagaaa actcatcttt ctttgaagaa tcatatagct tattggaaga catctagatg 360

tgctataatg acacatggat gaaccgatac gaggaagacg atgacctatt tactaatttt 420

ggtaaattat ccacttggaa ctatgttttg aagtctgta 459

<210> 2037
<211> 418
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2037

ggatcttata gaactccttc ttcttacggt gcttcatatt ttcttaccat tgtcaatgat 60

tgctcacctg cagtttgggc ttttttgttg attgataaga aagaagtatc acgggcactt 120

acaaattttt ttgctattgc agaaaggcaa tataaaaaaa tggttaaaac tatgagaagt 180

aataatggaa cagaattcat ttgcatgaaa aaatattttc atgagcgtgg gatagttttc 240

caaccttctt gtataggaac accttagcaa aatggcaggg tcaaaagaaa gcatcggcat 300

atcctcaatg tggtgcgagc tttgtgattt caaagaagtt tacccattga attttggggc 360

gaatgtgngt ngacaacatg atacttgatt aatcgtactc caagctcagt cttaaaag 418

<210> 2038
<211> 311
<212> DNA
<213> Glycine max

<400> 2038

ttcgagtgtc tcgatatatt acttgactca atcagacatc cgagttaaaa gttattgtcg 60

tttgaaattg ctacgagctt ccgttatcaa ttgcgagcgt ctagatatac taacggacac 120

aatcgtacat ccgacaacaa agataatgtc gtttgaattc gctcagagct tgcgttttat 180

atttctgagc gtctcgatat actacaggac tcaatcggac atccgagtaa aaagttatta 240

tcgttggaat tttctaggag cttctatctt taatttggag cacctcgatg aattgccgga 300

ctcaatccga c 311

<210> 2039
<211> 445
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2039

agcttgctat ccnctccaag aaaaggatta aaatttcctc atccgattct gatgatgatg 60

tcgaactaga tgtctcgaca tctaagaggg ccaagaaatc tggaagaaag gtgcctggaa 120

atgttcctga tgcaccattg gacaacatct ctttccactc cattggcaat gttgaaaagt 180

ggaaatatgt gtatcaacgc atacttgcgg ttgaaagaga actgggaaga gatgccttgg 240

attgcaagga gatcatggac ctcatcaagg ctgctggact gctgaagact gtcagcaagt 300

tgggagattg ctatgaaggc ttactcaggg aattcattgt caacattcct tctgacataa 360

ctaacagaaa aagtgatgat tatcaaagag tgtttgtcag aggaaaatgt gttagatact 420

cccctgctgt gatcaacana tatct 445

<210> 2040
<211> 438
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2040

cgtctcgacc cggatactta agtcacctga cgctgcagct ttgcaacttt ataaanaatt 60

gtttcttatt tgacattagt tctatattaa aattaacttt tcatatgttt caatgtgaaa 120

tatatagttg aaaccataaa ggtatcacat gtgatatata tatgagttac tttttaacta 180

tgcacatttt tttacttaaa gtaaaatagt gtgatatttc atatatcttt aattgatata 240

cttcacgatt aagagaagaa acacgatgat taatatgata acgaatgtga taaaaagaga 300

tgaatgtgtt caattaggtt tcatatgaat ataaaattgg aaacttaaca tagttgacat 360

aaatacgatt attaaatagt gaattctata gcatataatc agatgatggt gggaacttat 420

tatacacaga taatatat 438

<210> 2041
<211> 409
<212> DNA
<213> Glycine max

<400> 2041

atttcgagcg tctggatata ttacgggact caatcaaaca tacgagaaaa atgttattgt 60

cgcttgaatt tgctctcagc ttcaacattc aatttcgagc gtcccgatat attacgagac 120

tcaatcagac atccgagtaa aaagatattg tcatttgatt tggcacagag cttcaacatt 180

caagttcgag cgtctcgata tatgacggaa ctcaatcaga catccgagta aaaagttatt 240

gtcgtttgaa tttgctcaga ggttcaacat tcaatttcga gcgtctcgat atattatggg 300

actcaatcag acatccgagt aaaacgttat tgtcgttaga attgtctcat aggttcaaca 360

ttcaatctcg agcggctcga tatattacgg gactcattca cacatccga 409

<210> 2042
<211> 393
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2042

gagtntggag tgcacattgt agttactaag atgtggagag acatgaaaga agcaaagcca 60

ctagtggaag ggaatgagag gaaacaatat gccaaagtat ttgattatgc acatgaattg 120

ttgaggagca ttcctggatc aacagttaag atcaacacag tgccaagtcc aggaggtcca 180

ccataatttc agaggctata tatttgtctt gttggctgta agaaagggtt tgttgctgga 240

tgtagaccat tcacaggtct agatggatgt ttcctaaaga gtgcatttgg aggaaacttg 300

ctctctgttg ttgggcttga tggcaataac cacatctttg ttatttgcta tgctgttgtg 360

gacatcgaga acaaagacaa ttggaaatgg ttt 393

<210> 2043
<211> 296

<212> DNA
<213> Glycine max

<400> 2043

atgttgttag tcgtcatctg gatgtcgaga gtgttatctt gttggattct gagaagaaga 60

tcaataaaat cttggtcctc taattcagct ccatcttctt ttgcaatatt gttcttttct 120

tgatgctctc tgatgatgtt ttccaggacc ttgtcaacct gcttgtgcaa cttcttcaat 180

ctggtcatgt ttccagttag gaaatataac aatggaattg aaggaaagac atcagcaatg 240

tcgaatcctt ccccggattc tacgattctt cggatcaaag acacaacaaa ctcatc 296

<210> 2044
<211> 363
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2044

tgtaatcgat tacacacata ctgtaatcga ttaccagagg agtttttcag ataacattct 60

caacagtcac atctttttat ctgtttctta aatggccatc aaaggcttat atatatgtga 120

cttgagacac gaatttaaca agagttttca agaacaaaaa ggtcttatcc tcttaaaaag 180

aaaaatagtt ntatcctctt acaaattcct tggccaatac acttgtgatt caataaggaa 240

ttatttgagc gctcaaattg ttgaatctat ctcttccaag agagatttct tcttctcttc 300

ttctttattc tgaanaggga ttaagagacc gagggtctct tgttgtgaaa gaattctaaa 360

cac 363

<210> 2045
<211> 413
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2045

gcttttggag gtctattngc ataatacacc taggggttct tccctttata gtataccccc 60

tcatcaactc agttgcaatg agaatatgat tgtgaacgac ttgaccgggc acaaaagctg 120

cttggctagt atgaacaata tcctgaatca cactccctag cctcctagtc aaaaaatatt 180

atatcactct ataaaaagta gagcaacctg caataggcct gtaatccttg acagtcttag 240

cagtaataga tttaggaatg agtgtcacaa gagtactatt aaaaaccttt aatagagttc 300

ctttctcgaa aaattcattc attgcagcaa taaaatcttt ctttactata tgccagctat 360

ttttgaagaa ttgtgcccta taaccatcta tgccaggtgc tttcatatca cca 413

<210> 2046
<211> 315
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2046

gcttgcttct cataagaggc atgctaagtg ggtagagntt ctacttctat cttcatatgc 60

catcaaacat aaaaagggga atgggaatgt aatggctgat gctgtgtcta agatacatgc 120

tttacttgct atgcttgaga ctaaactgtt tggtctcgag tctttgaaag tcatgtataa 180

tcatgaggtg gactttgctg aaatttttgc tgcatgtgat aagttttctg aaactggtac 240

tataggcata atggagtttt gttaaagcaa ataaatttgt gtgcctaagt ggtccattaa 300

agagttgctt gtgag 315

<210> 2047
<211> 338
<212> DNA
<213> Glycine max

<400> 2047

ttcgagtgtc tcgatatatt atgttctctg tatcggacct ccgaatgaaa agtgatgacc 60

atttgaattt cttgagagct acctttgttc aatatcgtgc gtctcgatat attatgcgcc 120

tgaatcggac ctccgagtga aaagctatga ccatttgaat ttctcgagag cttccgatgc 180

tcaatttcga gcgtcttgat atattatgcg cctgaatctg acctccgtgt gaaaagttat 240

gaccatttta atttttcgag agcttccgtt gatcaatctc gagcgtctct gactatgatg 300

cgcctaaatc gacatccgag cgaaaagtat gaccattg 338

<210> 2048
<211> 307
<212> DNA
<213> Glycine max

<400> 2048

tctcgatatg ttatgcgtct gaatcggaca tgcgagtgaa atatttgacc atttttatat 60

tccgagagct tccgttgttc aatttctagc atctcgatac gctatgtgcc tgaatcggac 120

atgcgagtga aaaggtatga ccatttgaat ttctcgagag cttgcgctgt taaaattcta 180

gcgtcttgat acgctatgcg cctgcatcga acatgcgagt gaaaagttat gaccatatta 240

atttctcgag agatttcgtt ggtcaatttc gagcgtctcg atatgttatg tgcctgaatc 300

ggacatg 307

<210> 2049
<211> 451
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2049

actaagcttc tacattcaat ntggagctgt tcgatatatt acgggactca atcggacttc 60

cgagttaaaa gntattgtag gttgaatttg ctcagggctt cggtattcca tttgagcgtc 120

tcgatatatt acgggactca atcggacatc cgagtaaaaa gctattgctg gtagaatttg 180

ctcagagctt ccggattcca tttcgagcag tctcgatata ttacgggact caatcagaca 240

tccgagtaaa aagttattgt ggtttgaatt tgctcagggc ttctgtattc catgtcgagc 300

gtctcgatgt attacgggac tcaatcagac atccggagta aaagttattg gtcggtgaat 360

tagctcagag cttctgcatt caatttcgag cgtttcgata tattacggga ctcaatcaga 420

catccgagta aaaagttata tgtcgttgaa t 451

<210> 2050
<211> 413
<212> DNA
<213> Glycine max

<400> 2050

taaggaggga attccagggg tggaacatgc tctattcaaa gcatgattgg tgggacgaag 60

tttcacacaa tgtgagggaa ttgactacaa ttaagtgttt ttacctgttg tgaaaaacac 120

ttcaatcaaa atggttttgg ccttagttgc acaagaagac atggaattgg aacaacttga 180

tgtaaggata gctttcttac atattgagct tgaagaagaa acctacatga ctcaagcaga 240

aggttttgtc aaaatatgtg aagaaagaaa ggtatgcttg ctaaaaatgt ccctttatgg 300

ccttaagcat taataaaatg gcttaaaaag gtatgagtat gactggtgtg tctacttgaa 360

gaatattgag catgatgtta ttgtctactt actgctctat gtaaatgata tgc 413

<210> 2051
<211> 389
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2051

atatatgtat gtgngtntat gtagcatgat accttggata tgcatgtata taacagagat 60

acctcacaaa atatatatat gtatgtttag gtagcaagat accttggata tgcatgtata 120

tagcaaaaat atctcacaaa acatatatat gtatgtttag gtagcaagat accttggata 180

tgcatgtata tagcaaaaat atctcacaac atatatatat gtatgtttag gtagcaagat 240

accttggaca cacatgtata tagcaaaata cctcacaaaa atatacatat gtgtaggtag 300

caaaatacct catggaaaaa gaaaaagaga taaataagaa aaaaaataat tattagttgt 360

ctagctaaaa aaacaacatg ctttgtgaa 389

<210> 2052
<211> 430
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2052

ttatttaatt nggacgaatc tgcaccgttt aacatgactc ttattaaaaa gtagtagcat 60

caacatcaaa ttacattcaa aatttcaaat agtaatagta ttatttatgt aagttttttt 120

tttctcactc agaatcacat gtatttctta ctttttctca ctcagaaaat tgacctaata 180

atcaatggcg tatccagaaa gtttttccag tgggagcaaa aaatagtcta atatttttc 240

aaataaaaaa ttatataagt ttttctaaaa atggtaataa aaaattaaaa actataaaat 300

ttaaaaggat aaagtgattg ctcattaaag aatttggcta gacagcagaa tgacgtgatt 360

gctcattaaa gaaatatcat tccttccctt agaattttaa ttatcattaa aaatanataa 420

agatagactc 430

<210> 2053
<211> 429
<212> DNA
<213> Glycine max

<400> 2053

ccttctatta cggacctatg aaactaagct tttttctttt tatctaagca gattagaaat 60

gttcacctaa ttaatttaaa tttaatcact tgataatata ttaaaattaa tttatctgtt 120

ttttacgttg aaattaattt atgtgtttgt ttctatcttt ctcatgtaaa ttaaaatttg 180

actccaaatt gtttgtgctt ttaattggcc aatattagtt ttgtgtttta aatagttttt 240

aattggtcaa tgttgttagt tttaatttat tgttgtaatt aataattaaa tgcaaatatt 300

tgtatttaaa tttggattta ttattaattg tacttagata ttagttgttc tgtaattatt 360

ttttatataa cattgataaa ttattcatac tcatattagt tgtacttaat agtgattatt 420

catacttaa 429

<210> 2054
<211> 394
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2054

gggaagaagt gtacatggag attccacctg gatatggtgc cactaatgga ggaaataaag 60

tttgcagact aaagaaggtc ctatacagtc ttaagcagtc ttctcgggct tggtttggta 120

agttcactca agttatggta tctttggggt acaagcaaag ccaaggtgac catactcact 180

ttataaaaca ctcccaagat ggaaaactta ctttgctctt ggtctatgtc gatgatataa 240

ttattgcagg cgatgatgaa cttgaaaaat aaaacttaag ggagaggtta gctgcccaat 300

ttgagatgaa ggatctcggg aagctaaagt acttcctcga gatagaggtt gcacactcta 360

ngcaagggat cttcatttct cagaanatat atac 394

<210> 2055
<211> 391
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2055

tgtgcatcca ataccatgat gaggatgtcc catatgttct taatactgga ctgatccatt 60

tgcttccaaa gtttcatggc cttgcagatg aagacccgca caaacatatg aaagaatttc 120

atattgtctg ctccaccatg aaacccccag atatccaaga ggatcacata tttctgaagg 180

cttttcctca ttctttatag ggagtggcaa aggactggat gtattacctt gctccaaggt 240

ccatcacgag ctgggatgac cttaagagag tattcttaga aaaaaatttc cctgcttcca 300

ggaccacaac catcangaat gatatctcag gtattagaca actcagtgga gagagcctgt 360

atgaatactg tgagagaatt aaanactatg t 391

<210> 2056
<211> 284
<212> DNA
<213> Glycine max

<400> 2056

gacactctga gtaaaaaagt tattatcgtt tgaatttgct gagagcttca acattcaatc 60

tcgagcgtct cgatgtatta cgggacttaa tcatacattc gaataaaaag ttatcgtcgc 120

ttgaatttgg tcagagcttc cacattcagt ttatagcgtc tcgatatatt acgggactca 180

atcagacatc cgagtaataa gttattgtcg ttcgaaaatt cttagagctt cggtattcta 240

tttctgagcg tctttgatta ttacgggact tatcagacat ccga 284

<210> 2057
<211> 336
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2057

agcttgcctt gccccttgat atattagagg gactcatggt cactatgaat gacaaattcc 60

ttgggataaa ggtagtgttg ccatgttttc aaagcccgta ctaaggcata caactcctta 120

tcataagttg aatagttaag ggtaggacca cttaactttt cactaaaata agcaattgga 180

tggccttctt gcatcaacac agccccaatc ccaacatttg aagcatcaca ctcaatttca 240

aaagattttt gaaagtgtgg caacgcaagt atggnggcat tagttagctn ttgcttaaga 300

acattgaaag cttcttcttg tttctctccc catttg 336

<210> 2058
<211> 450
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2058

agcttacctt gctcggcggg ctcttgatta cttgattggg tttaacattt caccattact 60

atggaggaag ttaccaggtt gccaatcagc tggaagagtt caatctgctg cactttctct 120

tatatgtgat agagaaatgg aaattgatga atttaaaccg aaggagtatt ggactgtgga 180

ggttcaaatg aaaaagaaag agctgagatc aaacaagaac cttacttttc ctgctcactt 240

gacccatttt gattcaaaaa agttgaataa gttttcaatt acttctgata ccgaggcaag 300

agatattcga agcaatataa actcagctga ttttcatgtt gttagcttga aaaanaacaa 360

aagtcgaaga aatcctccaa caccttatat aacatcgaca cttcagcaag atgctgcaaa 420

caagttgcat ttcactgcaa gtcacacaat 450

<210> 2059
<211> 217
<212> DNA
<213> Glycine max

<400> 2059

agcttatctt atggatgctt gcgatatggc tacttattat aattccaagc aacttctggg 60

cagtggaagt aaccgtgttt gtcaagcaag gcacaacaat ggaaaggaac ctgggccaga 120

acttgcatat accaacagcc ctcctatgga actttgtgga ggacaccatt ctcatttgtc 180

tccccattta cgaacgttac tatgcaccat tcatgcg 217

<210> 2060
<211> 315
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2060

agcttgtaat ctattacaca catactgtaa tcgattacca taggagttnt tcacaaaaca 60

ttctcaacag tcacatcttt atatctgatt cttaagtggc catcaaaggc ttatatatat 120

gtgactagag acactaattt tatcataagt tttcagatca aaaaggtcta atcctcttaa 180

aaagaaaaat ccttttatcc tcataccaat tccttggcca gaacactggt gactcaataa 240

agaattattt gagtgctcaa attgttcaat ctatctcttt taacagagat ttcttctttt 300

cttcctctca ttctg 315

<210> 2061
<211> 441
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2061

agcttcctta tgaagatntc ctaaaaagct agagcttagt tacacatacc tctctaatgg 60

ctaagctcac cttcttgaga tgagaagcta gagcttagct acacacctcc tataatagct 120

aagctgaccc catgaaaata caaaaaaaaa tccctactac aaagactact taaaatgcct 180

cgaaatacaa ggctaaaacc ctatactact agaatggcca aaatacaagg cccaaacgaa 240

ggaaaaacct attctaatat ttacaaagat aagctggctc atacttagcc catggactcg 300

aaatctaccc taaggctcat gagaacccta gggcattccc ttgaatctct ggcccaattt 360

acttggagtc ttctatccaa tgcccttgcg gggtaggatg gcatcacaag taccctccac 420

ttgaactgat ccacaagaga t 441

<210> 2062
<211> 239
<212> DNA
<213> Glycine max

<400> 2062

agcttcaaca tcagaccact tccagggtgc tggatctact tcacatggat ttgatggggc 60

ctatgcaagt tgaaagcctt ggaggaaaga ggtatgccta tgttggtgtg gatgatttct 120

ccagatttac ctgggtaaac tgtatcagag agaaatcaga aacctttgaa gtattcaaag 180

agttgagtct tagacttcaa agagagaaag actgtgtcat caagagaatc aggagtgac 239

<210> 2063
<211> 357

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2063

agctttgagc aaattcaaac gacaataact ntattatcgg atgtccaatt gagtccccta 60

atatatcaaa ctgctccaaa ttgaaaatgg aagctcgtag caaatttaaa cgagaataac 120

tttttactca aatgtgcgat tgagtcacgt aatatatcga gacgctctaa attgaaaacg 180

gaagctcata gcaaatgtaa accgtaataa cttttaactc ggatgtccga ttgagtcctg 240

tgatatattg agacgctcaa aattgaaaac agaagctctg cgcaaattct aacaacaata 300

actttttact cggttgtccg attgagtact ggtatatgtt gagacgctcg aaattga 357

<210> 2064
<211> 362
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2064

agctnttaac tcggaggtcc gattcaagcg cataatatat cgagacgctc gaaattaacc 60

aacggaagct ctcgagaaat tcaaatggtc ataacttta actcggaggt ccgattcatg 120

cgcataatat atcgagacgc tcgaaattga acaacggaag ctctcgagaa attcaaatgt 180

tcataacttt tcacacggag gtctgattca ggcgcataat atatcgagac cctcaaaatt 240

taacaacgga agctctcgag aaataccaat ggtcataact cttcactggg atgtccgatt 300

caggcgcata atacattgag acgctccaaa ttgaacaacc gaagctctcc acaattcaaa 360

tg 362

<210> 2065
<211> 396
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2065

agctntataa ctngngtcan agctaccagg aatgagtata ctcccatcaa taaactcaaa 60

tgtgttctta gcacctaagg cgcgtctcat aaaacgagcc catgcatggt aattagagcc 120

atttagcaca ggagtgactg ttacagacga aggtccatct cctacatgaa cataatacgg 180

gctggaagga tcttgcgatg gatctgcaag accacctcca tgattgttgc cggaaccacc 240

tggacgagcc atcagagtta cgcagatatg gagctagacg ctctgtgata ccatgttaat 300

aaatgaatat aaaagcaagg aaggagacaa tatggagaaa tgcattgaca ctcaattcat 360

ggaattacat caggctgatg cttgttattt atatga 396

<210> 2066
<211> 278
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2066

agctntatgt tcaattgccc caatgacatc tattcttcac atggaanaag gccaagaggc 60

ggacatgact ttcagacgat ggggcagaac attgacattg ttcgcatacg ctcgacatat 120

atggcattta cttacatggg tgcagcaatc gctttccata acgagccaag aataacctgc 180

tctaaggatc ttcctggcca tagcatgccc attggcatgt gtgccaaatg aacccccgtg 240

gacttactca atcatgtagg tcggctctat ggcatcta 278

<210> 2067
<211> 389
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2067

agctntacat tactcctcat gcttctcacc atgtctaata aggttcgatt tcttcattct 60

accacaccat tctgatccgg agaaccaggc atagtgtatt gggcaacaat cccatgttct 120

tgaagaaatt tcgcaaatga acctggtgct tgtccatcct ctgtgtatct accatagtat 180

tccccacctc tatctgatct cacgatctta atttgttttc cacattgttt ctcaacttca 240

gccttaaaaa ctttaaaggc atctaaagct tcattcttag aatgaagtaa gtagagatac 300

atatatcgtg aataatcatt tataaagctt atgaagtatt tctgactatt tgcgtccatg 360

tctagacaac atatgtctgt atgtatgat 389

<210> 2068

<211> 465
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2068

agctntacta attaanaaat gtactcttct aaggctttta cttatgttgt taagagaata 60

aggagtagaa gagaaactta accaaacgta aaagtggaaa ttaaaatgca cagcggaaag 120

taaaagagta gggaagaagg agacaaacac acaagagttt ttaaattggt tcaacaacaa 180

cccgtgccta catccaatcc ccaagcgacc tacggtcctt gagatttctt tcaaccttgt 240

aaaaatcctt ttacaagcaa agatccacaa gggatgtacc ctcccttgtt ctctttgaac 300

ctagtggatc taccctccac tagaactgat ccacaagaga tgtaccctct cttgttctca 360

gtcaaaccca agtagatgta ccctctactt gtaccacana ggatgtatcc tccaatgtgt 420

taagacaaag atctcatgca gtcaaacctt tgatactttg tgaat 465

<210> 2069
<211> 391
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2069

gcttgcatgc ttgctaagat gcattntgaa gaatcatacc aagaaaagta ttacaattta 60

taatctgagg cttgcacatc atgtcatgtt gacatgagaa gcatatataa ttgaacaaga 120

aggaacataa attgtgttta ttttattgaa tacataccaa gaataccagt ataatatgaa 180

agcggaacat cggtgtgctc aatgttgaaa agtatttgag ttggggacac caagctgaat 240

tcttcccatt ntgtagatcc ccacactaaa gcacctttct tgaatctggg tgccagattt 300

aggactatta cactccatac cctgtaatgg ctgatgtaca caacggtaga gttagaccag 360

ccaaatttat gatcccaaga gtatntcaaa c 391

<210> 2070
<211> 415
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2070

agctagagta tcattccaaa tgtatggctt caattacctg ctaaaggcaa caggcacaat 60

tccagctcta tattcagcaa tttgcaagaa ggcaggttca gccatatcaa agtgttgcag 120

aggagggttg caccaacccc cattgttgtt aggcaaagaa cggtttgggg ggcagaagtt 180

agtggcagtt acagtaatgg agccaggttt gcaccatctt gggtcatcat cacatctcat 240

ttcatagcaa gatccacagc ttaagccatt gttgaacaaa gcagtgctta tagccacagt 300

gtcagttcca tagccctggc tatacaaatt tccataccca catgctccac ctgcatgtat 360

anaatacana gcataaacat acaactcatc acttaacttt cataaacaca ctcta 415

<210> 2071
<211> 421
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2071

acacgttaac tcgcttntga tctctatgaa tctgctgcaa atcaactatc aagacgtcaa 60

cgattgcgcg agttgcttaa acaatcccaa tcagctcctc ttaccgagga agaacagata 120

ataactattt atactggaac gaatggttat cttgattcat tataaatggg acacgtaagg 180

aaatttcttg ttgagttacg tgcttactta aacacgaata aacctcaatt caaagaaatc 240

atatcttcta ccaagacatt cactggggaa gcagaagtcc ttttgaagga agctattcaa 300

gaacagatgg aactcttttt actacaggaa caggtagaag aaaattgatt aatcgtttaa 360

taactctata atgtcacttt caaattctta tacattagat cttttaatat ctctttattt 420

c 421

<210> 2072
<211> 359
<212> DNA
<213> Glycine max

<400> 2072

agcttcctct tattagtgca cagctccttc aagaatttgg catattttgg aattttcttt 60

attgcatcca gcagaggtat gtttacctct acttttctga atgtctccaa gatctctttc 120

tctgcctctt ccatttttt gttggaaact gctcttggag ggaatggaag aggagggatg 180

tgctgcttct gcaaattacc agtggaagat tcacctgcac agaaattgtt aggtaaattt 240

ttgtcatcac ctttttctgg agtagagtga agtttggcag attcatttgt agatgaggaa 300

ggtgctatgg gttgaggtcc ttgacactgc tttcccgacc tcaatgaaat ggcactgac 359

<210> 2073
<211> 410
<212> DNA
<213> Glycine max

<400> 2073

tgcagctttg agcaattcaa atggtcataa ctttttcgg aggtccgatt caggcgcata 60

atatataaag acgctcgaaa tttcacaacg gaagctctcg agaaattcaa atggacataa 120

cttttaactc ggatgtccga tttatgcgca tcacatatag agacgctcga aattgaacaa 180

tagaagctct cgagaaattc aaatggtcat aacgtttaac tcggaggtcc gattcaggcg 240

cataatatat cgagacgctc gaaattgaac aaaggaagct ctcgagaaat tcagatggtc 300

ataacattta actcggatgt ccaatttagg cgcataatat atcgagacgc ttgaaattga 360

acaacggaag ctctcgagaa attcaaatgg acataacttt taactcggat 410

<210> 2074
<211> 304
<212> DNA
<213> Glycine max

<400> 2074

taccttgctc tgcgggctct cgaatactat tattgggttc aacatctcac cattattatg 60

tgttgatgtt accatattgc caaacaactg gaatagttca atctcgctgc actttctctt 120

atctgtgata gagaaatgga tattgtagaa tcttaacccg cagcaccttg gactgtggac 180

gttcaactga aaaagataga tctgtaatca aacaagaacc ctacttttcc tgctcacttg 240

acccattttg tattcaaaaa gttgaatata gtttcaatta cttctgatcc cgaggcaaga 300

gata 304

<210> 2075
<211> 338
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2075

agctntggag tttccaagtg ccaattcgtc ttcttctttt gtccagtctt cttctggctt 60

caattcatta gagggctttc cttctgtgtc cagcatcttg ggatgttccc agcctttgat 120

gacagctttc caggttctgc tatccagtga tttgaggaag gccaccatcc ttgctttcca 180

gtattcatag ttggttccat ccagaattgg tggtctgttc acttgtcctc cttcttttct 240

catgttcatc agaaattatc tccctagatc tcactcagtg atttcgagtg cctgctctga 300

taccaattga aattctgata ctggggacag atgtcgta 338

<210> 2076
<211> 398
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2076

actaagctat gctgcaatat tacaatagac ctcctcaacc tcatcagctt aatcaaccac 60

agcagaacaa ttatgacctt tccagcaaca gatacaaccc tggatggagg aatcacccta 120

acctcagatg gtctagccct cagcaacaac agcagcctgc tcctttcttc caaaatgctg 180

ctggcccaag cagaccatac attcctccac caatccaaca acagcaacaa ccccagaaac 240

agccaacagt tgaggccccc ccacaacctt ccctcgaaga acttgtgagg caaatgacta 300

tgcagaacat gcagttttag caagagacca gagcctncat ttagagctta accaatcaga 360

tgggacaatt ggctatccaa ttgaatcaac aacagtcc 398

<210> 2077
<211> 261
<212> DNA
<213> Glycine max

<400> 2077

atacttagac tatcctaaaa aatgatagct ctttcaattg gaaacccaag attgctaacc 60

agacctttaa gtcagatccc atcctttatt gcttctatta gagcatgcac tctacctttg 120

tagtggataa aaccacaatg ggctaaagag tttccttcca actatcaaga gagttgccaa 180

tcatgaatgc gtaccttgtc atagttctcc ttgcatccaa atctacagca tagtcaaaat 240

ctaaataacc aacaagagca c 261

<210> 2078
<211> 289
<212> DNA
<213> Glycine max

<400> 2078

agcttctcct ttgctcccta taactgattg cagttctcga gagtgttgga cctcttttta 60

gcattagggt ggaaattaga taccgagcta ttacagagag ggtcggagtt tcgcctattg 120

tatagaagat ggtggaaaat atacttaggt ggtttgggca tgtacagaga agaccggaag 180

actctgtatt gaagatgagt gacctgatgg agagaatgca cacacttcga tgcagatgaa 240

gacccacaaa gactattcga gaggctatca agaacgatct cgaacttaa 289

<210> 2079
<211> 412
<212> DNA
<213> Glycine max

<400> 2079

ctatttcaat tacgagcgtc tcgatatatt acgggattca atctgacatt cgagtaaaaa 60

gctatcgtca tttgattttc ctgagagctt cagttgtcaa tttcgagcat ctcgatatac 120

tacacgacac aatcggacat ccgagtcaaa agttattgtc gtctgatttt tcttagagct 180

ttagttctta atttcgagcg tctcgatata ctaccggata caatcggaca tccaagtcaa 240

aagttattgt tgtttgaatt ttctcagagc ttctgttttc aattacgagc gtctccatat 300

attgcgggac tcaatcggga atccgagtaa aaaggtattg tcgtttgatc tttcttagag 360

cttcaagttt taatttcgag cgtctcgata tactacggga cacaatcgga ca 412

<210> 2080
<211> 310
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2080

tctatcctca attacgaggg tctcgatata ttacgagact caatcggaca ttcgagtcan 60

aagttattgt cggttgactg ttcttagagg ttccgttttc aatttcgagc gtctcgatat 120

attacacggc tcaatcggac atccgagtta aaagttattg tcgtttgata tttctcagaa 180

cttcccgttt caattacgag cgtctcgata tccttcggga ctcaatccga cactcgagtc 240

agaagttcta gtcgattgaa tntactcaga gcttctggtt tcaattacga gcgtctcgat 300

atattacgag 310

<210> 2081
<211> 322
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2081

agctntgaga aaaatcanac gacaataagt nttatctcgg atgtcctatt aagccctgta 60

atatatcgag acgctcgaag ttgaaaacgg aagctctaag aanagtccaa caacaataac 120

ttttaactcg aatgtccgat tgagtcccgt aatatatcga aacgctcgta atttaaaaca 180

gaagctctga gcaaaatcaa acgacaaata cttttaactc cgatgttcga ttgagcccta 240

taatacatcg agacgctcga tatgaaaacg ggagctctta agaaagtcaa acgacaataa 300

cgtttgactc ggatgtccga tt 322

<210> 2082
<211> 390
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2082

agcttactnt aagtatttct aatatttctg ttgtgggaat tcttttgtat nttttaaag 60

cagattccca ttcttttata ctttntttta aacaagttag aacctattac ttccaaagcc 120

agtggaaggc cagaagcata agttactgca cgttgcaaga cctccacgta atttggatca 180

gctttttcct ttttaaaagc tttccatgta agtaactgaa gagcatcgtt ctcatccaat 240

tccttcacct catatgttgt aataacttga tgaggtgcta gcaattgttt gtcccgagtt 300

gtgatgatga atttgctgcc gggaccaaac caatctggtc taccaacaat tgcctgtaat 360

tgctcgtgct tgtcaacatc gtctagaatc 390

<210> 2083
<211> 379
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2083

tctatgatca atcaagatta taaagtggtg ccctanaaga tactgtctcc attntttaac 60

agcaatggtg attgtagcga gttcacgaac ataagttgaa gaagaaagta acttgcggca 120

aaactgcttg ctaaaaaaag ctatcgggtg tcttccttgg gacagcaccg cacctatacc 180

cgaacctgag gcatctgtct ccaccacgaa aggtttcgtg aagtcaggca atgctaagac 240

tggagaatgt gtcatagcat gcttcaattt gttgaaggca acatcagctt ccacggtcca 300

gtggaactct tccttggtca acagacttgt aagtggtgtt gccaacgttg cgtagctcct 360

tataaatctt cgataaaag 379

<210> 2084
<211> 443
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2084

ntagcttctt aaggagagtt tctcacagaa gcttctcaag gaagttttct taagaaagct 60

tctcaaggaa gttacctagt ctataaataa aagcatgtgt aacacttgtt ataactttga 120

tgaatgagag tcttgtaaga cacaactcan agttcaactt ctctcccttt ttcttccttc 180

aatttcgtgc tccctcctct ctttctttta gcaaatgctc acccccccct ctaaaattta 240

attggattgg gcttcttcca attcaattaa atntattttc aaccacacac atcaaatatt 300

cacttaatgc atgccaaatt agaaaactac ccctaataca aaaaactagt ctaggtgccc 360

tacaatacaa gagatgaaaa atcttacatt tctagggtac cttaactata ttgtggagcc 420

ctaaatacac ggccaaaaat aat 443

<210> 2085
<211> 223
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 2085

tgtcctctgc caaccaattn tccaacagat ttttcttgtt ctgtttcaca accaaccgcg 60

ataattctaa tgattcagag gcatttcagc tttccctttg taaaaagggt caaaatactg 120

aacagaggag gagttgccca gcttgcacag gaacactctt gcacgtaaag gagataatcg 180

gcaccttaac attataacta attgaccaaa caaaaggaca cca 223

<210> 2086
<211> 351
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2086

ctgcagctta tgtaagtcaa tttaggaggc atctcggata ggatcttttc cgtgcatatt 60

tgcgcanaat ctcttgaact aggaagatgt tgtccatcat ctttctgttc ttaatgaagg 120

cagtttgagt ttccccaata atagtctcaa gcactggggc tatgcggttg accaaaattt 180

tagacataat cttgtataac aaattacaat aagatatggg tctaaaatgg gtaacctggg 240

agggctaatc atgcttagga ataagtgcaa taatagcatg gttgatctgc tntannaatt 300

ttctagttgt aaagaattca ttaaccgcct caaagatatc atcaccaatg a 351

<210> 2087
<211> 367
<212> DNA
<213> Glycine max

<400> 2087

agagaggtgc aagtaaggaa gcaagtgaag ttggatattt cgattggaaa gtacaatgat 60

aaggtgtttt gtgatgttgt ttctatggag gccaaccact tactcttggg gagaccatgg 120

caatttgata agacggataa tcatgatggt ttcaccaaca agatcccttt cacgtattaa 180

ggaaaaaaag atagtgctca aaccattgag tccacaagaa gtgtgtgagg atcaaagaat 240

aatgagagag aaaattcttc ctacaagaga gaacatgaga aagagagcta aacacttgag 300

agttcaaaag tgacgacaat aagagggaaa cacaagagag gaaaaagatg agtgaaacac 360

ttgaagt 367

<210> 2088
<211> 403
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2088

tttgattgct ctggtagagt tcccaaacgt caaagagaat gagaagggat tgaagcctnc 60

attctgtact gtcttcgtgc aattntgttc cctctctccg tggatattag taaatcccaa 120

cagtgaaggt gtgtggaatt gaatcgtgac caacatatca aaattttacg acaatccaat 180

ggttaacgag ttcaggatcg tagttttacc gagacagttt tggatttctg cgggaaaaga 240

aaaggctacg atgcgaactg tatttctctc agctccgaca tgatttcgaa attcccaatg 300

gtgaaagtgt tcataattga gttgcgaact tggtatttaa atttcacgac gatccaacgg 360

tgaatgagtc tgagattgtc atttctctga gatagatttg gtg 403

<210> 2089
<211> 382
<212> DNA
<213> Glycine max

<400> 2089

gatgcaacat atggagaggt taatgaaaca acgagatgat gcgctccatg agagggtgga 60

tcaaatggag aatagagatc ataatgaaga agaaaggagg agaagaggga atgatggtgt 120

tcctagacaa aaccgaattg atggtattaa actcaacatt cctccattta aaggaaagaa 180

tgatccggag gcctacttgg agtgggagat gaaaatagag catgttttct catgccacaa 240

ctatgaggag gaccagaacg tgaagcttgc cgccacagag ttttccgact atgctcttgt 300

gtggtggaac aagctacaaa aggagagagc aagacatgaa gagccaatgg ttgatacatg 360

gacggagatg aacaagatca tg 382

<210> 2090
<211> 284
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2090

agcttcaaga gatcatccnc tcgacaacat tattggtgat atctcanaag gggtaacaac 60

tagacactct cttaaagatt tatgcaataa tatggctttt gtatccatga ttgaacctaa 120

aaatataaaa gaagccataa tagatcataa ttggatcatt gccatgcaag aagaactaaa 180

ccaatttgaa agaaacaatg tgtggaaatt agtagaaaaa cctgaaaatt atcctgtcat 240

aggaacaaaa tgggttttta gaaataaatt agatgaacat ggta 284

<210> 2091
<211> 412
<212> DNA
<213> Glycine max

<400> 2091

acgtgcattt gtgtgcaata cacaattcct tgtacaccac aacaaaatgg tgtatcagaa 60

aggcggaata aaactttaat ggatatagtt acgagtatgt taatcaatta gactttatcc 120

gtatcctctg ggatgtatac cttgaaaact gccttgtagt tgctgaacaa ggttcctagt 180

aaggtagttc caaagacacc ttttgaactg tggacaaata ggatacctaa tataaggcac 240

ctgcatgttt ggggttgcca ggcagaaata aggatttata atccgcacga aagaaaattg 300

gatgcaagaa caatcagtgg atatttcatt ggttatcaaa aaaaaaaaaa gttaacaggg 360

tatatgtctg attggtctaa tcatagtatg agaactttca aaactggaaa tg 412

<210> 2092
<211> 317
<212> DNA
<213> Glycine max

<400> 2092

agcgtctcaa tatattacgg gactcaatca gacatccgag taaaaagtta tcttcgtttg 60

aattagctct gaggttcaga attcaatttc gagcgtctag atatattacg ggactcaatc 120

agacatccga gcaaaaagtt attgtcgttt gaattagctc agaacttcat aattcaattt 180

cgatcgtctc aatatatttc gggactcaat cagacatctg agtaaaaaag gtatggcgtt 240

tgaatttgct gagagcttca acattcaatt tcaagcgtct cgatctatta cgggactcaa 300

tcagacattc gagtaaa 317

<210> 2093
<211> 394

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2093

cttataatcg attaccacaa gtttttttaaa ctttntataa catcctctag aaatttgaat 60

ttaaattcta aagcttgcaa tcaattacaa cttgtgtgta atcgattacc agacatgaga 120

attcaaattt caaatctgaa gagtcacaac tcttcagaaa ctaactgtgt gatcgattac 180

aacaattatg taatcaatta ccagcaagga attgtcgaac ataactccca agagtcacaa 240

ctgttcaaga agttttgaat ggctatcaag gtctataaat aggtgacttg ngacatgaaa 300

ttctgaaaaa gagaatttcc tgacaaattg tctatcctct caaaccaaat tgcttatact 360

ctcaaaagaa ttcttgtcaa acacttcaaa ttaa 394

<210> 2094
<211> 472
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2094

taatggcttc tttagattct ntgtctntca naagtttttt catgtataga ttattccaag 60

atcatgatga agacgaagtc aatttgtgtc tcatgacaga atctgatgag aataacaaag 120

aagattctat aatgaagaaa tggtacatag acagtggatg ttctaagcac atgacgggtg 180

atgtatccaa attcacaacc atttcccccа agaaaagtgg acatgttaca tatggtgaca 240

acaacaaggg caaaattatt ggagtaggta aaataggaac gagttcttct actcctattg 300

aaaatgtgtt acttgtagaa ggtttgaaac atagtctatt aagtgttagt caattatgtg 360

ataaaggata taaagtatct ttcgattctg aanaatgtgt tattaagcat gagcttgaca 420

aagatattga acatatacgt tttagagaaa ataatgtcta catgattgat ct 472

<210> 2095
<211> 386
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2095

ctgagcaaat cgaaatgaca ataactntat actcggatgt ccggttgagt cccgtaagat 60

atcgagacgc tcaaaattta tatccgaagc tctgagaaaa ttgaattgac aataacttta 120

tacacggatg tccggttgag tcctgtaata tatcgagacg ctgcaaaatg aaaacggaag 180

ctcgtaggaa attcaaacga caataacttt ttacttggat gtccgactga atcgggtaat 240

atatcgagac gctcaaaatt gagactagaa gctttgagca aattgaaatg acaataactc 300

tatacacgga tgtccggttg agtcccgtaa tatatcgaga cgctctcaat ttagatccga 360

agctctgaga aaatcgaatt gacaat 386

<210> 2096
<211> 262
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2096

catgcaagct nntcatttca tatttcgacc atctcgaata ttaccggact catccggact 60

tccgtgtata aacttattgt caattcaatn ttctcagagc ttcggatcaa aattttgagc 120

atcttgatat attacgggac tcatttagac atccgagtaa aaatttattg tcgttagaat 180

ttgatacgag cttccgtttt caatttggag catctcgaga taaaatgaga ccctctgtcg 240

ggcatcccga aaaaacgtta tt 262

<210> 2097
<211> 420
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2097

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ttctncatat gtaattcttc agtgctgcat ctaaactcac tcacaatatc ttcaaagaaa 120

catttatata catcctgaat tattgaaact tgagtatgtg catcctctat atcatcctta 180

agcttctgaa tgggttggaa caaatttttc tgtgtcagtt ggtgctgtga acaattttcc 240

acagaagcag aaagctggga agatagactc ttaaattcct ttttcttatc tgatagtgtg 300

tccttcagtt gatgattctc cgattgtaag aagtccaatc tatcctttaa actgctaaga 360

gattcaatgg tttcactgaa tggatgtact ttctcatttt catcaacgga ttcattcaat 420

<210> 2098
<211> 374
<212> DNA
<213> Glycine max

<400> 2098

cttgagagga atactagaga agctagagct tatttacata cacctctcta atagctaagc 60

gcacctcctt gagatgagaa gctagagctt atctacgcat cccctataat atctatgctc 120

acccccatgc caaaatacat gaaaatacaa aaaaagtccc tactacaaag actactcaaa 180

atgccttgaa atacaaggct aaaaccctat actactagaa tggccaaaat aaaaggccca 240

caagaaggaa gaacctatta taatatttac aaagataagc aggctcatac ttagccaatg 300

ggcccgaaat ctacctcaag gctcatgaga accctatggc cttcccttgg atctctggcc 360

caatctactt ggag 374

<210> 2099
<211> 332
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2099

agctagagga aacccttcgc attgtacctt ttatttcccg caaaacccaa aactgtctca 60

gaaaactatg atcctggatt tgttaaccgc tggattatat tcgaattgng atatgttgtt 120

agaaattcaa ttgcacaaac tttcactgtt gggatttgca agataatatt tgtggaggga 180

gaaaaatgaa tcacatgaag atagtgcaag tggagacttc aattccttct cattctctcn 240

taacgttggg gaccctatca gagcaaccag aggaatctca agaacttgtt atagatgtct 300

ctattcgctg cggaagacat gtgaacccgc tt 332

<210> 2100
<211> 424
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2100

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ctatgtcatt ttcttctccg gccacaggta tgccaggaat gactgcttat gctggtttct 120

ttgaggtagg ttctcccaaa aaaggagaca ctgttttcgt ttcagctgcc tctggtgctg 180

ttggtcaact tgttggccaa tttgctaagt tgactggttg ctatgttgtt ggaagtgctg 240

gaagtaaaga gaagggattt gtttaattat tgttggtata tgtccctgga taaacgaata 300

atcagcttaa atgttggata tttattctac tgcttaaaat actattattt tgaattaacc 360

taattacaat aacagccacc anagcctttt ctataatgta gagttgaatt ggcccaatta 420

tatt 424

<210> 2101
<211> 458
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2101

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cagtttaatc gattaccaga agacaatttt aaaaatcaga ttttaaaaaa ggttttgaat 120

tagaatttcg aatcatgtaa tcgattacta gatgtttgta atcgattacc agcaacgaca 180

cttcagaaaa aactttgaaa agtcatgacc cttcaaaata taactgtgta atcgattacc 240

agtgaagaat tttagaaaaa gctttttgaa aagacacata tcttcaaaca attttcaaaa 300

ggcacaaagg gcctatatat gtgtgtctgc attgtaaaat caagagagag atattctaag 360

agaacttaat tgccaagtgc tctctcaaca acttttggga aaaacacttc caaatctatt 420

gagaattcat ccaggaactt caaantgtat tatcatct 458

<210> 2102
<211> 470
<212> DNA
<213> Glycine max

<400> 2102

ttaagtcacc tgcggcatgc aagcttctta gtttcgtact tggtgacttg gcaatcaacg 60

cattgagcaa caaagcgaga gacgtcatct tgaaggccgg gccaataaaa attggtcatg 120

agacgagcca cggtcttggc gacgccggcg tggccaccgg tgggggtggc atgatactct 180

gtcagcaggg tggtgatgat gggtatatcg gaaggcaacc agatacggcc tttatacaac 240

agcagtttgt cagcaatgga gaactcacgg tggtggtcgg gatgattctg aacatcaagc 300

atcttttgct gaaaggtcga attcgtgcgt gactggtcat ggagctcatc taaaaaagtg 360

agacaaggga cggagagaat gagaaaggct tgagaagctc ctttcggtaa cctagataag 420

gcatctgctg cctgattatg gctccctgag cgatactgga tatgataatc 470

<210> 2103
<211> 338
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2103

agcttgaaat tgaacaatgg aagatcttga gatattcaat cggtcttaac ttttcactcg 60

gaagtccgat tcaggcgcat aatatattga gacgctctcg tgaaattcac atggtcataa 120

cttttcactc agaggtccga ttcaggcgca taatatatcg agatgcacat aattgaacaa 180

cggaagctct cgagaaattc atatggtcat acctttaac tcggagttct gatctangcg 240

cataatacat tgagacgctc gaaattgaac aatggaagct ctcgagattt caaatggtct 300

aactctaact cggaggtcca atcaggcgca aatatatc 338

<210> 2104
<211> 448
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2104

agcttctcag atccggtcat ggaaagactt ggctactgcc ttcattangc agtaccaata 60

caacacggat atggctcctg atcggaacca gcttcagagt atgaccaagc gagaacatga 120

gtccattaaa gaatatgccc aaaggtggag agatctcgca gcccaagtcg tcccgcccat 180

gactgagagg gagatgatca caattatggt agatacgttg cctacgttct actatgagaa 240

gctgatagga tacatgccag ctaactttgc agacctcgtc ttcgccggag aaagaatcga 300

gtccggactg agaaaagggc aatttgaata tgcctccaac gttgccccca acaacaacag 360

aagagcccca gtggtgggcg cgaggaaaaa agaaggagat acccacgcgg tcaccaccgc 420

cccaacatgg atgaaagcgc cccaaatg 448

<210> 2105
<211> 418
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2105

agcttaacct acttaggttt ctatgttgaa ggattgtggt tctatcttnt ctagagatta 60

gattggatta ataaaatttt taaggggttg aataaatatc tactctaatt aattttgatt 120

aacatttaca gttaaagtta accattcaca ttatagttta acgattaaaa tttcaacaat 180

tttgtaattt cctttacata ttaaagtatt ttataatgat tttagttatt agttcttaat 240

gttattaaaa agtcaaaata tcatttgatt gcaaacttgt aaactaaatc taaattttct 300

taaaaaatgg acctgacagc gggaggggat ttataaccat acatctaatt tattctctgt 360

tcaatgtaga aaatgcattt tgattagatt gcgcttcaat agtgtataac taaaaaat 418

<210> 2106
<211> 421
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2106

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aatggccctt tagatgaaga agtttatatt cagcaactcc ccggatatga agtcataggc 120

agtgaagaca aggtgtacat acttagaaag gctctatatg gactaaaata ggctccaagg 180

gcctggaata aaagaataga ctcctttcta catggtgaag actttaaaaa atatattgta 240

gagcatggta tctatgtgaa ggcaactaag gatggtggag tcctgctaat atgcctatat 300

gtggatgatt tgctgattat agggagtaat ccagctgaga tagaaaagtt gaagggcaat 360

ctcaaatctg aattcgagat gtcagaatta ggcttgctat catacttcct tggtattgag 420

t 421

<210> 2107
<211> 421

<212> DNA
<213> Glycine max

<400> 2107

agcttgtgct attccaagtt cattaatcat acctttaagc cagaatgctt ccttcactcc 60

ttcagctagg gccatgtact ctgcttcagt tgttgaaaga gcaacaactg attgttgatt 120

tgctttccaa ctgattgttg taccaaacaa agtaaacaca tatcctgtta aagatttcct 180

tgtgtctaca tttcctgcaa aatctgcatc tacataacct gtgattgctg cctcatatgc 240

tgtcttcttg taccttaatc caactttcga agatccattt agatacctta gtgtccactt 300

cacaacttcc caatgtgcac tgccaggatc tcccatgaat ctgcttataa tacttacagc 360

atgagctaag tcaggtctgc tacaaaccat tccatacatt atgcttcaac accactggca 420

t 421

<210> 2108
<211> 458
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2108

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accagcatct caggcttgat ggtggttgag ccgtccatgg attgactatg ctggtgtcta 120

actctgggcc tttcattagt cccaataaca acattctcgg tagaagaggt gggtgcccct 180

gacgccggtg ttgaagccga tgctcccaca gcattagacg gctcaaccat ttgaaacgtg 240

gacgttgccg acgatgaatt gaacttatcc atatcaaggt acatggacag caagtcctcc 300

tcggcatcat cggagaagga aggaccatca ccacctccaa caacaccaag gtcactgtcg 360

aaactaatat catccggtaa agtgagaatc tccgaatgag cacgcctatg acctctattt 420

ctcggnggat tatcaggcat tctgctaata tcatgact 458

<210> 2109
<211> 457
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2109

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taatgcatca ccaattgaaa aatttgaatc actaaaactc caagcaagaa tcttagcact 120

gtctattatc ctccctgttg aataattatt tgatatcagt agtgatgttt ttgttcttca 180

actgggtgtt gacatcagcc acaaacagtt cacttttcct ggttcctgat gctgtagtag 240

tcttcgtatt gtgaaatttg aaattaatat tgttgcaaag gcagaacaat ggaaatttca 300

aaatatgaaa gtgcgaactc acatgtggaa atctatcaat gaattttgct gcattagcaa 360

cttcagtggc agctctgatt tcttcatttg ttgccccatc cttaccatag gcaatgtttt 420

ctttgatgct gcaactgaag agtattggtt cctgact 457

<210> 2110
<211> 338
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2110

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ggttatcaag acgctcggaa ttgaaaacgg aagctcttag aaaaatcaaa cgacaataat 120

ttttaactcg gatgtgcgat tgagtcccat aatatatcga gacgctcata attgaaaact 180

aaagctctga gcaaattcaa acgacaataa cttttgactc gaatgtccga ttgtgtccta 240

taggatatcg agacgctcgt aattgagaac ggaagctctg agaaaaatca aacgacaata 300

actcttaact tggatgttcg atggagccct gtaatata 338

<210> 2111
<211> 457
<212> DNA
<213> Glycine max

<400> 2111

gcttgcacac aagattctcc ttggctggca cttcataact ctttggttgg gtcttataga 60

tgtcttcctc taaatcccca tgcaagaatg cagttttaac atctagctgc tccaagtaaa 120

gattctctgc agcaacaata ctcaaaataa ctctgatggt agtcatcttt acaactggaa 180

aggagtctct gtgatatcaa ttccctgttt ctactgaaac cctttcacca caagtctcgc 240

cttgtatctt cttctaccgt cagattcttc ctttagccta cagacccacc tattttgtaa 300

cgctttcttt ccttctggca atttagttaa agaccacgtc ttattcttct gaagggatgt 360

catcttatct ttcatcgcta gcttccactc aatagtgtca ttcccctgca tagcctcact 420

gaaacattct ggctcaccaa catcagttaa caacaaa 457

<210> 2112
<211> 361
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2112

agcttaaaca ttcaatntcg agcgtctcga tatattacat gactcaatca gacatccgag 60

taaaaattta ttgtcgtttg aattggctca cacgctcaac attcaatttt gagcgtctca 120

atatattacg ggactcaatc agacatccga gtaaaaagtt attgtcgttt gaataggctc 180

agagctttaa cattcaattt cgagcgtctc gatatattac gggactcaat cagacatccg 240

agtaaaaaga tattgtcttt tgaattggct cagaggttca acattcaatt tcgagcgtct 300

cgatatatta cgggactcaa tcagacatcc gagtaaaaag ttattgtcgt ttgaattggc 360

t 361

<210> 2113
<211> 436
<212> DNA
<213> Glycine max

<400> 2113

agcttccagc aaggtcctta taatcagcaa ggtctttgaa ggaaacaccc cgacaaccag 60

ttcaataaag accagggtgg atcctcaaac aagccaattc aacaagggcc taacatcttt 120

cagaggacga ctaagttgga agagaccttg actcagttta tgcaggtaat gatgtcagat 180

cataatagta ttgagtcaac actaaaaaac cttgaggttc aggtgggaca actggccaag 240

cagatagttg acaagtcatt caacagtttt ggagcaaata caggcaataa tcctaaggag 300

gaatgcaagg ctatgatgac taggagtaaa aagtttgtgg aagctgagga tgaagagagt 360

gtggtgtaca aggagcaaat gggtgaaaag ataggtgctg aggttaagga aaatgatgtg 420

aagggtaaag agaatc 436

<210> 2114
<211> 383
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2114

tgcaagctat cccatgacag ctaagtgacc gggatatgtc actccggaga cagctccaag 60

aagacttgtg ggtagctgca caacatcatg aatctttgct tcgtcagaag tcgagagcaa 120

gatgggtcaa ggagggagat tctaattccc attattttca tttgctagta aatgcaagaa 180

gaagagataa ttctctgcaa ggtttatgga ttgatggagc ttgggttgaa gatccgccaa 240

gggtcaagga gacaggaaga caatttttca tctgcagatt ccaaaaagtg gttcacaata 300

gacccctcct agatggngta gaatntcagt cattagatca gtaccacaat aacttgctga 360

gtgggagatt tacggaggaa gag 383

<210> 2115
<211> 402
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2115

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atgttaggtc ggctctaact gcaatggtat atcgaaaggg gctaaggata tcaagcttgg 120

ccaagcaaag tcacacgagt ggggaggttg ttaactacat ggctattgat gttcagaggg 180

taggggacta ctcttggtat cttcatgaca tgtggatgct tcctctgcag attgttcttg 240

cccttgcaat nttgtataag aatgttggaa ttgctgctat tgcaacactg attgctacaa 300

taatttccat cgtcgtcact gttcctattg ccagngtcca agaaaaatat caagacaaat 360

taatggctgc taacgatgaa aggatgaaga aaacatctga gt 402

<210> 2116
<211> 402
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 2116

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atactanttt catgtttggc gctgcatctc aagttcagac ttgcgtaaaa gtggaagcaa 120

ctacgagtag cttccacgtt ttttgtgata gtataacgcg atttgagcat taaatgcata 180

tacttgaagt ggctccatgc tatgactctt aattcaaaat taagttattt ttaatgtttt 240

ctattttctt tgtcatgaat agaaatatgt tgatttgaaa aaggagttga gcacaacaga 300

tagacatatt ttgatagaaa cgggattcat tcgtcaatgg tgaacatcct cataagttca 360

tattaaatta ccttgctacc ctcgaaacac ctacagaatt ga 402

<210> 2117
<211> 459
<212> DNA
<213> Glycine max

<400> 2117

agcttatgct gcaaacactt ataatagacc ccctcaacag cttaaccaac aacagaagaa 60

taattatgat ctttcaagca acaaatacaa tccaggttgg aggaatcatc taaatctgag 120

atgggcaagt cctccacaac aacaacagac tatccctcct ttccagaatg ttgctggtcc 180

aagcaagcca tatgttcctc ctccaatgca gcagcaacaa caacaacaac aacaaagaca 240

acaagcaact aaggcccctt ctcaaccttc cttagagaag ttagtgagga aaatgactat 300

ccagaatatg caatttcagc gagacaagag cctccattca gagtctaaca aatcagatgg 360

ggcagatggc tacttagttg aaccaagctc aatcccaaaa ttctgacaaa tttccttcac 420

aaactgtgca gaatccacaa aatgtgagtg tcatcatct 459

<210> 2118
<211> 411
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2118

agcttcttat actaacgtca caaggaatgt ggttgttaga ttcataaaga aggaggtgan 60

ttgtcgatac ggactcccca agaagatcat tactgataat ggcaccaatc taaacaataa 120

gatgatgcag gagatgtgcg aagacttcaa gatccagcat cataactcta ccccttatcg 180

gccaaagatg aatggggctg tagaggctgc gaataagaat atcaagaaga ttggtcaaaa 240

gatgacggtg tcatacaagg attggcatga gatgttgcct ttcgccctac acggatacag 300

aacctcggta cgaacttcta ctgggggcaa caccgtattc ttggtttatg ggatggaggc 360

agtactccca tttgaggtag aagttccttc tcagaggata atggcggagt c 411

<210> 2119
<211> 383
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2119

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catttgcttc caaagtttca tggccttgca ggtgaagacc cgcacaaaca tttgaaagaa 120

tttcacattg tctgctccac catgaaaccc ccagatgtcc aagaggatca catatttctg 180

aaggcttttc ctcattcatt agagggagtg gcaaaggact ggttgtatta ccttgctcca 240

aggtccatca cgagctggga tgaccttaag agagtattct tagaaaaatt tttccctgct 300

tccaggacca cagccatcag gaaggatatc tcangtatta gataactcag tggagagagc 360

ctgtatgagt actgggagag att 383

<210> 2120
<211> 422
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2120

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taaggacctc attgaagctc acagatccag cctccgtaga agccccacaa gcaagtttcc 120

atcatgaact ntgaactata attctaaaat gatcaaagtt cacaaaatgc acacatatgg 180

cctctattta tagcgtaagt gtcacacaaa attggaggaa aatttgaatt tctattcaaa 240

tttcacatga attagaaatt gaatttgtgg agccaaaatt tcactaatta tgattaatga 300

attntatnta tggttcagcc cactaatcca agatcaagtc caagattctc caataagtgt 360

gcttaggtgt catgagacat gtaaatcatg aacgacatgc acacagtgtg actatatgat 420

gt 422

<210> 2121
<211> 450
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2121

actcggatgt ctgattgaga cccgtaatat atccagacgc tcgaaattga ataccgaagc 60

tcttaaaaaa ttcaaacaac aataactttn tactcggaag tcagattgag tcccgtaata 120

tattatcgag ttgctcaaaa tggaataccg aagttctgtg caaattcaaa ccacaataac 180

tctttactcg gatgtctgat tcacgcccgt aatatatcga gacgctcgaa aatgaatacc 240

gaagctctga gaaaaattct aacgacaaca acttttgct cggctatccg attgagtcct 300

ggaaaatatc ggaatgctcg aaattgaatg ctgaacctct gagcaaattc aaacgacaat 360

aacattctta ctcgggtgtc tgatggagcc ctgaatatat cgagacgctc gatattatat 420

accgatgctc tgagaaaatt cacacaacaa 450

<210> 2122
<211> 333
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2122

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atacatccga gtaaaaagtt attggcgttt gaatttgctc agagcttcng catgcacagt 120

cgagcctctc gatatactac gggactcaat cagaccaccg agtaaaaagt tattgtcgtt 180

tgaatatgct cagagcttcg gcatgcaagt tcaagcgttt cgatatatta cgggactcaa 240

tcagacatcc gagtaaaaag ttattgtcgt ctgaagttgc tcagagcttc gataatctat 300

ttcgagcgtt tcgatatatt acgggactca atc 333

<210> 2123
<211> 378
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2123

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ctccaacaac agattatcct ttggggagtt ctacaagctc ccatacatca ttattctgaa 120

actggtctag ctcttcttgc attggtttga cccaatatta atcagacatg gnatcatcta 180

tgtgtttttg ctcaatctca tataagaatg atgtgttctt aagagagttc cttctctgta 240

cttatgccat aggatcacat atgatctacg ctctagatgt tgtttcctca acaggcatac 300

agttggttct ctggcctctt caggttggtt gtccactggt gagttagacg caagttggtt 360

ctgactcgac acaacagt 378

<210> 2124
<211> 319
<212> DNA
<213> Glycine max

<400> 2124

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cttcatgatc ccgactcgtt ggtggaggat gcatgaatga caatcaattc atggggctcc 120

gaataaaagt ggagattgga ggataggcga atagcgctag gcaatcaatt cgcggtgttt 180

ccgactcgtt ggtggaggat gaatgaatga caatcaactc atggggcttc gaataaaagt 240

ggagaatgga ggataggaga atagcgctag gcaatcaatt cgcggtgctg cagactcgat 300

ggtggaggat gcatgaatg 319

<210> 2125
<211> 340
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2125

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aaagttattg tcgtttgaat ttgctgagag cttcaacatt caattttgag cgtctcgatg 120

tattacggga cttaatcaga catccgagtt aaaagttatt gttgtttgaa tttgctgaga 180

gcttcaacat tcaatttcga gcgtctcgat attttacggg actcaatcag acatccgagt 240

taaaagttat tgttgtttga atttgctgag agcttcaaca ttcaatttcg agcgtctcga 300

tgttttacgg gactcaatca gacatccgag taaaaagtta 340

<210> 2126
<211> 470
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2126

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ggtacaaggt ttatagtgtg acagcaggaa catctcacac ttgtagcacc acgtgtgtac 120

attagcaatg tcgtacagcc tccacaataa agttgtgaca tgtccattcc tgcacgggca 180

acatgaaatt aaagggttcc ccagatgtaa ccatttagtt aaagtccaat acatgttaat 240

gaatacttaa tcaagctgaa tgcatagttt cttatcagat tatctctgtc tccagctctc 300

tccacacaca cacacacaga gtatctttta aaataatatg ccaatgttag ctacacacac 360

aatttcttga ttctttttat cttaataaaa gcatatagct aacatttcta ttgatctttc 420

atcatcattg atcttcaatc tcttgaagaa tctattanac aagcataatc 470

<210> 2127
<211> 472
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2127

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ttgctgatgg cttcttcccg ttccaagctt caattggagt cttgtctttt acagacttag 120

ttggacatct gttgagtatg taaacagcag tgtagactgc ttcagcccag aatttgttag 180

gtagtccctt ctccttgagc atcgatctag ctatttccat aactgtgcga ttctttctct 240

cggacactct attntgttga ggagaatatg agactgtaag ttgtcgctca atgccttcat 300

cctcacaaaa tcttttaaac tcgcgagagg tgtactttnt gccgcgatca cttcttagta 360

cttttatccg ttttccactt tgattntcag caagggcctt gaactntntg aatactccac 420

agacttctga ttttatttaa aanatatacc atgtcatcta gagaagcatc at 472

<210> 2128
<211> 414
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2128

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acttctttga gaagcttgat gcaatccttc ctacgaaggg accaatcact agaaccagga 120

gcaagaggct ccaagaagat tgggctagag ctgctgaaga aggccctagg gttctcatga 180

aattcagggt agatttctga gcccatgagc caaggttgag tccaattatc tntgtacata 240

ttagactacg atgtcattat atttggtcct tatatttagg gcttcatatt gtaggtaggg 300

taccctagaa atataggatt ttttcagccc ttgtatttta nggcacctag actagttntt 360

gtattaaggg tagtcttgta atttcacatg cactaagtgg atatttgatg tgtg 414

<210> 2129
<211> 463
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2129

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tggattaatt attgtgatgt aaatttcaaa attaaaaatg aagtgaatta ctcatagaat 120

tagaattggt agaatcatta aaagacgatc cttttatcaa gaaacctcaa tttcaactca 180

tttttattta ttggctgata tcttataaac taataaagca aatctataca cctataaaaa 240

aaattgcagc tccaatgata atagctggag agactcggtc atatgcattt gcaatatacg 300

caacaagaaa tgccaataat cctgccaaca gtgtcccgaa tcctctgttg agccctttgc 360

ataaagttac ccctagaacc aaaagaaatt aaaaaaatat taagatcatg cacaaataac 420

atgcnacaga aacacattat ntaacatagg aatatagaaa tat 463

<210> 2130
<211> 282
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2130

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acacttgcac agtggccaaa gatgcatggg agatcctgaa aaccactcat gaaggaacct 120

ccaaagtgaa gatgtccaga ttgcaacttg tggctacaaa attctaaaat ctgaagatga 180

aggaggaaga atgtattcat gacttccaca tgaacattct tgaaattgcc aatgcttgca 240

ctgccttggg agagaagatg acagatgana agctggtgag aa 282

<210> 2131
<211> 453
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2131

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gaaggccttg atatgacttt ctaggtctaa tattaaaaag tgtgaaataa atatgatgct 120

tatttttatt gatctatata ttattcttgt gtaatgtcta agattattat cctttcaatc 180

gtaaaggaag aaaaaattaa gaggaagacc aggcagcatc ccaatgagca atcccacatt 240

ntgattgagg ttgatttact tgctaatatt gttgacataa ggctttggca agctcaagaa 300

attatagaat tgctcaaacc tacggtaagt tccttcacac catgtcttaa tcttctgtcc 360

tgtgggttat gttgtgtgaa tcgactgcta tcgagggtta ctttcatctc tggtcagtat 420

tattaagttt gtgatcccta acagtgatac ata 453

<210> 2132
<211> 463
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2132

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tgtataagct gtaatcaaat agaanattcc tttccaatca tcaagattag tatccaaaga 120

anaaaaaaac atgaaaaaaa aggaaattct gatttaatat acaagcactg gccactcagt 180

catgtaccag cattgggcag ggctgccata aaggaattgt aagaagactc aagatcaaag 240

tgaagctgcc tcgcctgttg ttccgtcaac tcatcagctg cacccatctt agataacctt 300

gcaatccatt ccttcattnt ggttntcccc tcaaaatcag gcggcaggaa tgtcaactta 360

ttaagcgaag cataaaggtc cgagagcaat gggtgcacct gatccacagc caccatgtta 420

agtttcaagg aatccattga agtaataaaa ttctgaacac act 463

<210> 2133
<211> 421
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2133

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tatttgatca aataaagagt acactagatg aatttctcaa taaatattta taggagaaaa 120

aaataataag gtaaaatgaa ttaaatntct ttgtcttcaa ctaacacagc taatttaact 180

cataagtact tactgagaag tttatccaaa taaggtctaa agcttaatca gataccgaaa 240

cgggtatgga gggagtaaaa ntaattttaa caaaaagagt gtgacaaaaa acaatgaaat 300

gaaagagtac ttcgaaattg gtcttctaca ggtgtactga tggcccatcc attattacga 360

cagataanaa caacaggggg cctcatgact gctgcaaaat tcatagcagc atgaaaaatc 420

t 421

<210> 2134
<211> 458
<212> DNA
<213> Glycine max

<400> 2134

cggaagctct cgagaaaatc gagtggtcat atattttcac acagttgttc gattctgcga 60

aataatatat cgagacgcac gacattgaac aacggaagct ctcgagaaat ctgaatggtc 120

ataacatttc actcggatgt tcgatccggg gacataactt atcgagacgc tcgaaattga 180

acaaccgaag ctctcgacaa attagaatgg tcgtaactct tcacgcgaat gttcgattcg 240

gggacataac tcatctagac gctcgaaatt gaacaacgga agctctcgag aaatttgaat 300

ggtcataagt tttcacacgg atgttcgatt cgggaacata atatatcaag acactcgaaa 360

ttgaacaacg gaagctctcg agaaaatcga atggtcataa cgttccacac agatgtccga 420

ttcagggaca taactcatct agacactcga aattgaac 458

<210> 2135
<211> 392
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2135

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cagcggaatg gagaaggagg aaaggtgatt agagatgtca cttcaaggaa aaaatgagtc 120

aaaatcaagt tcaccaccat aggaagccat ggataagagc tagaaagtat ggaaagatga 180

gtggagggag agggagaaaa aagagggtac cttagtaatg taggattttt cagcccttgt 240

attttangac acttatanct agttttgtat taagaaataa tttataattt cacatgcatt 300

aaatgtatta tttgatgtgt gtatgttggt agataaaatt aattgaatta gaagaagcac 360

aatgcacatg atgtactacc atgtgagatg tg 392

<210> 2136
<211> 381
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2136

agcttgagaa tggagaatng cactaagcaa tcactacgca tagttccaaa ctcgaaggtg 60

gaggacacat gaacgaaaac acaattcatg gggctccgaa naaggggttg agaatggaga 120

attacactaa gcaatcacta cgcatagctc caaactcgaa ggtggaggac acatgaacga 180

taacgcaatt catggtgctc cgaaaagatt gagaatggag aattgcacta cgcaatcact 240

acgcatagct ccaaacgcga aggtggagga cacatgaatg aaaacgcaat tcatggcgct 300

ccgaaaagaa tgagaatgga gaattgcact aagcaatcac tacgcatagc tccaaactcg 360

aaggtggagg acacatgaat g 381

<210> 2137
<211> 424

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2137

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catatacatc cttcaatgtt tgaatggctt tttggccttc tggggtctcc ctgcctccaa 120

tgaggacacg gtccggattg aaaagatctt ggattgcagt tccctcagca aggaattcag 180

ggtttgaaag gatttggaac ttgattccct tgccattgtg agtcaaaatt ttctctatgg 240

cctcagcagt tttcacaggg acagtggatt tctccaccac aatcttgtca ctcttggata 300

catcagcaat catgcgtgct gcactctccc agtacgttaa atccgcggcc ttaccggctc 360

caagaccgcg agtttttgtc ggggtgttga cagagacaaa cactatgtct gcctcataga 420

catg 424

<210> 2138
<211> 413
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2138

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cccacaaaat catataagca taattagatg caacaactca ctcatctcca atcttcatat 120

gattgcacca aatgaaagcc caaacactga tgagaatgtt atctcacatt catccaacat 180

ttccataaag aactccaaga tggaaattgg taaatcatat ataagttaca atctttaatt 240

gcataattat tatatcttgt ccttaaatca ttcaatgaga atgcatagcc ctttaattcc 300

tagttntttt tataaggcta ctcaagtggt agatcctctc ttnaattttt tattaaaaaa 360

tatgtgatgg taaatattca ttttctcatt aagttgcaat cttatgtata aaa 413

<210> 2139
<211> 455
<212> DNA
<213> Glycine max

<400> 2139

tcatgtcaaa gagagaacgt ttttctctgt ccaaaagcac tctttgagct ttctccaatc 60

aacttaaatg cagcttctgc accagcaaag ttgtttttgt caggatgaag ttggagagca 120

aacttgctat attgcttctt aattattgca tcaccagctg tctgttcgac ctgaagaatt 180

tcataccaat ccatctcatt accatacaat ttctgctcag cagagcagtg cacatcacaa 240

acaacaagca tttgagctat attttccaga tcaaggtaca gctgctgagc ctttagagca 300

actttgcgag ccccaacaaa atccctgttt tccatcttct tttcagaatg tccttggccc 360

ttaaggcctc ttctttattg cagtccatca aagatccaga tgggaaaata ttatagtgga 420

tgctatggcc aagtgaagct acatttaatc caaca 455

<210> 2140
<211> 378
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2140

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aattagggat caacttgaaa cttatgtgct tcacgtgaga agaaatgctt ctttttccac 120

ttgtgaagat gttcaaagtt tggctatgaa gatggttcaa actgagaaac atttggtatt 180

tccattggtt tataaactta ttgagctagc tttgatattg ccggtgtcga cagcatccgt 240

tgaaagagct ttttcagcaa tgaagattat caagtctaaa ttgcgcaata agatcaacga 300

tgtgtggttc aatgacttga tggtatgtta caccgagcgg gagatattca agtcacttga 360

tgatatngat attattcg 378

<210> 2141
<211> 450
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2141

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gtatttaatg atccttttaa cggctgttaa gtgagattcc tttggattgg ccatatatct 120

tgcacacaag caaacactta gcatgatatc cggtctactt gcagttaggt agagaagtaa 180

tccaatcata cctctatatc ttaactcatc cactgattta cctttctcat ctaagtcaag 240

gtaggttgaa gttgcattgg agtatatgct tctttgcatt tttccataca gaatttctta 300

attagttata tacaataatt ggttcgacta aggaaggttc cattctttat ctgcttgacc 360

tggagtcaaa gaaagaagtt caattctcta atcatataca tctcanattc tttctacata 420

caacttgaaa attccttaca caaaatttca 450

<210> 2142
<211> 445
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2142

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tacattcact aggaaaacat tgtagtggaa ggaaattgta gcactgtgat tcaaaagatc 120

cttccaccta agcataaaga ccctgagagt gtaactattc cttgttcaat tggagaagtc 180

actgtgggaa aggctcttat tgacttanga gccagtataa atntaatgtc actctccatg 240

tgtagaaggt tgggagagtt ggagataatg cccactaaaa tgactttaca aatggttgac 300

cgctctatta ccagaccata tggagtaatt gaagatgtgc tggtcagagt gaaacatttt 360

atcttcctga cagacttcgt ggtaatggat atctgtgaag atactgacat tcctgtaata 420

ttgggaaggg cattcatgtt aactg 445

<210> 2143
<211> 432
<212> DNA
<213> Glycine max

<400> 2143

agcttcttag tttcagatga tgcagatggg tttgttttac ctcatgcact cctctaatga 60

ctatggcatc atttctggcg ctaaactgct gggagttgga ggccatcttc tcaattaaat 120

ttctggcttc aacaagagtc atgtctccaa aggctccacc actggcagca tctatcatac 180

ttctctccat attactgagt ccttcataaa aatgttggaa aagaagctgt tctgaaatct 240

gatggtgagg gcaactggca catagtttct taaatcgctc ccagtactca tacaggctct 300

ctccactgag ttgtctaata cctgagatat ctttcctgat ggctgtggtc ctggaagcac 360

ggaaaaaaat ttctaaaaat actctcttag ggtcatccca gctcgtgatg gaccttggag 420

caaggtaata ca 432

<210> 2144
<211> 453
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2144

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gacagcctca gtaattgcta ccatatcctc atctgcaatc atgtaaagag atcctcgctt 120

ctttccacga gccacaatga gattgccttt tgttaccttc caagctccat ctccaaaagg 180

ggtgtaatgt ccctcatcat ccaactgccc tatagatatt aaatttctct ttaaggcagg 240

aatatgtctg acattgtgca atgtccatag ggatccacta gaggtcttaa tgttgatatc 300

acctcttccg acaatgtcaa gagattttcc atctgcaagg taaacttttt caaatcttcc 360

agaaacatag ttagacaata aatctttaga gggagtagtg tggaacgacg cacctgagtc 420

catgatccat gaatcaacag gactatccaa act 453

<210> 2145
<211> 452
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2145

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atgcgttgag gcgcatctct ttaagttcct gtagctttac cttcctcctc tctctacatg 120

ttgtagagtc aaagttgagg aacttcatgg cccaataagc ttttatttct aactaccctt 180

gtaggtggca tgcttttccg tacaccattt gaaacggnga gaggccaatg ggtggtttga 240

aggttgtttt atatgcccat aggcaatcat caagctttgc agcccaatcc ttccttgaag 300

tagctacggt cttttctagt atcctcttga tcctccctat ttgaaacttc atcttattca 360

tatgtttgtg aataataggg tgatactact ttatgttgaa cattatagta ttggaggacc 420

tttgagagtt gagcattaca aaagtgtgta cc 452

<210> 2146
<211> 255
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2146

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catcttgctc cttcaagccc ttctctacga tatcccacac atcttgagct cctagtagcg 120

ccttcatctt gatactccca attatcatag ttgtctttgt gagcatcggc atttggaaag 180

gaaaaccttc attcgccatc ttttgaggat ctttgagctc tgataccact tntgtggaaa 240

taaggctttt tatgt 255

<210> 2147
<211> 430
<212> DNA
<213> Glycine max

<400> 2147

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gcagaacaat tatgacctct ccagcaatag atacaacctt ggatggagga atcaccctaa 120

tctcagatgg tctagccctc aacaacaaca acagcaacct gctcctttct tccaaaatgt 180

tgctggccca agcagaccat acattcctcc accaatccaa caacagcaac aaccccagaa 240

acaacaaaca gttgaggctc ctccgcaacc ttccctcgaa gaacttgtga ggcaaatgac 300

tatgcagaac atgcagtttt aacaagagac cagagcctcc attcagagct taactaatca 360

gatgggacaa ttggctacac aattaaatca acaacagtcc tagaattctg acaagctgcc 420

ttctcaagct 430

<210> 2148
<211> 375
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2148

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agtttcccac acctaaagta attcaaggta gtacattaaa agcatattcc tgatcctagc 120

aatatttata ttcataaata aacatggtaa gctgatacat cttttgaaat gttttttatt 180

tggaacagtg aatctgtctg gatggatgac tgatgaagag tttgcaagag agatgattgc 240

tggagtaaat ccacacatta ttaagaaact tgaggtaaat ttactattga actgttaagt 300

acataacact antaaacatt tatccacttg ttaaatttgc agttgataac cttaactcat 360

tgcaaattat attta 375

<210> 2149
<211> 379
<212> DNA
<213> Glycine max

<400> 2149

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ggtgtcgata aattcaaatg gtcataactt tgtcaacgga tgtccgatta tgcacataat 120

atatccagat gctcgaaact aaacatcgac agctctcgag acatacaatg gtcataactt 180

ttcacacgga agtccgattc aggcgcataa tatatcgaga agcttgaaat tgaacaacgg 240

aagctctcga gaaactcaaa tggtcataac ttatcacacg gacgtctgat tcaggcgctt 300

aatatatcga gacgctcgat attgaacaac gcatggtgcc gagaaattca aatggtcata 360

acttgtcaca cagatgtct 379

<210> 2150
<211> 340
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2150

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gaagtccgat tcagacgcat aatatatcga gaagcttgaa aatgaacaat ggaagctgtc 120

gagaaattaa atggtcataa cttgttacac cgaagtccga ttcaggcgca tactatattg 180

agacgctcga aattgaacaa cggangctct tgaaatatta aatggtcata acttattaca 240

cgggagtccg attcgacgca tatatattga gaccttgaaa ttgaacaacg aatgctctcg 300

agaaattcaa atggtcataa cttttcaaac ggaagtccga 340

<210> 2151
<211> 469
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2151

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gagatgcagc ggaagataaa ggagaagatg tgagatgatg tagcttcatg tagagcttgt 120

aggccttaga tcttcttcat caatagagac ttttgcttct tgaagatcaa tggcagcgga 180

atggagaagg aggaaaggtg attgtagacg ccacttcaag gagaaaatga gtcaagaaca 240

agctcaccac catatgaagc catggataag agcttgaagg tangagaaga tgagtggagg 300

gagagaggga gaangggcat ganatgtatg cctcaaatga ggtttgaaca ttgaagtgta 360

atttctcaaa tgttcanagt tgaaaaaata cacacacaaa agcttctatt tatagcctaa 420

gtgcacacaa aattggaggg aagattgaat ttctattcaa cttcacttg 469

<210> 2152
<211> 421
<212> DNA
<213> Glycine max

<400> 2152

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tcaaaagtta ttgcggtttg aatttgatgt gagactccgt tttcaatttg tagcgtctga 120

atatattatg ggactcaatc agacatctga cttgaaagtt tttgcggttt taatttctag 180

gggcatctgc tctgaatttc gaatgtctcg atacattatg ggactcaatc ggacatccga 240

gtaaaaagtt attgtcgttt gaatttgcta cgagattctg ttttaaaaat ggagcatctc 300

gatgtattac gggactcaat tggacatacg agtaaaatgt tattgttgtt tgaatttgcc 360

cagagctctc gttctcaatt tggagcgtct cgatatatta ccggactcag ttggacatcc 420

g 421

<210> 2153
<211> 446
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 2153

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taggctttta tttttctttt tattactaat tatagggatg caatctttgt tttgtaaagc 120

cataagtcca cttgtatgtt cttcagttaa ttttggaatt atgctttttt caaaattttc 180

gtaaagaaaa tctacagttt tttctatttg gtttagtctg atttccaaag tggaaatcct 240

attgttcata attttatttc catgatcatt ttctttctta aagtctggaa attctatttt 300

cagaatagtt tgtacactag ttntgcagaa attcttatag cataaactac agtgagctct 360

tagtgttttg tgtggatatc ttttacagaa ataacattct ttgtgatctg gtcctatgtg 420

gaattgtatt tcatgttcat ggtcat 446

<210> 2154
<211> 472
<212> DNA
<213> Glycine max

<400> 2154

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tctaatgact atagcatcat ttctggcact aaactgctgg gagttggaag ccatcttctt 120

aattaaattt ttggcttcag caggagtcat gtctccaagg gctccaccac tggcagcatc 180

tatcatactt ctctccatat tactgagtcc ttcataaaaa tattggagaa gcagctgctc 240

tgaaatctga tggtgagggc aactggcaca tagtttttta aatctctcct agtattcata 300

caagctctct ccattgagtt gtctaatacc tgagatatcc tttctgatgg atgtggtcct 360

ggaagcaagg aaaatgtttt ctaagaatac tctcttcagg tcatcctagc tcgtgatgga 420

ccgtggagca aggtaataca accagtcctt tgccactccc tctaaagaat at 472

<210> 2155
<211> 458
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2155

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ntcccattcg tcaatcctcc taccatgtaa gtaagatcca agaacttcaa gagctagtag 120

tagtcctcca caataagcaa ctacatttct tgcaagttca ttgaagtctt cttttggatt 180

tggttctcca aaagcgtgaa aacaaaaaag ctcaagagac tcattttcgt ccatttcctc 240

catttcataa acataatcaa ctntaaatag gttcagtaca cctgcatctc ttgttgtaat 300

gattattaca gatccttgac cgaaccattc acaatttcca cataaatctt ctaattggcg 360

aatctccttc acatcatcaa gtacaatgag caccctttt cctgaaagtc tattctctat 420

catagttggt cccatcccaa tgctatgtat cttgacct 458

<210> 2156
<211> 458
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2156

tttgagcaat tcaaatggtc ataaatagtc actcggaggt cttattcang cacataattt 60

atcgagacgc tctaaattga acaacggaag ctctcagaaa atttaaatgc tcataacttt 120

taactcggag gtccgattca tgcggataat atatcgagac gctccaaatt gaacaatgga 180

agcttttgag caattcaaat ggtcataaat agtcactcgg aggtccgatt caggcgcata 240

atttatcgag acgctctaaa ttgaacaacg gaagctctca gaaaattcaa atgctcataa 300

cttttaactc ggaggtccga ttcaggcgga taatatatcg agacgctcca aattgaacaa 360

tggaagctgt tgagcaattc atatggtcat aactattcac tcggaggtcc gattcaggcg 420

cataatttat cgagacgctc gaaattgaca acggaagc 458

<210> 2157
<211> 397
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2157

ctaagctgaa tagacattcg tgtgaaagta tgacatttga tttttcgaga gtttccgatg 60

tttaatttcg agcgcatcga tatattataa gcctgaatcg gacatccgtg tgaaaagtta 120

tgaccatttg aattttagag agttcccgat gttgaatttc gagtgtatcg atatattata 180

cacctgaatc ggaccttagt ggtaaaagtt atgaccatcn tgaattcacg agaagctttg 240

ttgttcaatt tcgagtgtca ctatatgtga tgcgccaaaa ttggacattc gagttaaatg 300

ttatgagcat ttgaatttct caagagcttc caatgttcaa ttctgagcgt ttcgatatgt 360

gatttgcctg aatcggacat ccgtgtcaaa agttatg 397

<210> 2158
<211> 341
<212> DNA
<213> Glycine max

<400> 2158

agcttcaacc tagaggagac ggaccattcc aagtgttgga gaatatcaac gacaatgcct 60

acaagattga cttgcctagt gagtataatg taagtgccac tttcaatgtg tctgatctat 120

ctctttttga tgcagatgga ggagccttgg atttgaggac aaatcctttt caagaaggag 180

ggagtgatga agacataacc aagggcaagg accatgaagc acttgaaggt tccatgacca 240

gaggcagact taaacaagcc caacacgtta tagagacaac gctggtcatt tgtatagctg 300

ccattgatga tgattgaagg cccaagtgga gaaagatgaa t 341

<210> 2159
<211> 462
<212> DNA
<213> Glycine max

<400> 2159

gtcttatttc agcagatgaa gatgaatcca tggccacatc atggactcct ctaaggacaa 60

tagcatcatt tcttgcactg aattgttggg agttggaagc catcttctca atcagattcc 120

tagcctcaac aggagtcata tcaccaagag ctccaccact ggcagcatca atcatactcc 180

tctccaggtt gctaagtccc tcatagaaat attgcagaag gagttgctca gaaatctggt 240

ggtgaggaca gcttgcacac aatttcttga atctttccca ttactcatac aagctctctc 300

cactaagttt ccagatgcct gaaatgtctt ttctgatggc agtggtccta gatgcaagga 360

agaatttctc caagaacaca ctcttaaggt catcccagct ggaaatggac ctcagagcaa 420

ggtagtacaa ccaatccttc gccactccct ccagagtata aa 462

<210> 2160
<211> 456
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2160

agcttctaaa ctntatacaa gaatgaagct ctgataccac ttgttagaca tgtggcctca 60

gatatcttaa gaaggggggt tgaattaaga tattacaaac tgtttcccca attaaaaatt 120

ctactttgat tctaatgcaa gttccaagtt cccttaaaga tgaatttcta aatgatgatt 180

caaattaaac aatctgaatg taactgttaa gcaacaataa ataaaagagt ttaagggaag 240

agaaagtgta aacacagttt ttatacaggt tcggcaaagt ccgttgccta cgtccgatcc 300

ccaagaaagc cgcttgggag ttccactatc tcgtaatcct ttacaccttc tgaaacacac 360

aaggacatcc cttcctttgt gttcagatgc tttacaacaa gagactctca gtctcttagc 420

cctttgatca gaaagagagg aagaagaaat gatctt 456

<210> 2161
<211> 452
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2161

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ttatgaggtg acgtttggaa gaaagccatt taactttcca gagtatatca aaggaacatc 120

taacatcgaa gcattgaatg cttattgact gacaaagatg ccactttcca aacgattcgc 180

aaaaagcttc ttaaagcaca ggaagctatg aaaaagtagg ccgatagcaa gaggcgcaac 240

aggcaatacc agataggtga ttgggtcttg ctccggcttc gtcctctcca ccagacatca 300

gccaaagggc ctcaaatagc ttctggtaaa ctcgcaaaac gattctatgg acccttccag 360

gtaatagatc gcattggcat tatggcctac aaactgaaat tgccggagac agctaanatc 420

caccctgtgt tccattgctc taaacttaaa cc 452

<210> 2162
<211> 411
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 2162

agaagtagta tatttcacct tcaaaccaat tcaatcaact atcaaatatg anattacaac 60

acataaaggc gccaatgaac cgaatagcac tcaaaaaaga gtacatcgca tgctaaacgt 120

gacttacagg aaacgcatta tagaccatgt gatgctcaat atcaagcagc tccccagtct 180

ccaaacacga aggtctgtga actggaaagc tagttttgag aaactgttcc aatcgatgcg 240

catcgatgtt tgatctgtag cctccgtctc actaaaacca atcagaacca cgttcacttc 300

aagcggaact cgaaacggga cctacacgaa ccacagacta aagcattcac acttaatata 360

acacatcaat taattggata gcgaatgtga atttgatttt tgtggtgacc a 411

<210> 2163
<211> 448
<212> DNA
<213> Glycine max

<400> 2163

agcttagaaa gacaatactt cattcatgac atcaaataaa ctttaaagtc atccgcaata 60

ttcaaataaa acatatatga attattggaa aagataaaac acaatgccaa atgtgagtgc 120

ataccactag tcatatatca ttaaagtaat taagtttaag acacataatc atgaacaacc 180

tagagcacgt caatataatc ataatgttca gtcatactaa gcaagtgtta aaagaaatac 240

taagtattca aatgtcataa aaacatagtc aaagacaagg cttaaaaaca aaatataatt 300

ataatctaaa tatattatca gagaatctaa gcttaggttt aagtaacaaa aattagttat 360

gaacacatac atggtgactc attacttatc ttgattaatt aaccactaga ttttaagtat 420

gatataacaa tcatgaacac atatcata 448

<210> 2164
<211> 455
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2164

ntggaagcaa tcttgtattg gtgcttcctt catcattcct gtttatgcct tcagcaacca 60

agtcaaacag tagggggcc aaaggatccc tttgtctcaa acctctttga ggcttaaatt 120

cagaggttgg gcttccattc actagaatag atatagaggc tgatgtgagg caccccttat 180

tccatccaat ccatatatca tggaacccca ttcttctcat catataaaan aggaattgtc 240

aagacattga atcataggct ttttcgaaat ccactttata aagacacacc cacacacaca 300

cacacacatt tcctctcaac taccttattt gcaaccagaa caccatggag ctactgtcta 360

cccttcacac agacacaccc acacacacac acattcacgt tgggacacac ccactcatac 420

tcacacacac acactcactc ggacacacac gcaca 455

<210> 2165
<211> 448
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2165

agcttcaaga aaaagatggc ctcagcaaat tccttatttc cagaagggaa ttctatcaat 60

agacctccaa tctttaatgg agagggttac cactactgga aaacccgaat gcaaattttt 120

atcgaggcaa tagatctaaa tatctgggaa gccattgaaa tagggcctta tatacccacc 180

acagtagaaa gaagttcaat agatggtagt tcatcaagtg aaagcataac catagaaaaa 240

cctagagata gatggtctga agaggataga aaacgagtac aatacaacct aaaagccaaa 300

aacataataa catctgccct aggaatggat gaatatttca gagtttcaaa ttgcaagagt 360

gctaaggaaa tgtgggacac tcttcgataa cacatgaagg aactacagat gttaaaagat 420

ctangataaa tgcactaact catgagta 448

<210> 2166
<211> 435
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2166

agcttgcctt gccccttgat atatttaagg gactcatgga cactatgaat gaaaaattcc 60

ttgggataaa ggtagtgttg tcatgtattc aaagcccgca ctaaggcata caactcctta 120

tcataagttg aatagttaag ggtacaacca cttatctttt cactaaaata agcaattgga 180

tggccttctt gcatcaacac agccccaatc ccaacatttg aagcatcaca ctcaatttca 240

atagattttt gaaagtttgg caacgcacgt atgggggcat tacttagctt ttgcttaaga 300

acattgaaag cttcttcttg tttctctccc cattcgaaac caacatttct cttgagcact 360

tcatttagag gtgctgccaa tgtgctataa ttcttcacaa atcgttataa aaacttgctn 420

accatgaaac tctca 435

<210> 2167
<211> 430
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2167

agctntatgn gatgtaaaga cctgcaactt ctctattgat catgctggag aaggaaatga 60

agtgcaacta agtgagctag atgagatccg tttacaagcc tatgagaatt ccaaattcta 120

caaggagaag accaagaagt tccatgaaaa cttgatagct aaaaaggact ntgtggttgg 180

acagaaagtt ttattgtata actctaggct cggactcaag agtggtaagt tgaggtcaaa 240

gtggattggt ccttttgtgg tggctaatgt ttttccttat ggtacagttg agatcaaaag 300

tgaatccaca tataagagtt ncaaggtcaa tggacaccgg ctgaaaccat tcctcataaa 360

tcccttctta gcggatgtag tggtggagga gaccctctta cttcacccta cttctcttcc 420

gccatgactt 430

<210> 2168
<211> 306
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2168

agcttgtagg gttaaagtct cacgattgtc atgtgttgat gtaacatctt gccaaacaaa 60

gtcaggttag ccataactcg cctgtgcttt ttcttccatg ccatatatag caaagtcgtt 120

gatcctgtca agtatgatga gctggaaaat gaggccgaaa ttatactatg ccagttggag 180

atgtattttt cccctgctnt ctttgacatc atgattcact tgattatgga tctggtcaga 240

gaaatcaaat gttgtggtcc tgtttatctg tggtggatgt acccggctga gcaatacatg 300

aagatc 306

<210> 2169
<211> 455
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2169

ntacattact cctcatgctt ctcaccatgt ctaataaggg tttatttctt cgntctgcca 60

caccattctg atccggagaa ccaggcatag tgtattgggc aacaatccca tgttcttgaa 120

gaaattttgc aaatgaacct ggtgcttgtc catcctctgt gtatctacca tagtactccc 180

cacctctatc tgatctcacg atcttaattt gttttccaca ttgtttctca acttcagcct 240

taaaaacttt aaaggcatct aaagcttcat tcttagaatg aagtaagtag agatacatat 300

atcgtgaata atcatctata aaggttatga agtatttcgg actatttgca tccatgtctg 360

gacaacatat gtctgtatgt atgatttcta ataaattaga actcctcttt gcaccttctt 420

agacttgtta gtttgcttac ccttaatgca atcta 455

<210> 2170
<211> 462
<212> DNA
<213> Glycine max

<400> 2170

actaagcttg tgctgtgtac ttttactctc tcaactctca attactgggg cctttagctt 60

gcgtttgtgt ccttctatgc tatattatgc agtaaaaaga tttgagagat ttttcttaca 120

gtaaaacact aaaacattct gtacttcatg atatggtttt gaagttctga ggggacattt 180

tattttcctg tggtggtttg catcttttgc aagtatcaga taacactcct tgatggggtt 240

gggagtgttt ggttctgttc tggttttggc actcttattc aagcatttgg catctcaact 300

tccaaatact gatgagttct ctgtgtctga gttcttgaag aagatgatgg gtttagcatc 360

tttccaaggc tacaacttct ctgcttctgt ctgttcatgg aaaggggttt cttgtgatgc 420

caatagagaa catgttgctg acttagtctt ttctggtatg ga 462

<210> 2171
<211> 532

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2171

tcaggctgct caattgctcc aggttgctgc atggaagggc aaaggtctgt atggtggtca 60

tcagaggagc acaaaccaca aacccttgcg acaggtacaa atttctgatt caaggccagc 120

tgggttacca agttgaccaa cgcatccagt ttgccttcaa gcttcttagt ttcagatgat 180

gcagatgggt ttgtagctac ctcatgcact cctctaatga ctatggcatc atttctggca 240

ctaaactgct gggagttgga ggccatcttc tcaattaaat ttctggcttc agtaagagtc 300

atgtctccaa gggctccacc actggcagca tctatcatac ttctctccat attactgagt 360

ccttcataaa aatattggag aagaagttgt tctgaaatct gatggtgagg gcaactggca 420

catagtttct taaatctctc ccagtactca tacaagctct ctccactgag ttgtctaata 480

cctgagatat ccttcctgat ggctgtggtc cttgaaacan ggaaaaattt tt 532

<210> 2172
<211> 514
<212> DNA
<213> Glycine max

<400> 2172

agcttcacat ggagctatat catgtggtat caagagcaac ttcttctatg taatgttctt 60

ttgctttctc tatcttttgt tcagtcaatt cactttcatt ccttgttctt catcttattc 120

tccatgtatc tcttccattt tcttatggtt tggtgttttt tagagtggat ccaaaaaaat 180

aaatcgatta aatcttagat ctacacttgt tcttgcattt ctatggttca aattttataa 240

atctactctt gaatcatgtt tttgtgttga ttttaggttc tataattttt cagtcataat 300

cttcttgtac taaaccttta aatttcaatt ttcttgcaaa atattgatta gaaaagaaaa 360

cacaaaaatc taagtgtaaa tcacttaatc catgttgtct tagagtcatg tttagtcata 420

ataattgtca cattatgttc taagtttgcg ttcatttttt attttgttga ttgaattcta 480

gataccattt ttttatttat tcttgcaatt ctta 514

<210> 2173
<211> 317
<212> DNA

<213> Glycine max

<400> 2173

agcttgaaat tgaacaacgg aagctctcga gaaatttttt gtgttataaa tttacacaca 60

gatgctcgat ccggggaaat aatatattgg agacgcacga attgaacta cggatgctct 120

agacacaggt gaatggtgat aacatgtcac tcggatgggc gagactgtgc caatttctat 180

ccagacgctt gaagtcgaac aaccgattgt ctaaacatat tacaatggac gcaactgttt 240

acgcgaatgt tcgattgggg gacaaaactc atgctgacgc tcgaaatgga acaacggaag 300

ctctatagaa attcgaa 317

<210> 2174
<211> 537
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2174

gtttgatctt ctgattcacg tgcttaaaat gctctcgata cttttattct tcctctcaaa 60

ctctttgaac tcttccttgc acttcctcat atcattatct aactcctatt ttatgaaaat 120

gaaagaaaaa aacaatgact agattacttc ctcaaaagct tatcattaag aatcatatga 180

ccagcaatat aatcatgcaa actgattcaa ttagaaaacc cgtctcatcc aaacctcttg 240

tcttttcata tagttgttgg gcgcagtttc aagctctttg agagtttgtt cactatcttg 300

gattttatcc ctggaataag ataccaccat gttcttcgcg aggaaagaat tcaaattcac 360

caaataaaga aaaaaaaatt ccccattgaa atccaaatgt acctttctgc cttgagatnt 420

cttttagagt agcaacattc ccttgtaact cattcatttt tccacctgta tcatcaaggg 480

ccaactttgt agctttctgt gccatttaaa cagagacaac tccttaacat gtatgct 537

<210> 2175
<211> 500
<212> DNA
<213> Glycine max

<400> 2175

agcttgtagg gttaaagtct cacgattgtc atgtgttgat tcatcatctt gccaaacaaa 60

gtcaggttag ccataactcg cctgtgcttt ttcttccatg ccatatatag caaagtcgtt 120

gatcctgtca agtatgatga gctggaaaat gaggccgaaa ttatactatg ccagttggag 180

atgtattttt cccctgcttt ctttgacatc atgattcact tgattatgga tctggtcaga 240

gaaatcaaat gttgtggtcc tgtttatttg tggtggatgt acccggttga gcaatacatg 300

aagatcttaa aagggtatac aaagaatcct tatcatctag aagcatctat tgttgagagg 360

tacattgcaa aagaagtcat tgaattttgt tcagaataca ttgagaaggc taaacctatt 420

ggccttcctg agtctcggca tgatgacaaa gtgggtggta agggttcaag aagactgcat 480

gtgatcactc caagtctaaa 500

<210> 2176
<211> 475
<212> DNA
<213> Glycine max

<400> 2176

tccgactatg ctcttgtgtg gtggaacaag cttcataggt ttatacaaga aatgaagagc 60

ccatggttga tacatggacg gagatgaaaa agatcatgaa gaagcggtat gtgccggcta 120

gttactcaag ggacttgaaa ttcaagctcc aaaaactaac ccaaggcaac aaggggggttg 180

aggagtattt caaggaaatg gatgtgctca tgattcaagc aaatattgaa gaagatgagg 240

aggcaactat ggctcgattt cttaatggtt tgactaatga tatccatgat attgctgagc 300

tgcaggagtt tgttgaaatg gatgatttgc ttcacaagat gtccgattca gtagcataat 360

ataacgagac actctaaatt gaacaacgga tactctcgag aaattcaaat ggtaataact 420

tttaactcgg aagtccgatt catgcgcata atatatcgag acgcctgaaa ttgaa 475

<210> 2177
<211> 500
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2177

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aaagaaaact ttagattttt tgtattttag agcccggcca aatgcagctt cctaatcaca 120

aaagatattc ttcaaaataa cattatcttg caaattttct ctagaaaaca atcatccacg 180

aataataaat gcaaaatccc aggtgctttc ccacaaatct taatgccatg aatatccctc 240

ctattttcaa cccttctcaa taaagatgta agaccttgag ctaaaattat aaatataaaa 300

aagggagaag ggatctcctt gccagagatc tcccagggga gataggatca accttgtcat 360

gattcactac cactacatac taaacagttt tgacacacat catcatccac tcggtccatt 420

gattgcaaaa tcacaacttg acaaggattg catctagaaa ccccagtcaa cgaggtcata 480

ngccttacat atatcaatct 500

<210> 2178
<211> 529
<212> DNA
<213> Glycine max

<400> 2178

tgatggacga atggcctcac tccaagcaac aagaatgttc accgcaggag ctcctaagtt 60

aggctttaga atttcaaggg tgagaaaatt aggccttctt gatgaaaatg ctggtactac 120

aggagatggt ttgattccca accttgtgcc tttaaaagct agagttgcag tagaactttt 180

acttgatagg agataacttt tgagcttttt tccttctttc tctcctattt caactactag 240

aaggaggtga gaatctgcaa ccaattcttc tccattggct tccgtgtttg tgagaatcat 300

tcccacccct cctaaacttc tcaccacatc acccttttgc actctaggac taaggcttct 360

atcacaaatt actatctttc ctgacagcac tttaggatcc aaggtccctt ccaagcatat 420

agatcttgga tcaaccctac tagaattgct caccatgtac cacccaaggt attgtttctc 480

aattgatagc acatttttcc atttatagag tgaaactcca atcattttt 529

<210> 2179
<211> 515
<212> DNA
<213> Glycine max

<400> 2179

agcttgatag acctgtaatt cttacacttg ctgggttacc actctcaaca ttgggcaatg 60

cttgtccgta cttaggggct cgacaaaatt atcacccccc acctgtcaag gctaccaccc 120

cggacattag acaatcttca acgcaggaca atctcttttg cctgcaagtc ggctcagagc 180

ttggtgttag acaagtggcc tcagaaatct taagaagggg gggttgaatt aagattatgc 240

taactattcc cccaattaaa acctactcag atttttatgc aagttctaag tttcctttat 300

aacaaattac ttagatgatg aatcaaatga gcaaactgaa atgagactaa taaacaacag 360

taaatataag agataaaggg aagagagaat gcaaaaccaa atttatgctg cttcggtcac 420

acccttgtgc ctacgtccag tccccaagca acccgcttga gagttccact atctttgtac 480

attctttaca agtactgaac accacaagga ctttc 515

<210> 2180
<211> 364
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2180

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tcttaagaag ggggattgaa ttaagatatc acaaactatt ccctaattaa aaattctatt 120

ttgattttaa cccaaatccc aagattcctt ttaaaatgaa ttcctaaata attattcaaa 180

ttaaacttac tgaatagaag ccatatacaa taagaaataa aagagtttaa gggaagagaa 240

agtgcaaact caattttata ctggttcgac cacacccttg tgccttcgtc gagtccccaa 300

gcaacccgct tgagagtttc actagcttgg aaaaatcctt tacaagctct ttaccacaca 360

agga 364

<210> 2181
<211> 415
<212> DNA
<213> Glycine max

<400> 2181

agcttttggt acaatgaaga agaagaagtt caaagagatt ttatgcttgt aaaggattgt 60

aagagattga ttggaagagt attcaagatt gaatgaatta atagaaaatg caaaaacaaa 120

gtcttgcttt tatagactct tcatgtctgg tcaagaagac catttagaag agttataaca 180

tttagaaaag cttaaaacca atttgaaaaa gtcaaaaacc ttttgaagag ttacatcttt 240

tgatttattc agaaacagtc actggtaatc aattactaaa tcagtgtaat cgattacaca 300

aagcttttat gtgaaaagat gtgactcttc acatttgaat ttgaatttca acgttcaaag 360

gcactggtaa tcaattacca aaacattgta atcgattaca gctttttgaa attaa 415

<210> 2182
<211> 554
<212> DNA
<213> Glycine max

<400> 2182

gctgcatgca tgctatcttg ccattgatag gttcacgaat cttgggaaac catttacctc 60

aaatcctctg cctcacacct ccgaactcgc aatcggagtt atgaggccct ccctttcgta 120

tgatgcatcc ttttgtagaa cctttcgctt gaaccatgtg aatcactatc gccccatttt 180

gtgtacaacc aacttagggc tgcctgatgt acttcttcca ctttgtaaga gaggcctcca 240

cagaatcact ttcagcactg caacatttcc gcgatttcct gtttctgcgg ccattccgaa 300

accaacaaat aaacagaaac atgttgcgac tttgcactta ctttcttcaa taaaacgttg 360

gctaacgtct cagactcgac acaatcacat attgaaacat aacggaagca taacaaaacg 420

gagcttatgc agctaccaca aattgattat aacaaatagc gcgtgaattg agactataaa 480

gaatatttac attgtccttc aatcaatcat aaactatcct gtgtgacaat ccatgaaaaa 540

taaatttgac tgaa 554

<210> 2183
<211> 615
<212> DNA
<213> Glycine max

<400> 2183

tttatgagtg gccaatatac caaaatcaac atttttttaa ctaaagtttt tgttttattt 60

tctttttaat gtaaaaatgt gtaaaactag ttgacactcc tctgtaattg gtttggatag 120

gatgttaagt acatgtaagg actattagta gcaaaatttc atcttgttgt tcaagtctaa 180

attataagca atcataagtt tacaattatt caactagttt ttaagtgtta ggagaatcta 240

cgtgaaaaag atcatccaca tcaaataaaa ttttagtaac atcaaaagag aatcaaattt 300

atatccacaa aaaagataag agtcattttt agatttttat taatttgtat cgacctgtct 360

tgttataaaa atttaaaata gttctttttt taattatttt atacttaata gttcttatta 420

aaattaaaag atttatcata tagacagtat aataatttgt gaataaataa tataaaaaag 480

taaataaatt atataataat cataattata atatataata aacttattga attttaaata 540

attaaatatg cacactgaaa tttgattaat agtcaacata attctcatat acataaaatt 600

aaaaacataa aaaat 615

<210> 2184
<211> 605
<212> DNA
<213> Glycine max

<400> 2184

agcttcagga acacaaaatg gaactcatga gactaaatct tcatgaagaa aatgacaaga 60

aaaagaaagg aatgacactt aaagttttat cttcagttca agaagaaagt gataaagaag 120

acttgaatga agtagaagag atgatgattt cagtttcttc gtaaagagat taaataaatt 180

cctaagaaac aaagaaaatc aaagaagatc aaacttcaaa ccaaagaaaa gaggagagga 240

ttcatctttt gttccaaagt gttatgaatg taaccaacca ggacatctga gagttgatta 300

cccgagtttc aagaaaagaa tggaaagatc taagaggaaa actttcaatg ataagaaagc 360

aaataaagct tacatcactt gggaatataa caatatggat tcatccgaag actcagaaaa 420

tgaagtcatg aatctaagtc ttatggcaaa aaaatatgaa agcgaagaag aggtaacatc 480

ttctaacaat aacttatcta tttcctttga tgaacttcaa gatgcattca ctgatttaca 540

taaagaatca gtcaaacttg caaaacttgt ttcattttcc aagaaaacta ttttaaactt 600

agaaa 605

<210> 2185
<211> 467
<212> DNA
<213> Glycine max

<400> 2185

ctacctgcat gcatgcttca caattatgaa ctcgtagcta ctatagaatt ttcattatat 60

gattcattat agtttactgc tctatgtaca ttctttctaa ctatttctag cattttccc 120

ccgttcaaaa tcatcattcc tgttttgatg ctctacaaca tctcatgtta aagtctcttt 180

gaactatcca taacatatga tgatgtacaa ttcccccatc ccacgcaaag tcatctatta 240

taactttaga tgaactcatt gtcaatgacg taattgaaag tccatatttt ccatctctaa 300

tggatagaga acaacatatt aaaggcagtg gtgatcttcg tagctgctcc aacaacactg 360

aaactgacat tcctcctatt tctaatccaa gcattgataa agtaattaca tcaagtccag 420

atgcaagatt tgttaaaaaa aggcgacatc gttgcttgga ggtaaca 467

<210> 2186
<211> 509
<212> DNA
<213> Glycine max

<400> 2186

ggtcggattt atcgtgaggc tctttgatag aagtctgtca gtggggtcga tttttgagca 60

taacccaatc ccctatttgg taattaacgt cacagtgtcg agtatctgcg tgttgtttca 120

ttaaagcctg ggccttgatc agcttctttt agatgtagtt gaagttgtct tccctatggg 180

ccaatattgc atcgacgaca gcaacgtttg aagttcctat tccgggaaat taaaaggctt 240

atggacaaac attatttcat atggtgtagt gtcggtgccg acattccacg aggtattata 300

cgaacactcg acccaaggga gtaatttgtg ttatgtcccc ggtcatcggt gaacaaaagt 360

gcacagatac tgttcaacga cgcgattcag aactttggtt tggctgtcac tttgcagttg 420

ataagctgag ctcatccgca attttgtacc actcaatcaa aaaattcttg ccaaaagtga 480

ctgacaaaga gtaggtcaca aatcgagac 509

<210> 2187
<211> 563
<212> DNA
<213> Glycine max

<400> 2187

agctttgagg agcccgcaag gtaatctgga aaggagaatg ttttgtgtcc aaatattatc 60

tcgtaaggtg tggagcctgt gctactattc cacgaagtgt tatgggataa ctcaacccac 120

ggcaataact tgccccatgt ttctggccaa cgatgcacaa aggcacgcaa atattgttca 180

attaccctgt tcattacctc tacctgacca tcactctgag gatggtaggc agaactcatt 240

cgaagatgag tgccactcag tctaaagagc tctttctaga agccgctgat gaataaggga 300

tcatggactg aaactaagct tctgggaatg ccgtggagtt tgacaacaat gtcaatgaac 360

aacaaaggta ccatgtgagc tgtatgagcc tgaggtataa tgccgaagtg aatccccttt 420

gaaaagcggt caacaaccac aaggagtaca atcttgccct gaaaaaaagg aagaccaatg 480

acgaaatcaa gggagaggtc ctcccatggt ctgaatggaa ctggaagagg gcacaacaag 540

cccacaatat gtttcgtttc ata 563

<210> 2188
<211> 541
<212> DNA
<213> Glycine max

<400> 2188

agcttgtagg gttaaagtct cacgattgtc acgtgttgat gcaacaattg ttagccgtgg 60

ctatacgaga catcttgcca aacaaagtca ggttagccat aactcgcttg tgtttttct 120

tccatgtcat atgtaacaaa gtcgttgatc ctgtcaagct ttagtcaaac agaaaaatcc 180

aaaaatgtca aagaattggg tgttgaaaaa gcataacaag actttctgtg attggattaa 240

agatacaatc tttgcagatg aaaatgcttc agaaacatta agaaatctag tagatgggcc 300

taaaagaaat gttattactt ggcaaggata cgacataaac aagtattcat tttacacaag 360

agcacaagac gataaaagta caatgcacaa tagtggggtc accctaaggg ctgaatctca 420

acaacttgca agtgtgcatg atgtcaatcc ctatgtagct tccatccctt actttgggtt 480

cattcatgaa atttgggagc ttaactatgg gaaatctact gtttggcttt ccaaaggaaa 540

t 541

<210> 2189
<211> 551
<212> DNA
<213> Glycine max

<400> 2189

tgtagggtta aagtctcaca attgtcacgt gttaatgcaa caattgttag ccgtggctat 60

atgagacatc ttgcgaaaca aagtcaggtt agccatgact cgcctgtgct ttttcttcca 120

tgccatatgt agcaaagtcg ttgatcctgt caagtttgat gagcagtgaa atgaggctgc 180

aattatactg tgccagttgg agatgtattt tccccctgct ttctttgaca taatgattca 240

cttgattgtg cagtggatgt acccggttga gcgatacatg aagatcttaa aagggtatac 300

aaagaatcaa tatcgtctag aagcatctat tgttgagagg tacattgtag aagaagccat 360

tgaattttgt ttagaataca ttgagaaggc taaacctgtt gaccttcctg agtctcgaca 420

tgatgacgga gtgggtggta atggttcaag aggactgcat gtgatcactc caagtctaga 480

agatttgtta caagctcact tgtttgtctt gaacaacaat aatgaaagtt tgccatacat 540

acttaagcat g 551

<210> 2190
<211> 530
<212> DNA
<213> Glycine max

<400> 2190

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tgcatataga gctacagacg tgttgaaatt gatacataca aacatttgtg ggtcatttcg 120

tacaccttta tggaatggtc accaatattt tatatcattc atagacgatt actctagata 180

tgcatacctg tttcttatac atgaaaagtc acaatctctg gatgtgttca aaaaatttaa 240

agttgaagtt gaaaatcaaa tcaacaaaag aatcaagagt gtcagatctg accgtggtgg 300

agaatactat ggaagatatg atggttcagg tgaacagcgt ccggggcctt ttgccaagta 360

cctagaggaa tgtggaatcg tcccacagta caccatgttg gggtcaccta acatgaatga 420

tgtggttgaa aggcgaaaca aaactcttaa ggatatgata agaagaatga tttgtcattc 480

caacttacta gagtcactct ggggagagac actaaagact gtagcttaca 530

<210> 2191
<211> 554
<212> DNA
<213> Glycine max

<400> 2191

tgtagggtta aagtctcacg attgtcacgt actcatgcaa caattgttag ccgtggctat 60

acgagacatc ttgccaaaca aagtcaggtt agccataact cgcctgtgct ttttcttcca 120

tgctatatgt agcaaagtca ttgatcctgt caagtttgat gagttggaaa atgaggccgc 180

aattatactg tgctagttgg agatgtattt tccccctgct ttctttgaca tcatgattca 240

cttgattgtg catctagtca gagaaatcaa atgttgtggt cctgtttatc tacggtggat 300

gtacccagtt gagcgataca tgaagatctt aaaatggtat acaaagaatc tttatcgacc 360

agaagcatct attgttgaga ggtacattgc agaagaaacc attgaatttt gttcaaaata 420

cattgagaag gctaaacctg ttggccttcc tgagtctcag catgatgaca aagtgggagg 480

gaagggttca agatgactgc atgtgatcac tccaagtgta gaacattttg ttacaagctc 540

acttgtatgt cttg 554

<210> 2192
<211> 571
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2192

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gagaaatgta gaaaaatccc ctttgttgac tcttaaaagt gatttcagaa ggtaaggttc 120

ataaaatgag ttacaaaaga gaaaaaaaca agatatggta cttatagatt ttaactaata 180

taattgtaat aatcgattac caaaacttgt aattgattaa ttcaatcaaa tacccttagt 240

tttacatttc tagaattgtg ctaatcgatt atcttgatca agaaagaaca aacataactc 300

ttttagaagc aatgtaatca attatgatat ttgataatca attatttcaa cttccagaaa 360

gcttcctaaa tttttcaaag gcaatgtaat tgattacaag aaatgataat tgattatctt 420

gatgtacaaa gccttccttc ttcttgatta tcttgatttg caatatttat tggttgttag 480

gaaatgatgt aaacccattt gcacaagggt tgaggatgga tctttaaagg nttctttttt 540

tacttgtatg aaaatttaaa aatggaatgg a 571

<210> 2193
<211> 509
<212> DNA
<213> Glycine max

<400> 2193

agctttgatg gtgttgagaa gaaatcacat gtttgttatt tcaaaaaggg ggagaatgtg 60

aatgtatgta tacatgattt tgatgatgtc aaaagaagaa tcaaacaagg ctcattttgc 120

ttcaagatta atacaagatt gtttcaacaa acaaagcctt gattcaatat ttcttcaaga 180

tcaagccttg cctcaaagtg tagagatttc aagtcatcca aggcacatgt aatcgattac 240

caatacatgt aatcgattac caaggcacat gaaagtgtgt aattgattac acatcatatg 300

taatcgatta ccagagactc tgaacgttgg gaattcaaat tataactgtg taatcgatta 360

cacaaacatt gtaatcgatt accagttgaa agttttcaga aaatctgcca acagtcacat 420

cttttcatta gatttgtgaa tggccatcaa aggcctatta ataggtgact tgggcacgaa 480

ttttatgcag aaagttttgc ttgcaaaaa 509

<210> 2194
<211> 484
<212> DNA
<213> Glycine max

<400> 2194

ttgatagatt gcaagtgtat aattagttaa gaaaactata tgagggaagt tttacccaaa 60

tcatttttgt atggcaataa tgctgcagtc ctatgcttaa tctccttaca ctaatctcct 120

tacacctaaa catgtacata aaaaaatgat ttgatcaggt aaaaggagga acattgagag 180

cttctgattc attccctact ggtcgacatc tagttgagtt atgggctcca aattcccaaa 240

agcttccaaa aacatcagtt ttgaacagca taaaacttca gcaacctaat ggcatttact 300

atgaagacat aacatttagg gacatcctct ttgattctag ctacaagggt ggagggatat 360

tcattgttga ttctgttaga acaaggatca acaactgctt tttcttgcat ttcaccacag 420

aagggattct agtccaaagt ggccatgaga ccttcataac aagcagtttc ccttggcagc 480

actc 484

<210> 2195
<211> 498
<212> DNA
<213> Glycine max

<400> 2195

tgaatcggac atccgtgtga aaagttatga ccattttaat ttcccgagag cttccatttt 60

tcattttcga gcgtctctat atgtgaccga atcggatatc cttgtgtaaa gttatgacca 120

tttaaatttc gtgagagttt ccgatgttta attttgagcg tatcgatata ttataagcct 180

gaatcggaca tccgtgtgaa aagttatgac catttgaatt tctcaagagc tttcgttgtt 240

caatttcgag cttgtcgaca tattatgcgc tcgaatcgga catctgtgtg aaacgttatg 300

accatttgaa tttctagaga gtttccgatg tttaatttcg agcgtatcga tatattataa 360

acctgaatcg gacctcagtg tgaaaagtta tgactatttg catttcgcga gagtttccga 420

tgtttaattt tcagccgatc gatatattat tagcctgaat cggacattcg tgtgaaaagt 480

tatgaccatt tgaatttc 498

<210> 2196
<211> 485
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2196

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tgtacctgtc gcaagagtct gtggtttgtg ctcctctgca gaccaccata cagacctttg 120

cccttccatg tagcaacctg gagcaaatga gcagcccgaa gcttatgttg caaacattta 180

caatagacct cctcaacctc agcagcaaaa tcaaccacaa cagaacaatt atgacctctt 240

cagcaacaga tacaaccctg gatggaggaa tcaccctaat ctcagatggt ctagccctca 300

gcaacaacaa cagcagcctg ctccttcctt caaaaatgtt gttggcccaa gcataccata 360

catttctcca ccaatccaac aacagcaaca gccctagaaa cagccaacag ttgaggctcc 420

tccacaacct tccctcgaag aacttgtgag gcaaatgacc attcagaaca tgcaatntca 480

acaag 485

<210> 2197
<211> 470
<212> DNA
<213> Glycine max

<400> 2197

ttgtttaagt ctatgtagtc aatacacatt ttccacttcc cattagactt tttcaccatt 60

accacgttag ccaaccactt ggtatactac acctctctaa tgaaagcaac acttagtagt 120

ttctttgctt cttcatctac cgcctttcct ctctcaggtt gagcttcttc tttctttggg 180

caatgggttt agcctctggg cagctgaata acttgtgata gtggaaattt gagtcaattc 240

ctggcatatc tgatgcagac catgcaaata ggccgacgtt ggctggtatc actcaggcca 300

ctaactcttc tacttttta ctctcatcaa acacctaagt ttggttaact ctgagggatc 360

tttgtcgagt tggaatagtt tgacttcttt ttttggcttg gctctctgtt ctgcttctca 420

tggatcgagt tcagactcta ctaggctttt tattaagaga ggtgcatgct 470

<210> 2198
<211> 477
<212> DNA
<213> Glycine max

<400> 2198

tgagttgttg tgtgctgtaa aagatgttcc tctaatctaa cattctgtat taccacgtgt 60

tatctcacag actttgactg cagttatggt caaactaatc catggctctc tgcttctggg 120

tacagattac agattacacc tgtttctgtt ccttccatta attgctgaag ggctatttct 180

actcactaat ttcctttgat taagttttat aaatttgaat tttaacaatt aaatttaatg 240

tatttcgaaa tgagtacatt ttaataacaa taagaataat gatatattag taataaaatt 300

tcttaactta atattattta ttttcaaata tatatatata tatatatata tatatatata 360

tatatatata tatatatata taaaataaaa tatgtcatta gtttaatatt acctttttaaa 420

ttttataatg taagtatata ttggctaata taaaacgtta acgaaattaa ctaattt 477

<210> 2199
<211> 352
<212> DNA
<213> Glycine max

<400> 2199

agcttatcta ccttactata acaaggccat atattttctt ttgttttaga agggtgagtc 60

aattcatgca gactggtcat tgtgatcatt gggatgcaga aatccgaatt ttgagataca 120

ttacacggac cccaggaccg tgactactct atgaagacca aggaaacact cacatagttg 180

gattgtgcga tgctaattgg gaaggatcac ctattgatag gcgtactatt tcaggatcta 240

gtgtgaatat tgttagaaat atcgtttcct ggaagagtga aacacaaaca gttgttgcac 300

cgctatttca aaggctgaaa taaagctgag gctgaagcca catgtagagc cg 352

<210> 2200
<211> 472
<212> DNA
<213> Glycine max

<400> 2200

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caattcatgc agtctcctca taatgatcat tgggatgcag taattcgaat tttgagatac 120

attaaaagga ccccaggaca aggactactc tatgaagaca aaggaaacac tcaaatagtt 180

ggattttgcg atgcagattg ggtaggatca cctattgata ggcgttctat ttcaggatat 240

agtgtgtcta ttggaagaaa tcttgtctca tggaagagta agaagcaaaa tgttgttgca 300

aggtctagtt caaaggctga atataaagct atggctgtaa ccacatgtga gctgatttgg 360

attaaacaac ttcttcaaga attgaagttt ggaaatattc aacaaatgaa gctatgttgt 420

gataatcatg cagccctaca ttagcttcta atccagtatt tcatgagaga ac 472

<210> 2201
<211> 499
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2201

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aatgccaccg agcaggcctt catcaaattg aaacatgcca ttacatcaac ccctgtattg 120

gcactgcctg actttactca gccttttgtg ttagaaacag atgaatttga aattggagta 180

gaggctgtgt tgagtcagaa tggccaccca attgcatact tctccaagaa attgctccct 240

agaatgcaaa aacaatttgc ttacactagg gagtttattc actgtaacag cagcattggc 300

taaattcggg cattatttgt tgggctagaa atttgtcata aaaaaaattg aaaagtttga 360

aaagtctctt ggatcaatcg ctacaaactc ttgaacaaca agcatgtttt cataaattca 420

ttggttatga ttntcgaatt gaatacaagc caggtaagga taatgtccca gctgatgctc 480

tttcccgagt gttctttat 499

<210> 2202
<211> 416
<212> DNA
<213> Glycine max

<400> 2202

tgtgaagaaa atggaggaat ggttcaggga taacggggca gagtatgcat atatggctac 60

ggagaaggac aacgttgcat ccgtcaagtt gttcaccgac aaatgtgggt actcaaagtt 120

tcgtaccccc tgcattctcg cgaatcctgt tttctcgcat cctgctagaa tctctcacaa 180

agtgactatc attgaactct ctccgagcga tgccgaaata ctctaccgca gcaagttttc 240

cacaacggag ttcttcccgc gcgacgtaga ctccgttctc cgtaataagc tctccttagg 300

cacttttctt gccgtcccca aaggcttgta ccgggctgac acgtggcccg gctcaacccg 360

ctttcttgag ggtccaccac cctgttcttg ggccctagtc agtgtgtgga actgca 416

<210> 2203
<211> 570
<212> DNA
<213> Glycine max

<400> 2203

agctttcatc tcattcatct gtagaattat atttgataac atacatgaat tgcttcagcc 60

aatgccatgc tacaagttac acattttcaa gatatcatta caaaatttta acttgtatgg 120

attttaatct atatataaat ataaaatcac caagagaata aattaaaaat aaaagcagat 180

gtttgcaggc aatctagctg ctgatactaa tacattatgt taagaaatca gggaaaatca 240

tagtaagcat aattcgacaa ggatctgcca tgtattacac tccatacctt gtattagata 300

agcaaagaaa attaattctg actgggtatc tgatctaggg caaaaacaac tgcaactttt 360

atttcacatg aacaagtgtt aaactaaagc tgagtgagct taaaccacaa aagtagtaga 420

ccttggttgt aaggtaggca ggtgaaaatt tgcactatga agattcaaca gcataacttt 480

ctatggtaat ttttcaatgc ccatacatac tccatatagg agatatacta atttatttga 540

tggaaaaata gtaaaactat gtgttgggtg 570

<210> 2204
<211> 162
<212> DNA
<213> Glycine max

<400> 2204

tctcgatata ttatgcgcct gaatctgatc ttcgtgtgaa aagttatgtt tatttgaatt 60

tctcgagagc ttccggtgtt caatttcgag cgtctcgatc tttcatgcgc ctgaatcggg 120

cattcgagtg aaaagctatg accatttgaa tttgtcgata gc 162

<210> 2205
<211> 558
<212> DNA
<213> Glycine max

<400> 2205

agctttctta cagtacttcc tgcaccatct gtaccaataa tgatgttaca gtgaatgttc 60

tgttctacac gcttcccttt aatgatagaa gatgcagtta ctgttacaaa gtcattgctg 120

gcatcaatgg aaacacactc atggcccatc attatttttt tctcacaaga ctgttcattt 180

ccttccaaac tttcaggcgc acatatttgg aagcctaggt tttcaagtcg cttgagtagt 240

aacatagtta gcttgtactg cgagaagtgt gcaacagaga ccgggctgac aaaatgctca 300

agatctgata acaagtacaa gatatatgaa tattctaaaa ctcaatattg tccaaaacga 360

acaatatcat gcagtctatg tgttgatata ctgcatattt tgaaggctat gtataaatat 420

tgtcaaaact acacttgaaa tagaaatctt cctattgcta tcagactgga aattggctct 480

catgaactac agaatagcac cttgaggttg tatgtgatca accgatccaa gaattgaacc 540

agagagggaa gttcaata 558

<210> 2206
<211> 561
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2206

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ggatgcctgt gaagacaaat agttcattga ttgtcattgc caattaggca atagatcatc 120

atgtatgtat tatgaataat aaacaagcaa atgctcctta caattttgtc aaataactct 180

cctccattca catactcaag taccatataa attttggttt tgctagccaa gacctgcata 240

attacaggta caaatcataa tcagaacatc aaggtttcat agagtcaagc tgctttgtaa 300

atgcaataaa tcactttatt gttctacaat ctgaggtttg aagctgttag agatgtgaca 360

aatcattcac atgtcttaca cctattagtt taaacatttg tgtctcaata ttcttctact 420

aaaaagctga atagtaatac aagacaaatg ttcttgtgca atatttacgt tttaagccta 480

aacccttcgt gtaaagggtg taatatataa tataaaatca ttcatgtgtt tctactangc 540

agattaatct tttggaatat a 561

<210> 2207
<211> 526
<212> DNA
<213> Glycine max

<400> 2207

agcttgtgag cgtttcttct tcattcttca aataagacaa ttctatgatt ttttatgagt 60

tctgttagtc caatacttgt aatcattgta tgtggcacaa ccgaaatcat tgtgttaaat 120

tatctaatgt ttgaattttt aaacttataa cctctggtaa caaacctctc aattcttgtt 180

gcagttcata aaccatctca tcaatttggt tgccaggcat cagtaaaaaa agatagcttg 240

ccaattggaa aagaagcaat gcttggagca ttttcgttac tcaaggttat tgagtctgag 300

ctacaagcat acttgtctac aactgagggt cgagtggtat gtatccttag aatttcccat 360

tgcacttttt ctttaatttt gtatgattct ttggtcattg ctcttatttt atttcaaata 420

ttcaacttgc ttgttcctct ttaatttgtc tgattatttt ttcacttggg tactcatgga 480

gtgaatacta attttctaga ccccttaac tttttttaa gtgggg 526

<210> 2208
<211> 418
<212> DNA
<213> Glycine max

<400> 2208

tcttctgctc aacagtatat gccgttcatg gctccttttc catactatta ttctccaatg 60

ccttatgtgc caaatgctgg aatccaagcc accattgctc cttcagctcc ttctcaagcc 120

aacatagcta ctgctagttc agcaccttca aacagatgga atccggattc tagtgcatcc 180

caccatgtca ccaatgtttc tcaaaatata cagcaattaa caccttttga agggtcagac 240

cagataacac ttggtaatgg acagctcctt gacattaact ccacaggtct aacttcattt 300

caatctcctt taaaccctac gtttcctcta attcttagca atttgctata tgttccttca 360

attactaaaa ttcttattag tgtgagttag ttttgtaagg ataatctaat ttattttg 418

<210> 2209
<211> 497

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2209

tcagcaatta caccttggac atttcaccaa tatgaattag tattagtttt ttggattagn 60

gaggaattac cttagaaact tcatcaacaa cttcgttgga gattttggtt cctccaaatg 120

aattgatgat atttccaaag tcattaaggc catggagatt ccattcccaa tagcaccaac 180

agaccccata aacatcaaaa aatgatccaa aggatcatca tatgagaaaa gcttctataa 240

gggcactgtt tttgcagatt catctttggc ctcactgttc tttgagtctt tcttgctggt 300

aggatctcca ttcaagtcaa tatcctctgc cattttcttc attgaagact ttacacaccc 360

ttatactaat tagtaatcac tgtaaacgga aaaaacctgc agaaaatgca ttacaggttc 420

aagttagtaa cacacaagat tgtgctcttc aaagcgtaac ctcatagtga aatttcattt 480

ttttcttctt cttggat 497

<210> 2210
<211> 584
<212> DNA
<213> Glycine max

<400> 2210

agcttgaagg tgcgtaaccc accatttttt catagtaaaa cactggtaat gggtctacta 60

ttattatgat cattttcttc tccatcattg gaggtgccac ttgagctgcc aagtctctcc 120

atctttaggc gtattctttg aaagatttgt gccccttttt acccatgttc tttagttgca 180

tcctatccgg agccatatca gaattgtact gatattgcct aacgaaggca accattatgt 240

ccttccaaga atggactagg gaaggttcca agttagtgta ccaggtgaca gctaccctag 300

taagactttc ttggaagaaa tgtatcagaa gtttctcatt ttttgcgtat gcccccatct 360

tctgacaata catctttaga tggttcttgg ggcaagtagt cctcttgtac ttgtcaaagt 420

ctggcacctt gaacttggga ggcgtgacaa aattgggtac taggaacaac tcttctatgt 480

tagcaaaggc ataatctctg cctcctttaa tggcattgag cctttcctct agatgatcca 540

actttcccat tttttccata gcatgaaggt tttacttgct gtgg 584

<210> 2211

<211> 572
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2211

tgaaggtgtg tagcccacca tcttttcata gtagaatact ggtaatgtgt ctactatcat 60

tgntattatt tttttctccg tcattgaggt gccacttgag ctgccaggtc tctccacctt 120

tgggcgtatt cttttgaaag attcgtgccc ccctttttgca catgttctgt agttgcatcc 180

tatctgaaga cattatactg acactgccta acgaaggcaa ccactaggtc cttccaagaa 240

tggactcggg aaggttccaa gttagtgtac caggtaacag ctaccccagt aagactttct 300

tggaaggaat gtataagcaa ttcctcatct tttgcgtatg cctccatctt ctgataatac 360

atctttagat ggttcttggg gcaagtagtc cccttgtact tgtcaaagtc cagcaccttg 420

aatttgggag gggtgatgat attgggtact aggaacaact ctcctaggtt agcaaaggca 480

taatcttcac cttcttcaat ggccctgagc ctttcctcta gatgatccaa ctttcccatt 540

tctgccacag catgagggtt tttacttgtc gt 572

<210> 2212
<211> 559
<212> DNA
<213> Glycine max

<400> 2212

tcattaatag caccaaaaac tattccttgc acaaagcttc attagtagca cctaaaacta 60

tgtcatgaac ataaatttgc acaagcaaca actcattgtt tgatctcttg ataaacagtg 120

ttttgtctta acctcttaca aaagattgct caattaagaa attgctcaac ctttcatacc 180

aagatataag tgcttgtttg aaaccataca gtgccttttc tagcttgtaa acatgattag 240

gatgtttgaa gtctacagaa cctacaggat tctcaacata tatctctttt tcgatgtata 300

cattgagaat aacacttttc ccatccattt gatataactt gaaacccata ttacaagcta 360

aagcgggaat aaccttatag ctttcaacct tgcaactgag gcataagtct catcatagtt 420

aatgccttcc tcttggttgt atcatttagc aaccaatatg gccttgttcc taactatgat 480

gcttgatgaa tcaagcttgt ttcgaaacac ccatttggtt ctgattggct tgtgagaggc 540

acgtttatgg actaaatcc 559

<210> 2213
<211> 459
<212> DNA
<213> Glycine max

<400> 2213

tgtaaggatt tgggtgggaa atgatagtga gactcaactt ggataccaag cttgtgcttc 60

aacaattgca acaagaccca ctatccataa tgagagaaca attttttttt aaaaccttgc 120

atctcgtatg aaatatgttc tctctttagg tttgggttag gtcagcggat ttactcccaa 180

ggagccttct caccattaga agatcacctt cttcataggg taaacctctt caatatgctc 240

atcacccatg gcttcacctt catttccact tgaggaagga gaagaagtag cctcctcttg 300

gctactatag atgtcttgac ccctcataat catggttttc tttgtggggg tattgagaag 360

caatggggcc tttcccaata catttaaagc acttaatgct actagcacta tcttaagaac 420

tagcccgttg gagtgatttc cttcctgcat ataccctta 459

<210> 2214
<211> 500
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2214

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aacaattatg acctctccag caacagatac aatcccggat ggaggaatca ccctaatctc 120

agattgtcta gccctcaaca acaacaatag cagcttgctc cttccttcca aaatgctgct 180

ggcccaagca gaccatacgt tcctccacca atccagtaat cgcaacagcc ccagaaacaa 240

caaacagttg aggctcctcc acaaccttcc cttgaagaac ttgtgaggca aatgactatg 300

caaaacatgc agtttcaaca agagaccaga gcctccattc agagcttaac taatcaaatg 360

ggacaattgg ctacacagtt aaatcaacaa cagtcccaga attctgacag attaccttct 420

caatctgtcc aaaaatccan aaatgtgagt gccattacat tgaagtcggg aaagcagtgt 480

caaggacttt aaccagcaac 500

<210> 2215

<211> 442
<212> DNA
<213> Glycine max

<400> 2215

agcttgcgtg gctctatcca tatttgaagc agagtatttc tctgctggag gatgttgagc 60

tcatatcttt tggatgaaac aacaactaga ggatttcggt atctttcttg atcacattcc 120

tttgatatgt gacaacacac gtgcaataaa cttgaccaaa aatcttgtca tgcattctag 180

aactaagcct ataaaaataa gacatcattt cattagatat catgtgctta aaggagattg 240

tgttatagta tttgtagata caaccaacca actagttgac atctttacaa aacccttgtc 300

tagggataga tttataaaat aggacatcat ttcattatat atcatgtgct taaaggagat 360

tgtgttatag tatgtgtaga tacaaccaac caactagcta acatctttac aaaaccccttg 420

tctagggata gattctactc ca 442

<210> 2216
<211> 421
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2216

tcatggattt ccttctacaa ttatatcgga taaggatgca atttttctca tcagttntng 60

gagggagatg tttaaattgg ctagaactag tcctaagcat agcacttctt atcatcccca 120

aacggatggt caaaccgaag ttgctaatcg gtgcttagag acctatctta ggtgctttgc 180

tggccctaag cccaagactt ggttgaattg gttgcattgg gctgagttct ggtttaacag 240

taactacaat atctttgctg gaatgacacc ttttaaacct ttatatggac gagatcctcc 300

attgttgatt aagagctgca ccattccatc aaagttggat gatgtaaatc agttggccca 360

acaacgagat gatttgcttg cggaattgcg acaaaaattg ttgaaatctt aagacccgat 420

g 421

<210> 2217
<211> 628
<212> DNA
<213> Glycine max

<400> 2217

actaagcttc cccggggcca tttcctgcga aggcaaacat ttggaaagtt agttttaccc 60

gtgggacact actcttaaaa caaaaatggc atacaacctc ctcccatata tacaaacatc 120

aatgtaaatt tagagcaagc ttatgcgcat atttccttac gaacgttcac ttgcacaaga 180

cattctatta actaagaaaa atgcacccat atacaatcaa ggcagcttcg ttacctagat 240

tatttacatg tacttccaag gtgtatttgt tacttacatc acacacatct ccttggctaa 300

atttacatac atgcatactc aaagcatttt ggggtaccaa aaattgcaca tgtgcacatc 360

ttggaatttc taatacctat acatacacaa acttcatgat gaatcttgac tatctacaat 420

aaggcgctac atttcttgct cttttcaaat ttttgctacc taaagccgca tgcaaattca 480

agtatatttt cctttgctga ctaaaattgt attcaaatta aaaggtatat attttttttgg 540

tatgtatttt ctttacataa catgcaacaa atttatatat atatttttt gggagaccat 600

ttgactacca aaaattacat gcacatac 628

<210> 2218
<211> 644
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2218

ntacaagtta gggtcactta taatttaact cattgatttg ccgagaaaac ttatgaatta 60

acgagagtgt gtaatgattt tttttttgt cttgtatgaa catcctttag taaaatgaac 120

atttctctct atatgattaa ctttggattt tgagtcatac cttatccaaa actagacata 180

catgactttt tatacaggta aagtttataa aattttgtta tctaataagt ataagttatg 240

caatagtttt ataaatactc tataaaagga aaaaaaatga aaacttgagt attaatataa 300

atttataatc cgataaatat atttatgtat aaatttggtt tgggttggat tagattgaat 360

tttaaaatca aatccaaaat ctgattttat ccaaaacaaa tgggtttatt aaattttaat 420

ttgttcgact attggtttat ttgattttca gttttttgct tgatttattc ataaagttat 480

ttgataaaat tagtttatga acattcctaa gaaaaccgat aaagtaaaga catcanatgt 540

acaattaagt ctattaacta gtaaagtacg ccttttgtga caaatctaca gtgttaaaca 600

ttcggagatt aatatgtata gtacattctt ttgcctatga ttct 644

<210> 2219
<211> 368
<212> DNA
<213> Glycine max

<400> 2219

agcttgcact gcccaaagtg gacaaccttc cagaaaacgt tgattctcac cattgatgtc 60

ccttatgatg tcgttcagta tctcaaaaaa gcctacgatg atttggaaga acccttgacc 120

tgttttctca aatcttccaa agttgattgg catttctatg acccatatat gttacagtta 180

ccaaaaaggt tcaaagagaa aaccaaatgg tgtggaatag taagccccgg ttgggcacca 240

tagttgaagg tattgagcca caaggcagtt ggtggggttt tgactcactc tggttggacc 300

tctgtggtgg aggttgttta gaacgaaaaa cctctagttt tgttaatgct tcttgtatac 360

catggatt 368

<210> 2220
<211> 285
<212> DNA
<213> Glycine max

<400> 2220

taacacctct cattcttatt acttttttcaa tattgaaaaa gtaataagaa tgaaaaatga 60

aaaggtcgtc ttattcaaaa ccccaaccaa ttatgaaatc ccctatctcc cacttcacac 120

ctcggaacgc accgttctta tagagagagg cgctttcaca tcttcttagg ctggggagag 180

gaaatgttcc catttttag gatactccgg ggaacagata tccagtggag atgacggggt 240

ggggcctgta cctcatagga ttaaagcacg tggctacgaa ccacg 285

<210> 2221
<211> 382
<212> DNA
<213> Glycine max

<400> 2221

atacgtataa taacggtgct attaggagct actataccta ttgctcaaca agatattaag 60

aaaaatttgg cttattccac actgtctcaa ttgggttata tgatgttagc tctcggtatg 120

ggatcttatc gagccgctac atgctttttg aatactcacg cttattcttt gacatggtag 180

aattattgtg agtgatcaaa ttatttcaca aactatttag ctcgattata tatacaaaac 240

ttgaatttat gactactaat taaagttcga ataatttggc cacaattaat tcaatcattt 300

tggcttttat aattcgttat ctggctgact ttacgtacaa atgttattta ccacctatct 360

gatccaattt aagtctacct ac 382

<210> 2222
<211> 483
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2222

ccgcttaagg ttatgcggng gtttggcggt tgttctggag tggcagtgag tgtgtttatt 60

ggaattggaa gggttcgggc gagttcgagt tcttcttctt ctgaggagga ggaggaggca 120

gtgagtgtgc agtcaaaagt gactcaaaaa gtatacttcg acgtgagtat tggaaatcca 180

gttgggaagt ttgtgggacg gattgtgatt ggactgtacg gcgacgatgt cccccaaacg 240

gctgagaact tccgtgccct ttgtactggc gagaagggct ttggatataa gggttctacc 300

gtccatcgtg tcatcaagga tttcatgatt caaggaggag actttgacaa aggaaatgta 360

tgtatgtttt aatggttgat gctttgcttt ctcattttcg attcattcta aattccttcc 420

cttccttgta gggaactgga ggcactagta tatatggtcg tactttccaa aatgagaatt 480

taa 483

<210> 2223
<211> 440
<212> DNA
<213> Glycine max

<400> 2223

agcttatttg aattaatgct cggaaatata tagaaccact ttctattaag atgaactatt 60

gatattatca gttaaaacaa ctaactaaag aaggataaaa ctgtcatcaa gaaagttttt 120

ttttttttt tacaaaacac atgcatcctt tataagaacc aattttattt gagaaggtaa 180

aattattatg agtgataaaa ttatttcaca aactatttaa ctcaattata tatacaaaac 240

ttgaatttat gactactaat taagtttgaa ataattggca acaattaatt caatcatttt 300

ggctttttta attcattatc tggttgattt tatgtaaaaa tgtaattcaa tcatatctga 360

tccaatttaa gtcgatctag attggatcga tttttcttat tttaatcata ctttttttaga 420

aaatattaaa taaatgataa 440

<210> 2224
<211> 502
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2224

tgtaagaaga ataacaatat aggagaatgt ttntggttga ttgataaaga ctatattnta 60

atcataggtt aaggagttgt acaactgatg gagatatatt acacttagtt agggatgctt 120

ttgaaaatga gaatgagata aatgtttatt ttcatcatga agtagatcca attttagaag 180

aagtcccaca gatgttgtac ttggaatgtg atccaattcc agaagctgtt gagaatgagg 240

atgatttaga tgatgtacct gttgctggcc atgaggaaac taagttttaa ttcatttgta 300

cttggtccga catggttact ataattaatt aatatgatta atttttactt gatcaccatt 360

gatgcagatg ttggtgctgg tgagcatgtt ggtgctggag agcagagaga tggtggtgag 420

caaagggatg ctgatgctat tgaatagaga gatggtggtg agcagaggga tactgatgct 480

ggtgagcaaa aggatgctgg tg 502

<210> 2225
<211> 445
<212> DNA
<213> Glycine max

<400> 2225

tattaaaact aaggtgtatg aaactgtttt cttttagtaa gaccttgttt ttacattcgt 60

tgacgtattg gtctactgta tttttattat tttttgttca atttttactg atttttttat 120

cctattttca gctagatgta ttggctattg aatttaattt atggatcttt tttactgttt 180

gattattgat acttgcatga tagagttttc tatatggggg tgacatatat atcaaacttt 240

ttgtggcaga gcacaagttg tgggatggcc accaattcga tcttttcgaa agaacacgat 300

gatggcttat aatttggcaa aatgtgacaa cgaagctgag gagaaatcag gagtaggttg 360

tctttacgtt aaggtcagca tggatggtgc tccatatctc agaaaggttg atctgaaaac 420

ctacagcaac tatattgaac tttct 445

<210> 2226
<211> 504
<212> DNA
<213> Glycine max

<400> 2226

tcatccaact gaaacatgga aagaagacag tatataccag acaccgaatg tttttgaaac 60

cttttcaccc gtatcagcga ttgaagaaag ctcttaatgg aagtcaggag aatgaaagtg 120

tgccgcaacc attagctaga aatgaagttt atgatcgggt gaaggacatc ataactatct 180

ttggtaagac ccaaaagtag acgtcatctg agatgaacat atggaagaaa aggtctatat 240

tctttgatct tccatactgg tctgatctac atgtgcatca ttgcctagac gttatgcatg 300

tcgagaaaaa tgtttgtgat aatttaattg gtacccttct taacattaaa ggcaagaaaa 360

atgatggttt gaaaagtcgt caagacctgg ttgacatagg aatacgagag cagttgcatc 420

taatatcaca aggtcgttga acatatctgc cccagcatgc cacacaatgt caatagcaga 480

gaagagaagt ttttgtcaat gtct 504

<210> 2227
<211> 433
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2227

cttcactaca tcaagaatca tcgggttgag tcttctttgt ggctctctta ctggtttagc 60

cncatcttct aaatttattc gatgcataca tgtggatggg ctaataccag gaatgtctgc 120

cacggtccag cctatagcct tcttatgctt cttgagaact gataacaact tctcctcttg 180

ctcatcaaca agggaggcag atataattac tggaaaactt ttgctatcat ccaagtaagc 240

atattctaca tttgatggca gaggcttcaa ttctggtgtg gatggctgga tagtggcaga 300

aagagatggt ttctcancct gtacctcata aagaaagtca gaggtattgt gtacttctga 360

cacatgcgta tttctatctg actctatana ttcaatctca agagggtaaa catcagcaga 420

catggtatca ata 433

<210> 2228
<211> 343
<212> DNA
<213> Glycine max

<400> 2228

agcttatctc actttttct tattatcttc tcctagaagc tctggagaaa tttatccaag 60

catgccctta gtaattattt tgctggaggt ttgcttgcta tacttggcta tatttacttt 120

tctttttaa atgtatgatg ataatactaa tcaatgttta cggatgacag gctcacacag 180

tgcttgagat gaactatact gagcagcaat taacagcagc tgtcgtttct gatggattac 240

ggcctgtcct tgctgccgat gacttgggta taccgtcaag attattatca atgattaaaa 300

aatgctggga tgcagatcct aataacagac ctgcttttga tga 343

<210> 2229
<211> 429
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2229

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tcaacagtca catcttttca ttgtgttctt aaatggccat caaaggctta tatatatgtg 120

acatgagaca cgaatttgct aagtttttt cagaacaaaa aggtcttatc ctcttaacaa 180

gcaaaattgt tttatcctct tacaaattcc ttggccaaaa cactcgtgat tcaataagga 240

attatttgag tgctcaaatt gttcaatcta tctctttcaa gagagatttc ttcttctctt 300

cttctttatt ctgaagaggg attaagagac cgagggtctc ttgttgtaaa agaattctaa 360

acacaaagga aggattgtcc ttgtgtgttt agaacttgta aaaggaatct acaagatagt 420

ggaactctc 429

<210> 2230
<211> 366
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2230

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cagccggtat tacgcctcat gagctttctc atatccagct tactggattt agtttgggtg 120

acttcccttt tagatactta ngtgttcccc tcttatcatc gagattaaat gtatgtcatt 180

atgctccctt gcttctcaag attactggcc tgacttatgg atggagcaag aagtctttat 240

cttatgcang taagttagag ttgattagag cacctattca acgaattgtg aatntctgga 300

tggagattct ctctttgccg ccatctgttc tggaccgaat caacgcttcg tgccgtaatt 360

ttctgt 366

<210> 2231
<211> 353
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2231

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ctaacaaaaa cttatattct tctttatgga caaagtatgg caagcccggg gcaagcaaat 120

tttggtgcca tcagaccctg gatgcaactg tgatcgaatc cacatatcag ctagatcttg 180

atgggtattc aagccatcct tcgtcttgcc ttgaatgtta agaagcgtcc ccatcacact 240

gtcacataca tttttctgca catgcataac atcaatacaa tgtctaacgt ctagatcata 300

ccagtacgga agatcaaaga gnatggacct cttatttcat atgcaactct tac 353

<210> 2232
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2232

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gcggtgactn tgtggcggat aatatggcaa tcgatctcga tatgcttagt gcgttcatgg 120

aaaacgggat ttgttgctat ctgaattgca gactggttgt cacaatacaa ggtggctggc 180

tgaatgaatg ctacaccaat gtcttggaga atatatgtta gccattgcag ctcacaggta 240

gtagatgcga gagcttgata ctcgacttcg gaggagctgc gggagacagc ggactgcttc 300

tttgactgcc accaaatgag tgaagaaccc agatagacaa ggaaccctgt agtggatgtt 360

tgagaatctt tacatcccgc ccaatctgaa tcactgaaag ctcgaagt 408

<210> 2233
<211> 411
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2233

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gataaacacg tcgtatttca tctctttgat caaaaggaaa ctcccacatc attgaacgca 120

atccaggatc ttgctctata ttaataacat ccatatcttc tacttcaatt cttctacatt 180

ttaaaggttg tacttcatca aattaaatta acaatcttgt gtgacatttg aagcttgtgg 240

aatacgaata agctgagatg aatcaataat attattgttg tctttcttct ttaagaatga 300

acaaagagtt ttttgagttg acatcttcaa caatacacct gtagtatatt tcttttacaa 360

acaaataaac atacaaaata aaagtaanat aataatatat taagttaaga t 411

<210> 2234
<211> 473
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2234

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ggaggttgaa ttaagatatt acaaactatt tccccaatta aaattatatt tcactttcta 120

ttcaagttac aaattccctt aacaatgaac tcttaaataa taattcaaat agaacaatct 180

gaatataaat ataaaacaat aataaataaa agagtttaag ggaagagaaa gtgcaaactc 240

agatntatac tggttcggtc acacccttgt gcctacgtct agtccccaaa caacccgctt 300

gagagttcca ctatcttgta naatcctttt acaagttctg aacacataag gacanaccct 360

tctttgtatt cagaattctt ttacaacaag agaccctcgg tctcttaatc ccttagagaa 420

atagaaagaa gagaagaatg aatctctctt gacagagact agatttacaa tct 473

<210> 2235
<211> 446

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2235

gctccttaac tgcacaaggc tcttaatatt ngaagagtat acttgtggaa ctcttacccg 60

atgaagacac tgacaaaaac ttatcttctc ctttntggac aaagtatggc aggctgnggg 120

caagtaaatt ntcttcccat cagaccttgg atgcaactgt gatcgtatgc ccatatcagc 180

tagatcttga cgggtattca agccatcctt cgtcttgcct tgaatgttaa ggagcgtccc 240

aatcacactg tcacaaacat ttttctccac atgaataaag agtttagtcc ncattgagca 300

tttcaagaag agcatggagg gagtgtgtca caattcggtg aagcagaagc cctttcttgg 360

acaataaaga gtggaatacc canngtagtg gtcttgacta tggcaatgac ttcgtgcaat 420

gtctggagac aaacaacaaa gttcta 446

<210> 2236
<211> 400
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2236

agcttatgct gcanacattt acaatagacc tcctcaacct tatcagcaaa atcaaccaca 60

gcagaacaat tatgacctct ccagcaacag atacaaccct ggatggagga atcaccctaa 120

tctcagatgg tctagccctc aacaacaaca acatcagcct gctccttcct tccaaaatgt 180

tgctggccca agcagaccat acattcctcc accaatccaa caatagcaac agccccagaa 240

acagccaaca gttgaggccc ctccacaacc ttccctcgaa gaacttgtga ggcaaatgac 300

tatgcagaac atgcagtttc aacaagagac cagagcttcc attcagagct taactaatca 360

gatgggacan atagctacac aatngaatca acaacagtcc 400

<210> 2237
<211> 342
<212> DNA
<213> Glycine max

<400> 2237

taaggaagca gctccattga tatcatttaa tttatgcaat gcttaagccc gaataagaga 60

acttgtatca caggaaaaga tctaatccaa gtcgaattag ggatcatact gattgtggtg 120

gtaaaactgg cttgaagtag ccatctgggt aatatccaaa ccacgaagtt tcctttggta 180

ttaaaacagt gtcgtgctca aactgttaat gtataaaata agattacaaa tatataagct 240

tttctcatga aatcaattag caatattcta ttcataatat cacacaaata cattcagagg 300

acttaccatg ataagtacca aattctgcta gctactaaat ct 342

<210> 2238
<211> 426
<212> DNA
<213> Glycine max

<400> 2238

tgtcagttat aatatatacc gtgctgagac atcaagacaa cattatacaa taacaacaag 60

ggtgtctgca atcatcattc acttggacga tatttctagt tcaatcaaat agggtcacta 120

gtcacaacag caataatctc tcaaccaaaa catcaagata aaaaacagga taatgcataa 180

caattttaag ataaaagctt gtcataaact ggatgatcca ctaatccaat tgacagacaa 240

ttataaatgg atcattcttt cttcttttac tggaggagct tcggaataga ttgactctct 300

ctacgaccca tcttattgac gggaattatc actacgttag cggctcactc ggttactcga 360

gaatccaaat tattctattt cctgactgta gcaatgcata gcggtcaata ggaacatttt 420

cttctc 426

<210> 2239
<211> 457
<212> DNA
<213> Glycine max

<400> 2239

acatgcctca tgacacctaa gcacacttag tggagaatct tgaactcgat attggattag 60

tgggctgaac catatatgaa attcactaat cataattagt gaaatattgg ctccacaaat 120

tcaatttcaa attcaagtga aatttgaatt gaaattcaaa tttccctcca attttgtgtg 180

acacttaggc tataaataga ggctatgtgt gtgcattttt ccaactttga tcatttaaaa 240

attaaaattc aaattttata gctctcttat agtacaaaat ttcgtgcttt tctcttgctc 300

tcacttcatt catctgcttc ttcctccaag ctcttatcca ttggcctcta tggtggtgag 360

cttcttctac gctcatcttc tccttgaagt ggcgtctcct ctctctcttc cttctccatt 420

ccactggcat tcatcttcca agaagcaaag gaatcca 457

<210> 2240
<211> 466
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2240

agcttgtgcc ttttcacgtc tggaatatga atgtagcata tagatccaaa gacccttagg 60

tgctntgttg atggcttctt cccgatccaa gcttcaattg gagtcttgtc ttttacagac 120

ttagttggac atctgttgag tatgtaaaca gcagtgtaga ctgcttcagc ccagaatgtg 180

ttaggtagtc ccttctcctt gagcatcgat ctagccatct ccataactgt gcgattcttt 240

ctctcggaca ctccattntg ttgagaagaa tatgcgactg taagttgtcg ctcaatgcct 300

tcatcctcac aaaatctttc aaactcgcga gaggtgtact ctctgctgcg ataacttctt 360

agtactttta tccgttttcc actttggatt tcagcaaggg ccttgacttt ttgaatactc 420

caaagacttc ttgattttct tttagaaaat atacccatgt cattct 466

<210> 2241
<211> 440
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2241

agcttaagag cgaanactac ggntgctaac ttattatcgn gtatggaata attcctttca 60

tgtatcttga gctgttgaga agcatangcc actacttgtc cccactgcat aagcactcca 120

cccaaaccca tcttagatgc atcacagtac accacanagg gttcactcgg gtcaagtaac 180

actaaaactg gtgcagtggt caacctttcc ttaagggtac gaaaactact ctcacactgt 240

gcatcccaca caaaagcttg acccttacga gtaagcttag tcaaaggtaa ggctagctta 300

gaaaaaccct ctatgaatct acggtagtat cctgctaaac caaggaaact cctaatctca 360

aacactgact taggactctc ccaactcatc accgcctcta ccttggaagg atctatngct 420

atccctcccc tggatataac 440

<210> 2242
<211> 310
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2242

agcttgcctt gccccttgat atattttatg gactcatggn cactatgaat gacaaattcc 60

ttgtgataaa tgtagagttg tcatgtcttc aaagcccgca ctagagcata caactcctta 120

tcactaattg aatagataag ggtaggacca cttaactttc ttctaaaata agcaatggga 180

tggccttatt gcatcaacac agtcctaacc catcatttga agcatcacac tcaatctcaa 240

acgatttatg aaaggttggc gacgcaagta tgggggcatt agtcagcgtt tgcttaacat 300

agaaagcttc 310

<210> 2243
<211> 419
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2243

ctgcagcttg acagaatcat tctaatttca agatttctgt aaaagatgaa ctgccctttt 60

gttctgcttg ttgtatggga aagattcata gatttccttc taagttttct canaccgtgt 120

ataattctcc tttggaatta atatacagtg atctgtgggg ccctgctcct atgaattctc 180

attgccaatt cagatattat atgtcctttg tagatgctta tttgtggttt acttggatat 240

atttttaaa gaataagtct gatgccttgt ctgttttaa acagttcaaa tctcttcttt 300

tctgtcagaa ttggggattg ttcataggct gacttgtcca cttacacatc accagaatgg 360

tatagtggaa agaaagcatc gtcacatagt tgaattaggt ctttctcttc ttagtcatg 419

<210> 2244
<211> 505
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2244

cgttattccg actacttgtc taaaccacta accaagcgac atgtatatat gcagctcttg 60

agaaccttat tcacaacata tcgttttctg tattagagta tgatttgact atatcttcgg 120

atggaataga tgtttcataa actcctttaa tgcattctat ctatattcat gaatcataag 180

acaagttatt ctcctcggat gatttggatt attaaaaatg tacataatgt tatatgtgtg 240

tatgtacgta cgtataagtt ggatgaggca tttcttattt atgagacttg ctngctttgt 300

gtcacggaat atatattgtg atgatataga tgcatgtgtg ggcgattaat gcagcatatc 360

ttacgaatct attctaatga caatgacaag agattgtgaa cgcttaatgg tgcgcataat 420

taaggagcga acaccganag accatatcga cctatctata tatatatatg aatcttctcc 480

acattatatt ttgcgttcct atgtt 505

<210> 2245
<211> 463
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2245

agctnntggg gcatatgtac tttaagtgag agatatgata tttaaaattg gaataataat 60

taatattacg agtaaataac atatacaaag atgattaatt nttacataat caatcacata 120

ttatcatata atgtaaattg attgatagta ataataaaaa tataaaattc atattaatta 180

tgatttaagt tctaaacatt atagatgata tgataaaaaa aatgtgtata aaaatgagaa 240

attaagcaat aatgagagat aataaaattg aataatgaaa gagagaaaga gtgtgaccgt 300

cacagcttcc aatagattgg tggtgtcgtg caagtacttg acgacccatg ttagaacact 360

tgctgtggtg tcatgtgcag canagatgac accaatgaga atatcaacaa ctcgagactc 420

tgtgtgctgc tgatagtaca tcttggtctt ctcacctcga gct 463

<210> 2246
<211> 491
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2246

actctacctt tacagctnta ctatttccac tgcttcatat tgttctcaaa ctaccacttg 60

taggccttgc attctgtcat ttgtttatga tttgctgatt atatttatca agaacgtacg 120

agatttgcat tgttatccat gatatttcta tttcattatt tttctttata gatttttaat 180

atgatattta ataatacatc ttacttggct acatgctcac agtggtataa tattctatat 240

gcagtgttnt tttgatacac cagggctcat gttgaattgc ggtggatttc cttatangga 300

tgtcaaggtc cgtgttgaaa gtgcttggag ttcagtcaat ctctatgaag tgctcatagt 360

catttctgac gttcatagac atattaccag gtcanagggt tatttattaa atggatgagt 420

agtcctatac tcgtgtttac cctatttctt ctatatatag acttgttcga taacttctta 480

taagactata g 491

<210> 2247
<211> 337
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2247

gcttcattaa tanatcgagt cctactagct ctagtcctct tcatattatc tattctgatg 60

tatggcggcc aacttcaata aatccaataa aaggatattc ctattatgtc atttttattg 120

atttattttc acattatgtt tgctggctgt atccaatgaa attcaaatcc gaaatttcca 180

ttattcttcc agtttttaaa tcctttgttg aaaaccaata aaatgtcaaa attaaaattc 240

tttatactaa caatgatgat gaatacatta agttacggtc gctccttcta acttatggaa 300

tatctcatgt aacaacttcc catacccgtg aatatta 337

<210> 2248
<211> 438
<212> DNA
<213> Glycine max

<400> 2248

agcttgcaat cactaagaga ctcttttaac atcgatagac taagacttag ctttcttatt 60

gatctttgtt ttcttggtct tgatttggac ttaaaataaa acttgtgttt cttttgtctt 120

ggcatcatca agaccatcat acacatacat tcacaaacat cgctatattg tcgtaacaac 180

ccattgtctt ttgaaccatg gatccctccc actcaagttt tggtgttatg cattgtaaat 240

cgcaacgtgt ctcatcaatc ggatgccctc tcttacacta aaccaaaaag ctccattaga 300

agtcttgttt catcgtccat caaattatag taaactaaca gcttttggtt atctctggtt 360

tccttgggtc actccatata caactaacaa acttcagacc aagtccgtac catgtgtttc 420

taggttacaa tcttactc 438

<210> 2249
<211> 432
<212> DNA
<213> Glycine max

<400> 2249

ctaagcttct tcccaatcca ttggcaaata ccaatgcaat ctgagttggt tactctaaag 60

gccaataata cttggtttct cacacctctc cctcctggaa agcaagctat tagttgccgt 120

tgggtctaca aaatcaagtg caaatcagat ggttctcttg aacgctataa agcacaatta 180

gtagcaaaag gctacacata acttgaaggg attgattacc atgacacttt ttcatctact 240

gctaaaatgc gtacaatacg ttgtttatta gctctggcag ttgctcaaaa ttggtcactt 300

catcaacttg atgtccacaa tgcatttctt cacgaagatc tttttgaaga aatttatatg 360

tctcttcctc ctggttctca gcgacagggg gagaacctag tgtgcttctc aacaatctta 420

tatggataaa ac 432

<210> 2250
<211> 451
<212> DNA
<213> Glycine max

<400> 2250

agcttaataa atcaatctat ggcttgtagc aagtctcctg ccaatggtat ttgaagtatc 60

atgatgtcgt cacttcattt ggctttgaaa agaacatcat ggatcaatgt atataccaaa 120

aggtcagtgg gagtaagatt tttttcttgt gttatacgtg gatgacattt tgcttgcaac 180

taatgataag ggtttgctat atgaggtgaa ataatctctc tcaaagaact ttgatatgaa 240

ggatatggga aatgcatttt atgtcattgg cattaagatc catagggaaa gatctcgagc 300

gaatttgggt ttgtctcaag agacttatat taacaaattt ttagagagat ctaacatgaa 360

agaatgttca ccaagtgtag ctcccattgt gaagggtgac aaactcactt tgagtcagtg 420

cccgaaaaat gattttgagc gggaacacat g 451

<210> 2251
<211> 416
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2251

agcttccaat catgcttctg tacagactnt gatcaacact ggtgccagct tcatcctttg 60

acagcttcaa gtgagtaggt gcaggtgttc ttttatggct ggaattttcc atcccaaact 120

tcttgacaat gttctttgca tacttgcttt gtgagaggaa catgaagtct tccatctgct 180

tcacttggag tcccagaaaa taagtcagct ctccaacaag actcatttca aattcagatt 240

gcatctgttg aacaaaatgt cgaagcatct cattcgacat ccctccaaac acaatgtcat 300

caacatatat ctgtgctatc atcaagtttc tagcatcttg tttgacaaag agagtcttgt 360

caattcctcc cttcctatac ccttgctgag taagggaact ctgtagcctt tcatac 416

<210> 2252
<211> 403
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2252

gcttggcaat aacacaacct cgactctcat tgagtgtaga acactttcaa gtggtgctca 60

gttggagaat agtcatgagc tatgatgcaa tcctaccccg caagggcatt ggatagaaaa 120

ctccaagtag attgtgccag agatgcaaga gaaggcccta gggttcttat gagccttacg 180

gtagatttct ggcgcatggg ctaagtacga gcccacttat ctttgtaaat attaaattaa 240

ggtttcatta tttttgggcc ttgtatttac ggctccataa tgtatgtagg gtaccctaca 300

aatatacgat ttttcagccc ttgtatttta cggcacctag actagttttt gtattaaggg 360

tagatntgta atcttacatg cactaagtgg atattngatg tgt 403

<210> 2253
<211> 461
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 2253

agcttctgag agtggtaaca accaaaataa agtgctatgg cctatgggta cagtcagata 60

agaacactca cagaatcaac ggtcttcata gcctgaggcc caggaaatgt cttgccagaa 120

ccatggctct ttggaagtag tcgcccctca acttcttccc cactgattcc tctagcaata 180

ttccacaacc aagtactgca atgctgtaaa agctagaatc aggaatagaa taccaacaga 240

ttgcaatgaa gacaatcaaa tggacagtca tgagtaatta agtaactaaa tcaaaactgc 300

atggcatgca attggagaat aacacaaaag ttgcaattta aaatatgaga tcccanaaat 360

gaaatcagca nagacagcca aatgatgctt tggtagtaga tatatataac atcatgtaag 420

aacttagaag acatactcac ccagtattga tcccatacca c 461

<210> 2254
<211> 458
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2254

agctntggag tttccaagtg ccaattcgtc ttcttctttt gtccagactt cttctggctt 60

caattcatta gagggctttc cttctgtgtc cagcatcttg ggatgttccc agcctttgat 120

gacagctttc caggttctgc tatccagtga tttgaggaag gccaccatcc ttgctttcca 180

gtattcatag ttggttccat ccagaattgg tggtctgttc actggtcctc cttctttctc 240

catgttcatc agaatttatc tccctagatc tcactcagtg atttcgagtg cctgctctga 300

taccaattga aattctgata ctggggacag atgtcgtaca ggatgtcacg acatcacgct 360

tcagaacatg cagattgtct ttgactgtat gaacaaatta aacaagttaa taacacaaga 420

gaattgttaa cccagttcgg tgcaacctca cctacatc 458

<210> 2255
<211> 486
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2255

gctttcttgg agaaacttnc ttgagaagct tctntgagag aactttcttg agaagctata 60

gcttagctac acacacccct ctaatgacta agctcacctc cttgagaagc ttgcttgaca 120

agattcctaa agaagctaga gcttagctac acacacctct ctaatagcta agctcacctc 180

cttgagatga gaagctagaa cttagctaca cccncnccta taatagctaa gctctacccc 240

atggcaaaat acatgagaat acaaaaaaaa aagtccctac tacaaagact actcagaatg 300

cctcgaaata caaggctaaa accctatact actagaatgg ccaaaataca aggcctaaac 360

aaagganaaa acctattcta atatttacaa agataagcgg gctcatactt agcccatggg 420

ctcanaatct accctaaggc tcatgagaac cctanggtct tccctgggat ctctggccca 480

atctac 486

<210> 2256
<211> 325
<212> DNA
<213> Glycine max

<400> 2256

cgcacccttc ttcaaacatt cggtcatagg acttgctata gtgctaaaat tctggataaa 60

gcgtcgataa gatgatgcaa gaccaacgaa agatctcacc tccgaaactg ttgtaaggct 120

cgggcaagtc ttgatagcat ccacttttgt ttgatcaacg gatactccat ctttagacac 180

cacatatcca acaaacacca cactctctac caagaaatca cactcttccc tcttcccata 240

gagtaattgt gctcttacgg tctcaaatat ctgtttaaat gagtgaaatg ctcctctata 300

gacttgctat acaccaatat gtcat 325

<210> 2257
<211> 206
<212> DNA
<213> Glycine max

<400> 2257

gactcaatcg gacatccgag ttaaaagtta ttgccgctta catttgctac gagcttccgc 60

tttcaactat gatcgtgtcg atatattact ggactcaatc gaacatcgga gtaaaaagct 120

attgccgtta gaatttgttc agtgcctccg ctttccattc agagccgctc gatatattac 180

gggactcaat cgaacattcg agtaaa 206

<210> 2258

<211> 391
<212> DNA
<213> Glycine max

<400> 2258

agcttgaaca gttaccaatc tccaaatgaa tcttccctga caacatgtta tcatagagaa 60

acattatctt caatttacca agcctcccaa cctctctggg gagatcaccc tgtaaattgt 120

tgcgaaacaa tgcaagtgtc tgcatgttag tgaggatccc tatgaaagga gagattgaac 180

caaccaaagt gttggtttga agcaatagat cagttagccc caacaaccca taaacctcaa 240

taggtattga cccattgaga aaattgtttg acaaatcaag ttgcttgagt gagtggcacc 300

gacccaactc agctggtatc tcaccatgaa ttccactacc tgacatcatt aaattctaca 360

cacttgtaac attggaacat atggttcttg g 391

<210> 2259
<211> 395
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2259

cttctcatca atggactcct gacgtatacg aatgagtgcg gttcgttcga taaattccta 60

tctctntatc tatttctgag atgtttggat ttttcaaaac tccatggaca tgcagaagag 120

aaatgctatt cccactcgga ccaagacata actttacttg ttcaaataac aattaaggtg 180

aagcagagtc aggaacaacg aatcccttta tgataaacag attcattttg caagttcgtt 240

attacgggta gttcctacaa aggatcggac taatgacgta tacaatactt gaattctcga 300

tgtagatgct acatagttgg ttctcatcct tcacagacta cgagtataat angagcatcc 360

gtcaacanaa ggatcaccct aagatgatca tctcg 395

<210> 2260
<211> 452
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2260

ctaagcttag tcctgttgat ctgangttga aggtaggacc cccatacttg gggtatccac 60

aactctggca tgctgtcctc ttcttgaaat ttatatgctc gcaaacacca cacatccaat 120

ctcctccaga ccagctcatt ttcctgatca atatccacac ttgaattttt gaattataag 180

aatttttggt tccatcaatt ctcggtgcaa ccagataagg actatatgtg catgtagcct 240

acttacacag taatgagaaa tattattagt ccttgtttta tgcattatga gttatgactt 300

atgaccctaa cttctattaa aggcatgcaa ttttctatcc atatataggt tatntgcaca 360

aagaactact gtcttgggtg atagaatact ctgtcaagat ggcatagcaa tcttgtcaag 420

ttttctactc tactcaatat taatctattc at 452

<210> 2261
<211> 455
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2261

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ctaatttagg gggaaaaagg ataaattgaa aacaatgaat gatatatgcc taaaaaatga 120

aacttattag acatatgaag aaatataaaa atcaaaattg atttattaat ataatatcca 180

gctcaatatt taaccagtta atttatatta tgaagttatt ttttaattaa ttgactgcgt 240

gacatttgtt ataaatctga attagaatat acattattgt tatcatttaa taagttgaat 300

ctagatatat actcgtggta gtaatttgaa tgcttaaatc ataaaaatta tacttattat 360

aacgacctta cttatgtatn ttttaataaa tagagaaata atacaaatta ttctacttca 420

atgaaatata cgatatataa tattttatat gaaat 455

<210> 2262
<211> 493
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2262

atgataaatc tttatatata aaanagtaga catgacggta ttattgtaat ttaaatcttg 60

ccgctcattt tgagggtaca tgcaattaat tctatcactt cttttgtttc cataatcaga 120

tttttaaaac gtaatttata actaattntg attacgatta tttcttcttc ttttaaaata 180

taagaatggt taaatactta attgcccatt ctaaattctc ataaattatt tcttattttc 240

cgttntatat tctatgtagt gtgtaaggat tttaacaaat tagtgtgtta gtgatcaagg 300

ttctctatta atatgagttc ttataagtca cattgtcatt tagtttgttt cctttcaact 360

gattgtaatt atcgtatgta aaaatcacga tgttggaaat ggatgatggt tggtccgcag 420

ctattgttgt tcaaaanaaa aatattngcg ggacacatgg tncactagtg agaactatgc 480

atatcttata tac 493

<210> 2263
<211> 312
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2263

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attaatttaa gattaaatat atctttaaca gatagtacag ttaattatat tatgagaaaa 120

aagtcacgca ttgacatata taaatgtgta ttatactctt actttttttt aacataccac 180

tcttttcttt atataccact ctgagctgat tatgtaaaag agttaagctc aagtttttct 240

tttaatttca tatattacat gttaagctca ttcttttaat tatcttatat aaaaacattg 300

attaaatatt at 312

<210> 2264
<211> 362
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2264

cattccaccc aaacgcaccc ttcttcaaac attcggtcat aggacttgct atagagctaa 60

aattctggat aaagcgtcga taaaatgatg caagaccaag gagagatctc acctncgaaa 120

ctgttgtatg gctcggccaa gtcttgatag catccacttt tgtttgatca acggatactc 180

catctttaga caccacatat ccaagagaca ccacccttc aaccaagaga tcacactttt 240

ccctcattcc atagagttnt tgtgctctta ggggctcaaa tatttgttca catgagtgaa 300

atgctcctct atagatttgc tatacaccaa tatgtcatca agagtaacaa caacacactt 360

ac 362

<210> 2265
<211> 373
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2265

gaagtgcctt atgaatcctc ccgtacttat gccaccagta cctggaaggc ctctcatatt 60

gtacatgaca atcttatacg agtcaatggg gtgtatgctg tggcaacatg atgaatccgg 120

agagaaagag cgcgctgttt actacctaag taagaagttc acgacctgtg aaatgaatta 180

ctccctgctc gaaagaacgt gttatgctct antatgggca tcccatctcc tacggcagta 240

catgctgagc catactacct ggttgatatc caagatggac ccggttaagt acatctttga 300

taagccagct ctcactggaa gaatcgcccg gtggcaagtg ctgctattcg agtgtgatat 360

agtctacgtc acc 373

<210> 2266
<211> 467
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2266

agctntatca aatttccctt ctaataagtt ttgtattcca agactttcgg tttggtatgt 60

atgatttcct agtcttggaa attagtggta taattntcaa ggggatacct gtgactcgat 120

tggtgaaata ggatctctct tcaaaaaagc atgtttttt taccattgca aaaagaaaag 180

attttgttgc gaatgaacaa gatatcgaga aattgtccat acgtaaaatc ataattattg 240

atacaggcct tttccacgta aaaagagaat cttttgttac aatagaagca gaagtgatat 300

tgattattca agaatcgaag tcaatttgct ttatacattt acataatata tggcataata 360

gagcctgcga ttctttgatt tgatgtctag tcaaatntca aggtggaagt tatagttctg 420

aatttatcca tgttangatg ggaaaatgtg aaaaaaagtt ggatatg 467

<210> 2267
<211> 284
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 2267

agcttcttct agacttatct cctcactact agataataca ctttcaacat cggttattta 60

gaacattcta catcggttct aaaaccgatg ttgaaagtga cgatgttgaa tgtatgaatt 120

ttaacatcgg ttttggagaa ccaatgttaa catacatatg acaacatcgg ttctccaaat 180

acccgatgtt aaacacaatg aacaacagca aaaaaagtgc aggcatgatg aacgttgaca 240

tcggttnttc agtaaaaccg atgttaatat gttagtttaa catc 284

<210> 2268
<211> 436
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2268

tatgccaaaa ctntcattat attcttcgga tatagtatct tcaaagcttg agtgttgaag 60

tgaccaaatc ttcaatgcca taaccatgaa tcatcaattg taactctcat ggcaatgcca 120

gtattagtag tatacttaaa gcttattgga aaaaacttat atttcctttc tccattttaa 180

ctntggcaat ctcttgcctt ttgggtattt ttatcataga taatgcacgt atcttcttca 240

aggtgaagat aatagccttt ctccatcatt tagccaatgc tcaagagatt atctttatga 300

tttggaacta gtaagacatc tttttatgat ctcttacctt tctttgtctn caccatgaca 360

gtgcactttt cttttgactc taccatggtg gtcatttcca attgaactnt gactctgaca 420

gtggtcgcaa tttcct 436

<210> 2269
<211> 342
<212> DNA
<213> Glycine max

<400> 2269

aattcatttt tatcgttttt gtaaaatact tggatgaata atacaattaa tattacgcta 60

cattgaaatg tgactttatg tataatgcat actctcactt atcactacaa ccaatatatt 120

atacataaat atgtactata atacactaca cctttatgat tctatgctat gcaattacta 180

ataatttata cataatttga tataatatac aatatcaacc attatctttt acaataaaat 240

attactatac aaatctatat aaacatatga taactatcct atgattttat tttttaatcc 300

taaacttatt catttaacat aaactataat actattgacg ta 342

<210> 2270
<211> 383
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2270

tctgttgttc aactttgagt gtctcgatat attatgctcc tgaatcgaac atccgagtga 60

naagctatga gcattcgaat ttcttgagag cttacgctgc tcaatttcga gcgtctcgac 120

atgtgatgtt cctgaatcgg tcccccgcgt gtatagttat gaccatctga atttcacgag 180

agcttccgct gctcaatttc gagggcctca atatgtgatg tgcctccaac atcccagtga 240

aaagttatga caattcgaat ctctagagag cttccatcgc tcaatttcga gcgtctncgg 300

atattatgcg cctgaatcgg acatccgagt gcaaagctat gaccatccaa ctctcttacc 360

cgcttcatag ttcgatttcc acc 383

<210> 2271
<211> 436
<212> DNA
<213> Glycine max

<400> 2271

tctacttcat agtctaccac attcatatga tcaattcatc atcaacatta ttgtcagtcg 60

tctaaccttt gatgatgttg ccagaactat tcctaaagaa gaattctaac aaaagaataa 120

gaaagatacg caggaaaatt ccaagcatgc aaaggcttta atgatgacga aggtagatca 180

atgtaatgtg gctctaatgg gagttaaaat catggcagat caaagtcttg aagaagaaag 240

aacctcatat actataattg tggcaggaga tgacacttaa agaaagattg ttggcctaaa 300

aagagtggag gagataaact atagagaatc gagctctcaa cgttgtgttg ctagcacctc 360

acataatatg gaagccatgt gtagtgaaac accaattggt tttagaggtg gaagacaact 420

tcatgatcgt tggata 436

<210> 2272
<211> 436
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2272

ggataagagt agtaaatgat gaagtgatac ctttaggcaa tgatgcactg ccatgaaatt 60

cctgaatgcc ttcacaaata tcagctccca tcgtgctcca acaagctttg aaaaaatcga 120

agttgaagct gtatggtcca aggcttttgt ctccagcaca gcttcaaaca attgctttga 180

tctcttcaca agaaaatgga gcttctaacc aattactatc ctcattgctt atctgtttga 240

aatccaccct ttccatctgg ggtcgtgaaa catagttctc ctaaagcatg ttagaaaaga 300

agcgtttaac ttctttctta acccctacca catcttcaat ataactgcat cagaattaac 360

gcactntagt ttattcttct gacattctgt tcaaaggcaa gagtggaaaa attgggtatt 420

gataatccca agtttc 436

<210> 2273
<211> 488
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2273

ntctacaaaa tcaaacgaac aataacttta actcggatgt ctgattgagt cgcgtaatat 60

atcgagacgc tcgtaattga aaacagaagc attgagcaaa ttcaaacgac aataactttt 120

tactcggatg tccgattgag tcctgtaata tatcgagacg ctcgtaattg aaaacagaag 180

ctctgagcaa attcaaacga caataacttt ttactcggat gtccgattga gtcccgtaat 240

atatcgagac gctcgtaatt gaaaacagaa gctctgagca aattcaaacg acaataactt 300

tttactcgga tgtccgattg agtcccgtaa tatatcgaga cgctcgtaat tganaataga 360

agctctgagc aaattcaaac gacaataact ctttactcgg atgtccgatt gagtcccgta 420

atatatcaag acgctcgcaa ttgaaaacag aagctctgag acaatcaaac gacaataact 480

ttttactc 488

<210> 2274
<211> 311

<212> DNA
<213> Glycine max

<400> 2274

tttcgagcgt ctcgatatac tactgtacac aatcggacac ccgagttaaa agttattgtc 60

gtctgaaatg gctcacaact tttgtttcaa ttacgaacgc tttgatatat tacgggactt 120

catcggacat cccagttaaa agtttatgtc gtttgaattt gcttaaagct tctgttttca 180

atttcgagcg tctcgatata ttaccggact caatcggaca tccgagttaa agtttttgtc 240

gtttgaattt tctcaaagct ctctgtttca attacaaagc gtctcgatat tctacgggac 300

acattcggac a 311

<210> 2275
<211> 488
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2275

cttcattntc aattacaagc gtctagatat attacgggac actttctgac atccgagtaa 60

atagttattg tcatttgaat ttactacgag cttctgtttt caataacgag cgtctcgata 120

tactacgaga cacaatcgga catccaagta aaaagttatt cctgtttgaa tttgctacaa 180

gcttccattt tcaatttcaa gcgtctagat atattacggg acacaatcgg acatccgagt 240

aaaaagttat tgtcgttaaa attttctaag agcttatgtt ttcaatttcg agcgtcacga 300

tatattacgg gacttaatcg gaaatccgag ttaaaagtta ttgtggtttg catttgctac 360

aacctttcgt tntcaatatt gagcgtctcg atatattacg ggacacaatc gaacattcga 420

ataaaacatt aatgtcgttt gaattgctat gagcatctgt tctcaataat gagcgtctcg 480

atatacta 488

<210> 2276
<211> 375
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2276

agctntgagc anattctaac gatagtaact cttttctcgg atgtccgatt gggtcccgta 60

gtatatcgag acgcacaaaa ttcagaacaa agcctctgag caaaatcaaa cgaaagtaac 120

tttttactcg tatgtccgat tgagtcctgc aatatatcga gacgctccaa attgagaaca 180

gaaactctga gcaaaatcaa acgacaataa ctttttactc ggatgtccgt atgaatcccg 240

taatgtgtcg agatgctcgt aattgaaaac ggaagctctg agtaaattct aatgacaata 300

actttgtact cggatgtccg aatcgtaata tatcgtgacg ctcgtaattg anaacagaag 360

ctcttagcat attct 375

<210> 2277
<211> 492
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2277

ntacatgaat tntattaaca taaaaaattt cttcaatcat agtacctttg atatatctaa 60

taattctctt agctccttgt agatgactaa cgcgtggctc ctcaatgaat ctgctaagca 120

aactaactcc aaattatctg gtcttgttgc aaccagatat ctcatatttc caatcaaact 180

cttatataga gttgcatcca cctttttttc cttcaacatc tcttgtcaac tttagctctt 240

cttcaactag tgtggaaaca tgctttgaat tttccatctc gaatttcttc anaatatcac 300

atgcatactt cctctaggag atgaanatcc caccatctcg ctaattgacc tcaatgccaa 360

gaaaatanga catcaggcct aaatctgtca tctcacaaca tcttatcata gcttccctag 420

attctgaaat caactntgaa ttcgtgtcag tgaagattag attatcaaca tacagacaca 480

caatgagaat at 492

<210> 2278
<211> 270
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2278

agcttgtcct ctccgatgga agaataccgt gacatatgtc tcctgggcct tataaaggac 60

aatgaagtca aagtcaacct atgcttgtac ctactncatg ccaattgaat ggccacagca 120

acccaagttc tccaccctgg tgagtaatac cttgcacttc tcttcacctt ttccttaaca 180

aatgtgtacc tgaaatgttg tgtcacatac ttcacgtcct gtgctataag gccgaacgcc 240

tcggtggttt ccaacgtgat gagtgtggat 270

<210> 2279
<211> 309
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2279

tatggacaat aaaatacgcg gtattgagaa gagcattttg aaagaagctt ctgtgcctga 60

tgctgagaaa gatgttncac tatcttacac cccgaatgtt tctgtgcctg atgatgagaa 120

agatgattct acatcttccg gcctaaatgc tgagggactc cctttatcca cgggagaaga 180

atcaacagaa gaagaggatt tagccctaaa tgagactcct gtaacgcggg cgcctgaagc 240

tgctgcagtg aactaatgac ctgtagacat taatgtgtga agaaccattg ccacacgtgg 300

ccctcgttt 309

<210> 2280
<211> 328
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2280

tgcaagctgg aatcatttat cctatctcct acagccaatg ggcgagtccc gtccaggtag 60

tcccgaagaa gaccggcctc acagtgataa aaaatgagaa ggaggagttg attcctactc 120

gggtgcagaa caggtggaga gtctgcattg actataggag gctgaaccaa gttaccaaaa 180

aggacaattt tcccctgcca ttcattgacc aaatgcttga acgcctggca agaaaatctc 240

actactggtt ccttgatggt ttttctggtt atatgcacaa tactattgct cctgaggatc 300

angaaaagac cacattcacc tacccctt 328

<210> 2281
<211> 347
<212> DNA
<213> Glycine max

<400> 2281

agcttatata gaaagttcgt tcctaatttc tctattattg catcacctct caatgagata 60

gagaagaaga atgtggcatt tacctgtggt gaaaaacaag agcaagcctt tgctttgctc 120

aaagaacagc ttactacggc acttgttcta tctcttcctg acttttctaa aacttttgag 180

ctacaatgtg atgcttctgg agtgggagtt ggagctgttt tgttgcaagg tgggcaccct 240

attgtcttat ttagtgaaaa acttcatggt gcgacccttа actactccac ctatgataaa 300

gagctttatg ccttaataag agcactcaga acttgggaac attacct 347

<210> 2282
<211> 313
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2282

agcttcggta ttcaatntcg atcgtctcga tgtattacgt gactcaatca gacatctgag 60

taaaaacgtt attgtcgctt ggaattgctg aaagcttcaa cattcaatgt cgagcatctc 120

gatatatttc gggactcaat cagacatccg agtaaaaagt tattgtcgta tggaatttct 180

gagagcttca acattcaatt tcgagcgtct cgatgtatta tgggactcta tcagacatct 240

gagtaaagaa gttattgtcg ttggatatgt gccagagctt caacactcaa tttcgagcgt 300

cttgatgtat tac 313

<210> 2283
<211> 294
<212> DNA
<213> Glycine max

<400> 2283

tcttgaaccc tcaccgcgca ctctttcata atacggagac tcctgacacc catcaagtgt 60

acccctttct atgctctctg gacatgaata cgcctggttg gtttgcacca accacgcgga 120

tatgaatgga aggcttcttg ccacttcatt ggctctttaa agtcgcatac ttcactatat 180

tattgctcgt atcttactcc ccagatcttc aaaccttgca cacgtttctg aagaagatct 240

tatagtcatg tgggcctttc atatcgaccg accaagcgat tgggccactt aacc 294

<210> 2284

<211> 312
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2284

agcttctcca nagaacacag gatcatcatc atactgcagg atatccacag gaaccttgtt 60

cttccccacc aggaagcttt tgaaacatgt ttgagatact tgttgcctca taaaccctgt 120

taggccttca gccactaaat caaagagaaa aggggccaaa ggatctcctt gtcgcagccc 180

tctttgaggt ttaaactctg aagtagggct tccattaaca agaatagata tggaagctga 240

agagaacagg cctttatcca tctaatccat ctctcatgag accccattct cttcatatat 300

aaatgagaaa tt 312

<210> 2285
<211> 463
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2285

ttgagcaatt canatggtca taaatagtca ctcggaggtc ctattcacgc acataattta 60

tcgagacgct ctaaattgaa caacggaagc tctcataaaa tttaaatgct cataactttt 120

aactcggagg tccgattcag gcggataata tatcgagacg ctccaaattg aacaatggaa 180

gctgttgagc aattcaaatg gtcataaata gtcactcgga ggtccgattc aggcgcataa 240

tttatcgaga cgctctaaat tgaacaacgg aagctctcaa gaaattcaaa tggtcataac 300

ttttaactcg gaggtccgac tcacgcgcat aatatatcga gacgcccgaa attgaacaac 360

ggaagctctc gagcaattca tatggtcata acttttaact cggaggtccg attcaggcgc 420

ataatatatc gagacgctcg aaattgaaca acggaagctc tcg 463

<210> 2286
<211> 486
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2286

tctagggatt aaacataatt aagggtattg aaaaacaaat atttaacaga aacattgtat 60

gattcttttt cttgggaatt ccaacggcat gaatgagttg ataattggtt gattttgatc 120

cacaggtcac tcaattgaga tttgaagcca aggctccaat tatgtggtaa attatgacta 180

ttattgttgg caacacctaa aggacatgac aacttcacga cgagcattta agatagatag 240

aacaatcttg gttcagatct ggctggagag actgcagcag ccatggtagt tacttccatt 300

gtgttaagga aaaccaaccc acattactct cacttgcttc tacaccaggc catgcaagtg 360

agtcattact caatgctttg tgtcctagag atcacaattg aatgcactat tatactntga 420

attaaaaata aaatagatta gtactgcagg tataattcaa tctacgtata gtatatatat 480

actact 486

<210> 2287
<211> 379
<212> DNA
<213> Glycine max

<400> 2287

atcttaagtc acctgcggca tgcagcttaa catttcaatt cgtgcgtctc gtatgttact 60

ggactcaatc agacatccga gtaaaaagtt atggtcgttt gtattggctc acagcttcaa 120

cattcaattt caagcgtctc gatatgttac gggactcaat cagacatccg agtaaaaagt 180

tatggtcgct tgaattggct gagagcttca acattcaatt tccagcgtct cgatatgtta 240

cgggactcaa tcagacatcc gagtaaaaag atatggtcgt ttgaattggc tcagagattc 300

aacattcaat ctccagcgtc tcgatatgtt acgggactca atcagacatc cgagtaaaaa 360

gttatggtcg tttgtattg 379

<210> 2288
<211> 271
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2288

agtgaacttt atagcggggg tgatcacaga atggaaggat attccagttg agcttttgat 60

gcagattttg tcacttgtgg atgatcaaac ggttatgata gcttctgaag tttgtcgtgg 120

gtggagagag gcaatttgct ttggcctgac tcggttatca ctctcatggn acatcatctg 180

ttttttacc ttcccttcta atgctttatt tcacttttga ggttattatg cttgtggagg 240

cagtgaatat tgaaaagggt gatttttttt t 271

<210> 2289
<211> 441
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2289

agcttcctta agaagattcc taaagaagct tgagcttagc tacacatacc tctctaatag 60

ctaagctcac ctcctcgaga tgagaagcta gagcttagct acacaccacc tataatagct 120

aagctcaccc ccatgacaaa aaacatgaaa atacaaaaaa agtccttact acaaagacta 180

ctcanaatgc cccgaaatac aaggctaaaa ccctatacta ctagaatggc caaaatacaa 240

ggcccagacg aaggaaatgc ctattctaat atttacaaag ataagcgagc tcatacttag 300

cccatgagct cgaaatctac cctaaggctc atgagaaccc tagggccttc ccttggatct 360

ctagccaatc tacttggagt cttctaccca atgcccttgc ggggtaggat ggcatcattt 420

ggcacataac taanatttca t 441

<210> 2290
<211> 395
<212> DNA
<213> Glycine max

<400> 2290

cctgtattgg ccttacctga atctacaaag actattttag tggaggcgga tgctatatga 60

gtgggggtca gagccgatct cataccagat caccattgca tagcctttat aagtagaagc 120

ttaaatgttc agcaacaatc catgtcaacc tataagaagg aggtactacc tgtggtgctt 180

gttgtacaaa agtagagaca ttacttatta cctaagcagt ctgtaatgaa aactgatcac 240

acaagtctcc agtatattct tgaccagaga ctttccacag ctttccaaca catatgcgtg 300

gtaaaaccta tggaatttga tttcattatt gaatacaagc acggaagtga gaaccaagct 360

gctgatgcac tctcaagagt tgaatgtgct actat 395

<210> 2291
<211> 495

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2291

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acaaaagaac tcatgtgaga attgactcat ggtcaagaag atgttctatt tattttaatt 120

actatcaatt tagaatttat ggtgaaataa aaaaataaag caacctgtta aactcggtag 180

aatgatagaa aatttagata atttatatgg catcttaagt atacatctta ttatcaccat 240

tatataaaac aaataaataa aattaacaaa aggagaaaat aatttatctg ccaaccatgg 300

attttttttt tatactttta tctaatcata aattaacata tacaataaaa ttgttgattn 360

ttttatagta attattttca agttatagtt atcataattn ttaattaact gatagtgtaa 420

aattatatat taataaaata taaattaaat tcattaacaa aagaacatta taaagtgtct 480

gtgcaaaatg aaatg 495

<210> 2292
<211> 259
<212> DNA
<213> Glycine max

<400> 2292

atataaactt cttcaaacaa atctctattc aaaaaagcat tattaacatc taattggaga 60

agacactagt ttctaacagc aacaacacag agcaaaactc ttacagtggt aagcttggcc 120

attggagaaa atgtatcaga gaaattgatt ccagcttatt gagtataccc tttggcaacc 180

aatcgagctt tgtatctatc cacaaagcca tcattttata tttaacctta tacacccatc 240

tacaaccata catgcttat 259

<210> 2293
<211> 502
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2293

atactcagct agaagaaata agactagtgg ctgaggatag atgattagta tctctggcgg 60

tttaagttat atgagtgaca acaactctgt acaatattnt gatgcacttc aagaacacac 120

acttgagggt tttaatctaa taagaaagtt tgagacggaa ttcacctaaa cttaaatntt 180

tataaaatgg atttatagaa ttattaattt gtgatatcga cgatactaaa agattatata 240

tattacgata gaaaatgtta ttatattaat ttattgaaat gatagatttt gcttgtatgg 300

ccgaagttat ggccacaaat atatatttta gagaaaatta ttaatttttg aaagtttata 360

tgtaacttga aaaacttagc caattgttat aatgtgaact tatgcttggt attcgactgg 420

cgacgattgt tagtggagtc ggggactgta acttaccttc tagagcctat attattacca 480

taactgtgat gtaatcatta ta 502

<210> 2294
<211> 486
<212> DNA
<213> Glycine max

<400> 2294

tatctctaga agacaaataa atgagtttct ttgtactctc aaattagttt atgcacttta 60

tagaaactct cttctctcat atatagctcc tttaaagatg aacaaatttc taaaaattaa 120

cttatataat ttatgtagaa actcttgatt cttctttttc ttaaagcgta tatgaaaaaa 180

cttaccaaaa aagactctgt cattaagaaa aaattatgaa gcttatccgt tggttttgtt 240

ttattataag ctttttatct tcatgtgcgt tgttccctga ttcgtagtaa ttgctaatgt 300

aacatgagtt taatggaaca tattgtcggt gtcaaattac agaataaaga aagtagaaaa 360

tcataactaa taagactctt aacccagtaa ataaactaat cttatagctt gatttgtaat 420

taaataatat tatacaacta cttttagtta ttgatacata gcctatccta tcatcttaca 480

tttcat 486

<210> 2295
<211> 315
<212> DNA
<213> Glycine max

<400> 2295

gcttgtaatc gattacacat atactgtaat cgattaccat aagagaattt cagaaaatat 60

tctcaatagt cacatctttt tatttcattc ttaaatggcc atcaaaggct tatatatatg 120

tgacttgaga cacgaatttg ctaagagttt ttaagaacaa aaaggtctta tcctcttaaa 180

aagtaaaatc gttttatcct cttacaaatt ccttggccaa aacacttgtg attcaataag 240

gaattatttg agtgctcaaa ttgttcaatc tatctctttc aagagagatt tcttcttctc 300

ttcttcttta ttctg 315

<210> 2296
<211> 471
<212> DNA
<213> Glycine max

<400> 2296

taaagtttgt aggcctgagg attctctatt atctctctca cacgcacata tataatagtt 60

ctatatataa taatatattc atgctgatag gctcgttggc gtatttgact tcgacaagtt 120

tcttcgcttg tttataaacc ttaattcaaa atagacttat tataaataga cttttgtgac 180

aaatctaact cttaaacaac tcagactaga cttaacaaat caataaatag tttctttgag 240

taatattaga ttctattctt ttaagtaaga ttttatattt aagttttatt gatagaaaaa 300

tatgattgga agaaaaaatc tcattaaaaa tagctcatta ggttctttga tagagattaa 360

ttatcgacaa aactaataaa tactctattc caatagcata attaagaaaa ataaattaaa 420

cttaacaagg atatataata ggcaaatgag ttacgctaga ctttgtaatt a 471

<210> 2297
<211> 431
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2297

cgcttgcctt agcacactnt acttncatct atttcagact atattattta tacgggttgg 60

acaaaatgtt tccgaagact aatatcatat tgttgattac cttgtatatg taacaattta 120

ccttattatt gtggagtttg gcattgggtg cataaagggc tcgatgacat aaaatcactt 180

tacaaacatc ttctttctac tcatcacatc tacaacaaat agaacaatat atccctattt 240

gctgatgagt acataataca tttgacttgt ttttgccaat atacggatga gttcatcaca 300

tttttcttat tttggcatca aaatattatt atttaagata aaatatgtgt tacatgttat 360

tctatatcat tatgtgatgt gtcggtttat gatataacta tgttcttcct actcgagata 420

tactcatttt t 431

<210> 2298
<211> 469
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2298

agcttacagc aaatgataga atgtctatag ttttatcatt tgacaattta ttggtattat 60

atgtcttatc cttcatatat atagactctc ttttttcatc tttttcaact gtgaattttt 120

acataattca taaattttat ttgatacctt gcatagcatt gcatttagca aatacaattt 180

aacatgcttg gtttataagt attgacacaa aaaaggctta tgaaaatacc ttgtattgca 240

tgttgctagg gcttattaaa aatatcaaat aattttacat gtgtctgtga aatcagactt 300

attaatgatg cgataaatta tgtaactatc atgtctctcg ttgatgttgc taaaaaaatt 360

gtttaggaag tatanggatt aaaagtgcat tttgcaaaaa gtttaaagat cgagaacata 420

attaacccat ttaaatatta tcaatanaat aaccttaaat ttaaaatac 469

<210> 2299
<211> 511
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2299

tcggacctat aaaactaagc tgggtatctc cttcttcact acatcaagaa tcaccgggtt 60

gtgtcttctc tgtggctgtc ttactggttt agctccatct tctaaattta ttcgatgcat 120

acatgtggat gggctaatac caggaatgtc cgccagggtc cagcctatag ccttcttatg 180

cttcttgaga actgacaaca acttctcctc ttgctcatca gcaagggagg cagatataat 240

cactggaaaa ctcttgctat catccaagta accgtatttt aaatttgatg gcagaggctt 300

caattctggt gtggtcggct ggacagtggt agaaggagat ggtttctcan cctttacctc 360

ataaagaaag tcagaggtat gtgtacttcc tgaaacatgg ttagtcctat ctgactctat 420

aanatcaatc tcaagaggta aaacaccacc accaggcatg caatcaatat cactctcaga 480

ttcactctca gcatcaaagt cagacatatg a 511

<210> 2300
<211> 449
<212> DNA
<213> Glycine max

<400> 2300

ctaatgtgtt ctcccttgta gaactactaa ctgcagtaac agttgcagcc caactatcca 60

gtagtgatga caatagaatc aatgccttca cctcatcctc aaatttaatc tgcacagatt 120

ccaattgggc aagaatagta ttaaactcat taatatgatc agttacagag ataccttctc 180

ccatcttgag gttgaacaac cggcgcatca agtatacttt gttggctgct gacggcttct 240

cgtacatatc tgataatgcc ttcattaagc ctgcagtagt cttctcgttc acgatgttga 300

acgcgacgtt cttggctaat gtcaatctga tcacgccaag agcctgtcga tctagcaagt 360

tccattcttc ttgcttcatg tcttctggct taacccctga taagggctga tacagctttt 420

tctgatatag ataatcctct atctgcatc 449

<210> 2301
<211> 337
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2301

ctgagcanat tcaaacgaca gatcactgtt tactcggatg tcttattgag tnccgcaata 60

tgtcgagacg ctcgaaattg aagaccgaag ctctgagcat attcgaacga cacataactt 120

tttactctga tgtctgactg agtcccgtaa tatatcaaga agctcgaaat tgattatcga 180

agctctgagc aaactcaaac gacaataact ttntacttgg atgtctgatt gagtcccgta 240

atatatcgag atgctcgaaa tggaataccg aagctctgag caaattcaaa cgacaataac 300

tttttactcc gatgttcgat tgagtatcgc aatatat 337

<210> 2302
<211> 378
<212> DNA
<213> Glycine max

<400> 2302

agcgttagga tcggaagagt gactatgata atctattatg gccaacggaa aaatgagggg 60

ttgattgtca atgcaatttg ggggtagctc tgctggcttc gacgtcattg gcaaaccgcg 120

gaatggtttg agtgtggaac aatggaaaat atggtgaatt cgtgctcctt ttggtacttg 180

caagcggtac gccatgggac ctattctctc tatgatctga aatggcccgt aatacctctt 240

tgctaatttg cccatactag ccggagttcc ttttgtcgat gtttctcggt atggtcggag 300

cttgactata acccagtcac cacattcata attgaccttg tgccgcttct tatcagcata 360

tgtcttcata catgcttg 378

<210> 2303
<211> 482
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2303

ngagcttaaa tctaaactca gttattcaaa tgagataagc tcatgctgta tatgtttgat 60

aaaagctcac aaacaacttg tgtttgtgta tgtgtatatt ctatacaaaa gattgtcatt 120

ttaaatgaga aaatgtatgt atactaataa taataattta tttattgtta ttacttagta 180

aattgttatc ttattgattt attactgtct actatttacg taacgctact tttcaaagag 240

tttctttact ctcttcaact tctagcataa agatatgtac tcaactaaat gctaaattaa 300

taaacataga aagaatacat tggagaaaat ttgaggtacg aaaagaaaat tattgttaga 360

atttagaata tgttgaatag taactgtcat gttgaatgtt ntatgactga aagttagcag 420

ttacatatta ttaaatatgc gtaatacggg aatagaggga tatgtgtgta tcggtttcta 480

gt 482

<210> 2304
<211> 424
<212> DNA
<213> Glycine max

<400> 2304

agcttatgac aattgaaatt ctcgagagct tccgaatacg tgtgaaaagt tatgaccatt 60

tgaaattttt gagagattcc gttgttcaat tttgagcgtc tcgatatatt atgcgcctga 120

atttgacttg cctgtgaaag gttatgacca tttgaatttc tcaagagctt ccgttattca 180

atttcgagct tctctatatg tgatgtgcct aaatcagaca tacgggttaa aagttatgac 240

catttgaatt tctcaaaagc ttcggtagtt caatttcgag catctcgatg tattatgcgc 300

ctgtatctga catccgtgta aaaagttatg accattttag tttatcggga gcttccgctt 360

ttcaatattg agcgtctcta tatgtgatgc gcctgaatcg gacatccgag ttaaatgtta 420

ttac 424

<210> 2305
<211> 468
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2305

tgtttcgaaa ccacccattg gttctgatag gcttgtgaga ggcatgttta gggactaaat 60

cccacacttc attcctttta aaatgaatta attcatcgtg catagccaac aaccaatgct 120

catcatgaaa tgcttcatat atggttctag gttcaatctg agaaacaaaa gttgtgttca 180

agatccttaa ccttggtttc atcttcaagt gcagcttgcg tatcctaaaa acctgcttct 240

tcattttcca aagcattttc ttgaacaaaa gagccagttt cctcacgaat aatattttta 300

ggttcttcca cacacaaagt tctcctatta agcactctat aagccttgcg ttgtaatgaa 360

taaccaagaa agattgctca tcagttttgc atcanattan aaagagatcc ttttcattat 420

taaatcaaca tttacatcaa accctaaatg gatatattgg ttcttcat 468

<210> 2306
<211> 473
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2306

tctatagaag gttcgttcct aatatctcta caattgcatc acctctcaat gagctggtga 60

agaagaatgt ggcatttacc tgcggtgaaa aacaagagca agcctttgct ctgctcaaag 120

acaagcttac taatgcacct gttctagctc ttcctgactg ttctaaaact tttgagctag 180

aatgtgatgc ctctggagtg ggagttggag ctgtattgtt acaaggtggg caccttattg 240

cttattttag tgaaaaactt catagtgcca ccctcaacta ccccacctat cataaagagc 300

tgtatgcctt aataagagcc ctgcaaactt gggaacatta ccttgtttcc aaggaattng 360

tcattcatag tgatcatcaa tcacttaagt acattagagg gcaaagcaag ttaaacaaga 420

ggcatgcaaa atgggtagag tacctagagc aatttccata tgttatcaaa tac 473

<210> 2307
<211> 443
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2307

agcttcattc ctttttcact catgtgtcca agtctttgat gccacatggt tgaattattg 60

acagcctcag taactcctac catatcctca tctgcaatca tgtaaagaga tcctcgcttc 120

tttccacgag ccacaatgag attgcctttt gttaccttcc aagctccatc tccataagtg 180

gtgtgatgcc cttcattatc caactgccct atggatatta agtttctctt taaggtagga 240

atatgtctga cattgtgcaa tgtccatagg gatccaccag aggtctttat gtcaatatca 300

cctcttccga taatgtccag agattntcca tctgcaaggt aaactttccc aaatcttcca 360

aaatatagtt agacaataaa tctttagaag gagttgtgtg gaacgacgca cctgagtcca 420

tgatccatga atcaacagga cta 443

<210> 2308
<211> 238
<212> DNA
<213> Glycine max

<400> 2308

tgtaatcgat taccccttcg gaactttccg agatggctcc caagagtccc tactgtatat 60

attgtattat gtatggcctc cctggtcttt caatatatta ccagacatgc aagttccaag 120

ttcaagtctg atgagtcaca acttttttata tactagttgt gtgatccgat tcaaccatta 180

tgtaatcgat taccatttgc gaatgttcga taatagctcc cgagagtcca cctattca 238

<210> 2309
<211> 496
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 2309

ggaaccttga tngaatttcc atccaatgtt ggagaaaggt tcttgtgtaa agtatagatg 60

tcaaagaggg ttaaagaaat gttaatctta taaaatatga tcttgtaaac aataaaagat 120

tattacttac tttttgctaa cattttcggt agtagttatc gctatgttca aagtaagcat 180

tgtttttta tattgattac tagtgagagt ttccatgatt ntcttattat tgttggaagt 240

aatcattgat aanaatgttt aagaaggaaa aaaattatat aaaaagtatg caaaatacta 300

gaaaggaata atttcatgtg aaaaagtgat tttgatattt ataatggttt tgaagtaatt 360

aactaacaaa aatagacact ccagtaataa taacataacg ttcatgtatc tttntctcta 420

gctaacttaa tttggatata acataacgtt ctttaataac annatatnga catcattgac 480

tttgagaaaa aacaca 496

<210> 2310
<211> 383
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2310

agctnggctg tcttcctatt catccatcaa catgtagaat gcttattctt tccatattga 60

tgatatgtct tgatccagct ttaactcttg cttgtgcatt cgagtttaat gatccatttg 120

tgcatcccat tttacctgat gaaaagaaga gagcttcagc tgctagatct gagcttggtt 180

ctttgtatgg gggttgtggt gaccagtttg ctatagtagc agcatttgaa tgctggcata 240

attcanagga aatgggtcta gaatcacggt tttgttctca gtactttgtt tctcaaagca 300

ttatgaacaa gttatctgga atgcgtaaga atttagcagc agaactatat cagaatgggc 360

ttattcatgg gcagtttaca agc 383

<210> 2311
<211> 409
<212> DNA
<213> Glycine max

<400> 2311

tcgattacta gaagttttta cgtttttaac aacctttaga aatttgaatt taaattttaa 60

agcctgtaat tgattacaac ttgtgtgtaa ttgattacca acatgagaat tcaaatttca 120

agtctgaaga gtcacaactc ttcagaaatt aactgtgtaa tccattacaa cagttatgta 180

atcgattacc aataaggaat tttcgaaaat aactcccaag agtcacaact gttcaaattt 240

tttttgaatg gtcatcaatg gcctataaat caattaccag acatgaaaat tcaaatttca 300

agtctgaaga gtcacaactc tttagaaact aattgtgtaa tcgattacaa caattatgta 360

atcgattacc agtaaggaat tttcgaaaat aactcccaag agtcacaac 409

<210> 2312
<211> 403
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2312

tgtagcagan tagaactaca ataactnttc actcggaagt ccgattgagt cccgtaatat 60

atcgagacgc tcgaaattta aaaccgaagc cagtagcaaa ttcgaacgac aataacaatt 120

cactcggaag tccgattgag tcccgtaata tatcgagacg ctcgaaattt aaaaccgaag 180

ctcgtagcaa attcgaacga caataacaat tcactcggaa gtccgattga gtcccgtaat 240

atattgagac gctcgaaatt ttaaagcgaa gctcgtagca aattcgaacg acaataacat 300

ttcactcgga agtgcgaatg agtcccgtaa tatatcgaga cgctcgaaat ttataaccga 360

agcctctagc aaattcgaac gacaataaca tttcactcgg aag 403

<210> 2313
<211> 436
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2313

agcttcggtt ntaaatttcg agcgtctcga tattttactg gactcaatcg gacttccgag 60

tgaaatgtta ttgtcgttag aattagctac gagcttcggt tttaaatttc gagcgtctcg 120

atatatttcg ggactcaatc ggacttccga gagaaaagtt attgtcgtta gaattagctg 180

cgagcttggg ttttaaattt tgagcgtctc gatatattac gggactcaat cagacttcct 240

agtgaaaagt tattgttgat cgaatttgct acgagcttcg atttggaatt tcgagcgtct 300

cgatatatta cgggactcaa taggacttcc gagtgaaatg ttattgtcgt tcgaatttgc 360

tacgagcttc gggtttaaaa tttgagcgtc accatatatt acgggactca atcggacttc 420

cgagtgaaat gttatt 436

<210> 2314
<211> 473
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2314

acaatggttt taaaatgtgg ctcataaact tggaatccct atccgacaca atgctcctag 60

gaaatccatg aagagtcact acctctttga ataaaagata caccacatga caagaatcat 120

ccnctttgtg acatggaatg aagtgtgcca tcctagaaaa cctatcaaca accacaaaaa 180

tcgaatcttt ctcctcttgg accttggaag accaagtaca aaatccatgg aaatgtcggt 240

ccaaggggag gtaggaattg gaaatagagt atacaaacca tgatgcatga ctntagactt 300

tgcgttatga acaaaanttg ataatatcat gtttcattnt aggccaaaag aaatgttcat 360

gcaaaatgtt caaagtcttt taaactccan aatgtcctgg ttaacccccc ttatgagctt 420

cacanatcat gagttcatga naggaacttt gaggcaacac aatcttttat ttt 473

<210> 2315
<211> 444
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2315

acattgagat gctataaatt gagatatgga agttcttgag agattcaatt ggtcataact 60

tttcactcgg atgtcagatt caagagcaaa atatacagag acgctcgaaa ttgaacaacg 120

gatgctctct agaaatntaa atggtaaaat tttttcacat ggatgttata ttcagacaca 180

taatatatcg agacgttcga aattcaagaa ttcaaaaatt aaagttctca agaaatatag 240

agatgaaaaa ttatgaccat gggtgtacga ttgagaccca tgatatatcg atatgctcaa 300

aattcaaaaa ttggtccaat tcanaaattc aaagagccct aactntngac atgggtgtac 360

gatngaggcc catgaaatat cgagaacgct cgtaatgaaa aattgaagtt cttgagaaat 420

tcanatagtc ataacattta actt 444

<210> 2316
<211> 399
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2316

agcnttatga gagagtcaaa gatcaaatgg agaggaaaaa ttataactat gctaaacaag 60

ccaacaaagg gagaaagaag gttgtcttcg aacccggaga ttgggtttgg gtgcacatga 120

gaaaagaaag gtttccggaa caaaggaaat caaagcttca accaagggga gatggaccat 180

ttcaagtgct tgaaagaatc aatgacaatg cttacaaagt tgagctgccc ggtgagtata 240

atgttagttc caccttcaat gtctctgatt tacctctttt tgatgcagat ggagaattcg 300

atttgaggac aaatccttct catgagggag agaatgatga ggacatgacc aagagcaagg 360

gcaaggatcc acttgaagga cttggaggac ctattgaca 399

<210> 2317
<211> 349
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2317

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acactggatg ggtttcatgt nttgttcttc gaacatcatt ggagtgtaat ggggagagat 120

gtctacaatt tcactagagc tttcttttag gatccaacaa aaattgctga agtgaaccaa 180

actttttaa ctctgattct gaagaaatgt gaggtcaatt ctattaaaga tatcagacct 240

cttagacttt gtaatgtgat ttatgaagct atgactcgtc ttatctctca acgcttgaga 300

ccaatgatgg tgaaattagt gggtcatttc caatctagcc ttaccccaa 349

<210> 2318
<211> 408
<212> DNA
<213> Glycine max

<400> 2318

tctgtccctg agaaactggt tcccagaaga caacatggag tgtagattgc tgtaaaccct 60

agccttgcaa caagttctag ggaagtagac acggagatgg acaagaaaat ccgcagtatg 120

gtgagtagca ttttgaaaga agcctctgtg cctgaagctg atgaagatgt tccaacatct 180

tccaccccga atgtttctat gcctgatgtt gagaaagatg ttccaacatc ttccggccca 240

aatgatgaag tactctcttc ctccagcaaa gagagatcaa cagaggaaga tgatcaagcc 300

gcagaggaga cccctgcacc aagggcacca gaacctgctc caggtgacct cattgactta 360

gaagaagtcg aatctgatga agaacccatt gccaacaggt tggcacct 408

<210> 2319
<211> 409
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2319

atgttctgtt atcaccgtaa cattaaattc aatgttaatt ataaccctat caaccattta 60

aagctagtat atctcatcat caggaatatc tggngttagg aatttcctgg gatctttact 120

tatttcttca tagtttaggg ttgatttcac cctttctggc actggcatga gaggaataat 180

gctatctcta tcgattacac catcaataat tccgtattcc actgcttcaa ttggagacat 240

atatttatcc ctatcaatat ctctttgcac ttgttcaaat gagcgtccag tgaaacttga 300

tataattctt gtgatattat tcttgttgtg cataacttct ttagcctgaa tttctacatc 360

tatagcttgt ccactagcac ctcctagagg gtgatgaatc ataattcgt 409

<210> 2320
<211> 433
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2320

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ctccatttga gataaccttc gggcggaagt cctttaattt tccagaatac attgcgggga 120

ttgcaaaggt ggaagctatg gaagatattc tatcagaaag ggaggccacc ttctaggcaa 180

ttcgaaagaa gctcttgaaa gctcaagaac gcatgaagac atatactgat atgaagcgcc 240

gggaggtcaa ttatggctcc gatgactggg tcttggtcaa gctccgacca tatcaataaa 300

catctgctaa aggaacacag gccattacag gcaaattggt gaagaggtat tactggccat 360

tccaaattaa agagaggata agcccagtgg cataccgcct acaattgccg aacggagcgc 420

gaaatcaccc tgt 433

<210> 2321
<211> 500
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2321

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aaggaaccaa taatattaag gtgtggaatt gcgagactgg cagtgacaat ggcagcgaga 120

tgcggaggca cggagttgcg atgaagacga tgacgcgggc gacactagag ttgcggcaga 180

gacttgaatg aattagggcg tggagccaat aatattttta aaaattgagt cgttaacatc 240

ggtttttcca tcaaaaccga tgttaacaaa gtgatgttta cgttaacatc ggttnttttt 300

ataaaaaaaa aattgatgtt aacttataat ttaccaacat cggttntttc aaaataccga 360

tgttaaggaa gtgatgttaa ccttaacatc gattntntaa gaaaatcgat gttaacttat 420

cattntccaa catcggantt ttgaaaacgg acgttgcgtn tcatgtaaca tcggttctca 480

aaaccgatgt aacctactat 500

<210> 2322
<211> 421
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2322

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acactattca naaagggcta gaaaggaaan ttgttgattg ttcaaatcta tgtagatgac 120

ataatctttg gtgcaacctt agaaaagatg tgcaaagagt tttctgggct aatgaaaggt 180

gaatttgaaa tgagtatgat gggtgagtta aagttcttgc tagggcttga aatcattcag 240

aaagatatga tggatattta tccttcaaga aaaatacaca aaggacatac ttaagatgtt 300

caaaagggat gaagccaaac ctatggctat tcctatgtat ccttctctag tcattgataa 360

ggatgaaaga ggtaatgata ctcgtaaaaa gataactgct agtagaccag atattgtatt 420

t 421

<210> 2323
<211> 310
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2323

tttaaattta tgatttaatt nnttttgagg tggagttgat attgagaagg aggaantaan 60

agatttgagg gtaaatnntt tttaagggga agaaaatgat gnaatntttt ntaggaaggg 120

annagtnatt agaagtatga gnaagagggt ttaagagaat tgggttagag ntgntgaaaa 180

agggggtagg gtttttatga anntnaagat agatttttga gnnnatggan naatgttggg 240

ttnaattatt tttgtanata ttaaantagg atggtattat atttggtnnt tgtatttagg 300

gttnnataat 310

<210> 2324
<211> 344
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2324

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ttcgtccaga ttntatttta tccatcttat cttatcttgt ccagatttta ttttatttcg 120

tttatgggct tggacttaaa atagatttgt aagctntgtg gctaagaacc tcatccatac 180

atttttaat agtatgctct ctttattttc ttttgatata ctttgtgttt taacgacttg 240

aattcaatat gaatttgttt atcaattatt tgtggagttg tacattactt atatgaaatt 300

ttataagttt attgttttag ttagatttca ctacgttcta aaat 344

<210> 2325
<211> 453
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 2325

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atgaaaagtt atgaccattt gaatttctcg agagctacct ttgttcaatt tcgagcgtct 120

cgatatatta tgcgcctgaa tcggacctcc gagtgaaaag ttatgaccat ttgaatttct 180

cgagagcttc cgatgttcaa tttcgagcgt cttgatatac tatgcgactg aatctgacct 240

ccgtgcgaaa agttatgacc attttaattt ctcaagagct tccgttgttc aatttcgagc 300

gtctctatat gtgatgcgcc tgaatcagac ctccgagtga aaagttatga ccatttgaat 360

ttctcgagag cttccgttgt tcacatttga gcgtctcgat atattatgcg cctgaatctg 420

acatccgagt gaaaagntat gaccatttga att 453

<210> 2326
<211> 225
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2326

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caagctgtga atgatagata tgcattcacc agcttgaggg ggagtgttgt gatacattcc 120

ataattaaca cagattntat tatgtacaga ttctattcca ttgtatttct ttccttaatt 180

aggttgcttg cagcatataa ataaatcttg tattcacttc tttgt 225

<210> 2327
<211> 449
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2327

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agtgaaaact caacagctat gagaatgttg tctctctacg acaacattgc tagaagacat 120

gttcccgcca aactgggaca gttctctgcg atggtggttc ttgatttgtc ggagaacaag 180

aatagtggac cgctgccaac cgatgccagc aagggacgta cactctagga cttggtcgct 240

cttgataaca tgttttctgg cgagatacca cacagttatg cgaactgcat ggtgctgtcg 300

aagtacaaag tgatctgcaa ccgtatggag gggtccattc ccgctggact catcaggttg 360

tgacacgata caatcattga tttgagtagc aacaactnta ccggtccggc tcctgagatt 420

aacggacatt ctagaaaatt atctgagct 449

<210> 2328
<211> 456
<212> DNA
<213> Glycine max

<400> 2328

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ttaaccttat ttctgtagca ttgtggggag aggttggggt aaagatatcc tttgagtcta 120

ataagatagt tatgactaat aataatgtat ttatggggaa gagatattgt gatcagggtg 180

tctttgtact caatgtttct gaagtgatta atgagaatgc atcttcttat gcttacttga 240

ttgattctta tgatatatgg catgctagat taggacatgt taatccaact tatgttatga 300

aattgcaaca atcatgttta attaatatgc atgagaaaca cagtaagaaa tgttaaatat 360

ttgttgaatc aaaattaact aagaaatcat gtccttctgt acaacatgaa attgaactgc 420

taggcttaat tcattatgat cttgcatatt taaaac 456

<210> 2329
<211> 384
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2329

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acaagcacat gcacccttgt atgacaaaat acaaagtcat tcaaagaagt ctgtgtattc 120

gaggtgcaca tctttcacat agttgtcagc ggtgttaagt ctggccaact tgaaggcatg 180

atttgcatgg agtgacaaga gcttcatcaa attgtttgtg ttattgaana gcatgctttc 240

tgaggataac acattgccga ggaatcacta tgaggcatag aagattgtat gttccgtggg 300

aatgcagtac cagataatct atgcatgccc taatgattgt agtttgtaca taaatgattn 360

tgtagagatg cgtacatgtc ccat 384

<210> 2330
<211> 402
<212> DNA
<213> Glycine max

<400> 2330

tgcctacaac aatctttaaa tatttatgta ggaataataa atcaaagaag ttactaatga 60

caaaaaaatc aaagaagtta aatataaatt taatttttgat caagaaatga caaatgaaaa 120

ttaatgtgtt tttgaaattg ccaagagctg attgaaaatg taaatttatg cacttcgatt 180

caaaggtcaa ggtaaaaaag aaatagaaca ttacatgtaa atttaatgaa aagaataatt 240

gaattgtttt ggttaagatg acgagttaga aaggaggaag tgaaattttc aaataacttt 300

tttatataaa actattcaag gatgatataa aaactatttt taaaatagtt ttagctgagt 360

gtcattaaaa taattgtttt attgaaaaat agtagtagat gt 402

<210> 2331
<211> 433
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2331

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cctgcgcaat ttatcaattn tttgagcaag gacagccccc aatgcataat ttgatgcatc 120

acacataagc tcaaaagggg ctgtccaatc gggtgcctgg atgatggggg tggtagtcaa 180

cgctcttttg aggcaatcaa aagcctcttt gcatctgtca ttaaagtcaa actccacctc 240

cttttgcaac aagttggaca gtggaagggc tactatgcta aaatcccttа caaagcgcct 300

gtagaatcct gcatgaccaa gaaaagatcg cacctctcgc acacaagagg ggtaaggcaa 360

ttgtganata acagaaattt ntgcaggatc tacttcaata cccttattgg aataatgtgg 420

ctanaactat acc 433

<210> 2332
<211> 368
<212> DNA
<213> Glycine max

<400> 2332

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acacagacct ttagccttct gtgcaacaat ttgaagcaat tgaacagctt gaagcttatg 120

ctgcaaacat ctacaataga cctcctcaac ctcagcagca gaatcagtca caacagaaca 180

gaacaattat gacctctcca gcaacaggta caatctcggg tggaggaatc atcccaacct 240

tagatggtcg aatgcttcac cacagcaaca acaacaacaa caaccttatt ttcagaatcc 300

taatggccca agcataccat acgttcctac accaatccag cagcaacaac agcaacagcc 360

ctagaaac 368

<210> 2333
<211> 491
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2333

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tcttaagaag ggggggttga attaagatat tccaaactac ttccccaatt aaaaatctat 120

ttcactcttt actcaagtta tgaattccct taatgacaat cttcttaaat attgattcaa 180

ataaaacaat ttgaatatga atataaagca ataataaata aaggagatta agggaagaga 240

aagtgcaaac tcagatntat actggttcgg ccacaccctt gtgcctacgt ccagtcccca 300

agcaacccgc ttgagagttc cactatcttg taaattcctt ttacaagttc taaacacaca 360

aggacaatcc ttcctttgtg tttagaattc ctttacaaca agagactcac agtctcttaa 420

tccgttagag aatgaggaga agaagaagaa taaatctctc tagaaagaga tggatttaca 480

gaatgagact c 491

<210> 2334
<211> 297
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2334

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gatttatttg gtccctctag aactatgagt ttaagtggaa attactatgt ctcggtaatt 120

gtggatgatt actcaaggtt tacttggacc ttgtttataa aaactaaaaa tcaagctttt 180

gatgttgttc gcaaacttgc caaggtgatc caaaataaaa aaaaaggtct ttacggtgtt 240

tcatctagaa gtgatcatgg agatgaattt accaatgagt cttttgacaa cttctat 297

<210> 2335
<211> 456
<212> DNA
<213> Glycine max

<400> 2335

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agacctccaa tctttaatgg agagggttac cactactgga aaacccgaat gcaaattttt 120

attgaggcaa tagatctaaa tatttgggaa gccatagaaa tagggcctta tatacccacc 180

acagtggaaa gagtttcaat agatggtagt tcatcaagtg aaagcataac tatagaaaaa 240

cctagagata gatggtctga agaggataga aaacgagtac aatacaactt aaaagccaaa 300

aatataataa catctgccct gggaatggat gaatatttca cggtttcaaa tcgtaagagt 360

gctaaggaaa tgtgggacac tcttcgatta acacatgaag gaactacgga tgttaaaaga 420

tctatgataa atgcactaac tcatgagtat gaatta 456

<210> 2336
<211> 462
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2336

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tttattattt gttcatttca ggttcaacac tgtagcatat ttgcagcaaa tatggtggtt 120

tgaggtggat ggggagttca gcttcccttt tcctgctgat atttatactc tctcctttag 180

gcttcacctt ggacgatttt ccaagaggct tggtcgacgt gtctgcagtt atgaacatac 240

ccatggttgg gatataaaac cagtgagatt tgagttgtca accatggatg gtcagcaagc 300

atcatctgag tgctacttgg atgaaactga acctgatgat ttacacggca atcacaagcg 360

tggacattgn gtagattaca aggtgggtga gtttatcgtc agtggatcag aacctacaac 420

taaagtaaga ttcttcatga tacagattga ttgacacact ct 462

<210> 2337
<211> 451
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2337

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tactctttga atatctcgag aatgaacaat ggaacatctc gagtaattca aatggtcata 120

acatttcaat cgaatctccg attctagcac gtaatatatt gagacacttg aaatcgaaca 180

tgaaagctct cggcaaattc aaatggccat aacttttgac tatatgattg aggcccatga 240

tatttccaga cgctcaaaat tgaacaacgg aagctcttga gaaattcaaa tggtcataac 300

ttttcacttg gatgtccgat tcaagcgcat aatatatcga gacgcttgaa attgaacaca 360

aaagctctga ccaaattcaa acgaccataa ctnttcacat ggataatcga ttgatgccca 420

tgatatatcg agacgctcga caatgaacaa c 451

<210> 2338
<211> 421
<212> DNA
<213> Glycine max

<400> 2338

agcttcctag acgactactc cggatacaac cagatcagaa tggatcctct agacgaggag 60

aaaatgacat ttatcactgc ggatgccaac ttttgctata gggtcatgcc tttcggccta 120

aaaaacatag gcacaacata ccaacgactg atggatcgag tcttcaaaca acagatcaga 180

ctaaacattg aggtatatat ggacgacatg gttggcaagt ctcacagcat accccaacat 240

gtggtagacc tagaagaagt cttcagggaa ctccgcaaat atgacatgca cctcaaccct 300

aaaaaatgta ctttcggggt tggcggaggc aagttcctca acttcatgat cacacaccga 360

gggattgaag ccaaacctga caaatgcact gtcatactgg agatgcgcaa cccagccaac 420

a 421

<210> 2339
<211> 432
<212> DNA

<213> Glycine max

<223> unsure at all n locations
<400> 2339

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ctattgtaga aagcaattta tttttggcct catgtctgtt cagtatcttt gaaatttcc 120

tgttagcata attactttaa ttttctcatt agtaaatgat agatttataa gccaagatta 180

tcatttcaaa tatagaatag ataattnttc tttattgttc tcatggcaat tcttacacta 240

ttaaaaaata tactttcaac atcaatttta aaaccgatgt tgaaagtacc aatgttaaat 300

gtaatattgt taacatcggt tttgaaaaac cgatgttaac ataaaaattc taacatcggt 360

tttcaaaata aacgatgtta tatacaaaga actacaacaa aataagtgta tgcataatga 420

atattgacat cg 432

<210> 2340
<211> 498
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2340

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agtctctgat gaaatcctat cccccaaggg cataggatag aagactccaa gaagattggg 120

ccagagatgc aagagaaggc cctaggattc tcattagcct tatggtagat tntgggccca 180

tgggctaagt atgagaccac ttatctttgt acatattaca ttaatgtttc attatttttg 240

gcctttgtat ttaggactcc ataatgtagg tagggtaccc tagaaatgtt ggacttttca 300

gcccttgtat tttatggcac ctagactagt tntttgtatt aagggtagtt ntgtaatttc 360

attcgcatta agtgaatatt tgatgtgtgt gttgngaaat aaatttaatc gaattgggag 420

aagcctaatc caattaaatt ntagaggggg aggtgagcat tngcttgcta cacnccattg 480

ccacatcata tagtcaca 498

<210> 2341
<211> 380
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2341

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tccctggagg tggcacttcg tttcccgaag gagtcgatgc ttatgttaat gctctaaaac 120

gtcttcttcc cgtgccttta taatctgggg atgtcaaaac aatgcttgat gttggatgtg 180

gggtgagtca ncttctatat cttattatgc tttctccttc cttggattct ctttctttat 240

tttctttcgt cctctcttaa ttgttcgccc tgttatcatt tcattcgcct tcttttagct 300

tgtactttta catgttacta caagaggagt ttcttgagca acanagacag agaggctttt 360

caatcaaatg agagcttatg 380

<210> 2342
<211> 430
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2342

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tctcgggtca atctaacatc gtggaactta agggtgccta tgaggataaa caatcggtgc 120

atttggtcat ggaactttgt gcgggtggtg aacttttga tcgtatcatt gctaagggac 180

attacactga acgcgccgcg gcttcattgc tgagaaccat aatgcaaatt attcacactt 240

tccattccat gggtgtcatt catagagatc ttaagcctga gaatttcctc atgttgaata 300

aggatgaaaa ttcacccgtc aaggtcacag attttggtct atccgtcttt ttcaaagaag 360

gtttcccttа attctatttc atatattctc tattattntt tctctcttcc acatcttttt 420

ttttttcaat 430

<210> 2343
<211> 452
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2343

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gtcttttggg gcctggttta ataaggcag gcaagatgat tgccttgcta tttgctcttg 120

attggttctg cgtaaaatat gtgagttctc aaaccaaata atgtcaataa gagaaatacc 180

gcagaagcta taaactgtag cttctgttgt gacacacgcc cgattgggta aaacaatcaa 240

atagaacagt ttcagtgttt cctgtttgtg ttcttagctt ggttccagaa ctttccttca 300

cttatcttga agaaacggtg tttcttttgg cttctttgag tgtcttttat gatatgcatt 360

gtgatttacg gagaacttat tgatcacatt ctctgtattt atatccctgc aactntgtca 420

agagtagacg aatattgcac tgatgataat ac 452

<210> 2344
<211> 407
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2344

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ggatggcctt gattttctca aggtccactt ggaccccatt tctaccaact acaaatccta 120

agaaaactat attatctaca caagaggtac acttctctat atttgcatag agggtgtttt 180

tcctaaggac tgaaagaact tgcctgagat gtcctaagtg atcatctagg ctcctactgt 240

acactaaaat atcatcaaaa taaacaacta caaatctacc taggaaatcc cttaagacat 300

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attcatacaa accaaacttg gtcctgaaaa gcggtntcca ctcatca 407

<210> 2345
<211> 343
<212> DNA
<213> Glycine max

<400> 2345

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cgatatatta taagcctgaa tcggacctta ttgtgaaaag ctatgaccat ttgaatttct 180

caacaacttc cgctgttgat tttcgagcgt gtctatatga gaatcgcctg aatcagacat 240

ccgaggtaaa agttatgacc atataaattt ctcaagagct tccgctgttc aattacaagc 300

gtgtcgatat gcgatgcgta tgaattggag atccgtgctg aaa 343

<210> 2346
<211> 654
<212> DNA
<213> Glycine max

<400> 2346

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ttgtccaaga atgaagaatt gaatttggaa aatgacaaat gacgagtctt ggtgtcgatc 120

tttgtttctt tcccaagttc ttctgatcta aagtaaaaat ctccaccgag tgacgtcgct 180

agatcatgca tgaggtcatg catcacaaac catttccgat catgcttgag gtcaggcatc 240

aaaaaccatt tccgatcaga ccaactactt ctatttgaac gttggaaaaa tgatctcgaa 300

accaaatcat caaaatactc atgaccaacc tcttctaaag tcctaccatt tcttggtttc 360

ttcaaaagat cttcggccat ccacaacaag attaattcat ttttttcaaa ctcgtaatct 420

tgaggataca aggaacaata aacaaagcac ctttttaaat gtggagggag gtaatgataa 480

ctaagtctca gtgctggaat aactttacac tcactttcag aaagttccca aatgtcacta 540

ttcagaatat tattccaatc cacgatgtca tgctttcttc tcaacatgcc tccaagcgac 600

tctgctgcta aaggcagtcc atcgcacttt ttaacaatct tctttccatt tttt 654

<210> 2347
<211> 593
<212> DNA
<213> Glycine max

<400> 2347

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tcatcagtgg gctttccttc tgtgtccagc atcttgggat gttcccagcc tttgatgaca 120

gctttccagg ttctgctatc cagtgatttg agaaaggcca ccatccttgc tttccagtat 180

tcatagttgg tcccatccag aattggtggt ctgttcactg gtcctccttc tttctccatg 240

ttcatcagaa tttatctccc tagatctcac tcagtgattt cgagtgtctg ctctgatacc 300

aattgaaatt ctgatactgg ggacagatgt cgtacaagat gtcacgacat cacacttcag 360

aacatgcaga ttgtgtttga ctgtatgaac agattaaaca agtaaataac acaagagaat 420

tgttgaccca gttcggtgca acctcaccta catctggggg ctaccaagcc agggaggaaa 480

tccactaaaa tagtgttagt tcaaggtcta acagccactg tttacaacct tctcacctaa 540

ccactacccg tgcgatctct acctaagagc cactcttaaa tatgagaaac ccc 593

<210> 2348
<211> 555
<212> DNA
<213> Glycine max

<400> 2348

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gttcttttga aagactacga tgagaaaatt acagaggaca tgaatccctg ggggaaacca 180

agaagaacac acaaaaataa aaacaagcaa cgacttcctt aattgcccca gatcttaagc 240

gtagtatcgc ttgacaacgt cggagttcac gggtgagggt agctcctcga catccatgtt 300

ggcgagcacc agggtccctc cggagaaatc ccttttttaca acgaaaggcc cttcgtagtt 360

cggggcccac tttcctctat tgtctttcag agcttgggag actttttttca acaccaagtc 420

cccttcactg aacctgcgcg agcgtacctt cttgtcaaaa gcattcttca ctcgtttctg 480

atataaacgc ctgtggctca tggcggccaa atgcttgcct tctatgagat taagctgatc 540

gaaacgtgcc tgagc 555

<210> 2349
<211> 539
<212> DNA
<213> Glycine max

<400> 2349

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ctaatgactc ctctgcggct tccacataat gcatagagga tgggaagctc accaagatgt 120

cttcctcgcc tgatacgatg accagatgcc cttccactat gaatttcaac ttttggtgga 180

gtgttgaggg aacaactcct aatgagtgga tccacgggcg ccccaacaga cagctgtagg 240

gagggttaat atccattatt tggaaagtaa cttgacaggt gtgagggcct atctgtactg 300

ggagatcgat ctctccccta acctctcggc gggtgccgtc gaaggcacga accaccgttg 360

aactcggctt taagtgggag gcattgaatg gtaatttctc caaagtgctc ttaggcatca 420

cgtttaaact ggaaccatta tcgatgagca ctttggctac gatatggtgc atacacttga 480

ctgatacgtg caaagcttta ttatgccctc tcccctcggc ggggatttct tcttccgcg 539

<210> 2350
<211> 604
<212> DNA
<213> Glycine max

<400> 2350

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caagtttcag aatttctaca cctagaccac tccttgaaac actccttttt tactctaact 120

ttgctctgaa cattttcatt ccaccaccac gattctttac ccctaggtcc aaaacctcta 180

gattcaccca acgtctcttt agccacttta ataatctctt gggacatctt gttccacata 240

tcatttgcac ttccttgtga ttgtccacac caaccctccc atatcttttg ttggaagatt 300

ccttgtttct caccccttcaa gtgccaccat ttgatccttg gtgctaccat aggacttctt 360

ctctttgccc tatctctaat tcttacatcc ataaccaaca ctctatgttg ggtagtcaag 420

ctctctcccg ggataacttt acagttcaag caatacttcc tatcagactt cctgataagg 480

aagaaatcta tctgagaaca tgtccctcca cttttgtcag tgataagatg ttcctctctt 540

ttcttacacc atgtattggc tatagaaaga tccaaagcct tcggaaactt caagatggat 600

ttac 604

<210> 2351
<211> 636
<212> DNA
<213> Glycine max

<400> 2351

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ccgtttccgt gatgacgact ctcgtctcta ttccttcttt tttcttctgc ataaaacaaa 180

atacaaacaa caacaagaac aacgaatata atatacatat acacatatac acatatccgg 240

cgaaggaacc gatccagaaa acaacagaat aacgtgtttc ccagtcacca gaggcttcgc 300

gcttgacaat ggaggacaca tgaatagcgc taggcaataa cattcatgag gctccgaaaa 360

ggggtgagaa tggaggattg ccttgagggt cctcacttag gcaatcatga aaccagctcc 420

aaactcgaaa gtggaggaca catgaacaac cctaagcaat aacattcatg tggctcccga 480

aaagggtgag aatggaggat tgccttaagg gtcctcactt aggcaatcat gaaacacagt 540

ttcaaactcg aaagtggagg acacatgaac agccctaagc aataacattc atgtggctcc 600

ggaaaacggt gagaatggac gattgccttg agggcc 636

<210> 2352
<211> 533
<212> DNA
<213> Glycine max

<400> 2352

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ataacaattt agtgcccaac ttgtcccaca aagttctcca aaaatggctt aggaacttag 180

agtccctatc actaacaatg ctctttggca aaccatggag tctcacaatc tccttgaaaa 240

acaaatcaac cacatgggaa gcatcatcaa ctttttttac atggaataaa atgagccatt 300

ttacaaaacc tatcaacaac cacaaaaatg gaatctctac cactgcttgc ttttggcagc 360

cccaaaacat aatccatgga taaatcaatc caatgatact ccggaatttg caatggagta 420

tacaattcat gaggctttac cttagacttt gccttttaca tacaatgcaa tgttcacaaa 480

atttcggctc atccttttc atatgaggcc aataaatatg ttcttgtata tgt 533

<210> 2353
<211> 337
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2353

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tccctcggtt cttcactttc tctttacttc cttcctcaac tcaaggtgtg attttgtggt 240

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tttctcgact gctcggcgct cgatctacgt ggttcat 337

<210> 2354
<211> 391
<212> DNA
<213> Glycine max

<400> 2354

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gagtagtggg gacaaaatta gagcattggg gatgattttg gagatgttga gcaacggtgt 120

tgatcctgat aggatcacat ataactcact gatatcaagt ttgtgcagag atggaatggt 180

ggatgaggcc attgggttgt tggtggacat ggaacggagc gagtggcaac ctacggttat 240

tagttacaac attgttcttc ttggattgtg caaagcacac agaattgtag atgccattga 300

agtgctggct gtcatggttg acaatggatg tcagccaaat gaaactactt acacgttgtt 360

ggtggaaggg gttggatatc ctggatggct a 391

<210> 2355
<211> 393
<212> DNA
<213> Glycine max

<400> 2355

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aaagttatga ctatttaaat ctctcgtgag catctgtcgt tcaatttcga gcgtctcgat 120

atattatggg cctgaatctg acatccgagt taaaagctat gaccatttga atttctcgag 180

agcttccgtt gttcaatttc gagcttctct atatgtgatg cgcctaaatc ggtcatccga 240

gttaaaaagt tatgaccatt tgaatttctc aagagcttcc gttgctcaat ttcgagcgtc 300

tcgataaatt atgcacttga atctgacctc cgagtgaaaa gttttgaccc ttcgaattgc 360

tccagacgct ccattgttca atttcgagcg tct 393

<210> 2356
<211> 449
<212> DNA
<213> Glycine max

<400> 2356

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gagcagtggg gacaaaatta gagcattggg gatgattttg gagatgtcga gcaacggtgt 120

tgatcctgaa ttgatcacat ataactcact gttatcaaaa tatggcatag atggatatgg 180

tggatgacgc cattgggttg ttggcggaca tggaacggag cgagtggcca cctactgtta 240

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aagtgctggc tgacatggtt gacaatggat gtcagccaaa tgaaactact tacacgttgt 360

tggtggaagg ggctggattt gattcatgct caatcaacaa attgtattca tttatcaaca 420

gcgtttttcc tttcatttga actaaattt 449

<210> 2357
<211> 471
<212> DNA
<213> Glycine max

<400> 2357

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ctcaaattcc tggaaaatgc aaagattcac gtacattcag cataccttgt attataggga 120

atagtaagtt tgacaatgcc atgctagatt caggagcttc tgttagtgtt atgcctctga 180

ctatgtttaa ttctttatct ctacgtccct tgcagtcaac tgatgtggta attcatttag 240

ctaatagaag tgtcgcctat cctgttggct tcataaaaga tgttttagtt agagttggta 300

aactgatttt ccctgttgat tttcatatta cgaatatcga ggatggattt cctcataaat 360

cagtttctat tcattctatg ctgacccttt atgataactg ctacaactaa tattgatgta 420

tatgcatgca cactatccat ggagtatggt gatataaccg gtccttttta t 471

<210> 2358
<211> 568
<212> DNA
<213> Glycine max

<400> 2358

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gcgcaacctt gctcatcttc ttgttgtgaa agaaattgga gtacatattc atttattcat 120

tctttaaaga gaaacaagat ggcaccactt agagctgaag atttagtatt tgttcatagc 180

aacctacgac ttctctcaag gaatactcca caatatcatc aagaggaaac taaaatgtga 240

gatgtaactg gagatgattt tgggttactt aatgaatgtg gcattcttga aatttctaat 300

ttgtctttag atgaaccaca gttagagggt gtctttttca atgatgattg ctagtttgta 360

gaattcttga agacttgaag ttgctaattc atcatcttgc tttataatta ttcttttcga 420

aagaaacaaa gtgtacaaat cgtataatga ggtctcttag tatttcttgt gacttattat 480

cataggaaaa gttttttga gatgatgatg aatatataaa tcttaacttt caattaagat 540

cctttatgca tatcgctcat atttaatc 568

<210> 2359
<211> 579
<212> DNA
<213> Glycine max

<400> 2359

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gtttttctac catgtttcag ttgtatgtag cttgtgtctt cttcacagat ggggcatgca 120

agatgaccct taacactgta accgctgaaa ttcttatatg ctggaaagtc attaatggta 180

caaaatagca ttgcacgcat ttgaaaagtc tccttgtgaa acccatcaaa tactaaaacc 240

cccttatccc acaactttct caggtcttca atcaaccgac ttaaataaac atcaatgtca 300

tttcctggtt gtcttgggcc tgatatcatc atagacaaca tcatgtattt tcgcttcatg 360

cacaaccaag gcggaaaatt gtaaaatact aatagaactg gccatgaact gtgttgagtg 420

cttaaattgc catatggatt cattccatca ctggctagtc caagtctaag atttcttgcc 480

tctttgccga aattcggata caaactatca atcctcctcc actgggagca atcagctgga 540

tgacggacca ttccatcaga atttctccca tttgcatgc 579

<210> 2360
<211> 614
<212> DNA
<213> Glycine max

<400> 2360

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gaaacttgga caatgacaaa gtacaaggaa ataagaatgt actgattatt cacctctctc 120

cttctctcag ctcgttcacc acacttaaaa ctgaatccat aatttggaag tgttcccacc 180

ctttgaggtt tggcatcttc tgtgttggaa cttctaggag gattaaggtt aaaacacaat 240

atacacagca ccacactcaa taataaattt aaataataga gacccagtag ttccagattt 300

tcactcataa atatacaaac ccaaaaaagg atacaaggaa gattctgctt ctccttgaac 360

tttatcaatg ggttcttttc tcgatgattt tggttttgtc ttctccctgt atccaaaaca 420

tcacagtcca ccagttaaat aataacaaca atctatcttt ctagcaatgg aacatagaca 480

agaaatacaa gcattacata cactgatact tcagaagatg ttgcatcaga cttcaaaggt 540

gctgagaaaa acaaagtgca aaaactatca gggaatgccc aaactataaa cttgatttcc 600

caaaagagat aaaa 614

<210> 2361
<211> 535
<212> DNA
<213> Glycine max

<400> 2361

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agatggcata tttctcccaa atgcatcttg agtaaagtcc cattgatatc gataaaattg 120

ctgtaatcag gctctacaca tgcagggtgt cagagggttc tcccagaggt cgtagttagg 180

gaaagtctct tctggcaatc ccgtccgagt ctggtgagta acaacaacat cttctacaaa 240

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aattgatttt agacggtgac ccatgtatct acgtgctcca atgatcaact tagcaaaatt 360

gcctccatgg gtcatcacga atacatttga cttcaagcac accaagaaat caagagctgc 420

caggcttgtc acatgctttc tgaaaccatc taactcctct ttagttgcca actcctcctt 480

ggaacctgtt gcaaatgggg gaaatattaa ttaccttgca aaagaatcaa aaata 535

<210> 2362
<211> 608
<212> DNA
<213> Glycine max

<400> 2362

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ttcaatgcaa agttaccact ccattccatc caaccttgag gattgataaa gccatcaaga 120

caagtcttca ttaaaactgt tcttgaatat tgcttccatg gtcttcgaag ataagtccta 180

accgggtttt gaaccagtct caaatctgaa gtagctgtga ctcaagaatt gcgaattgaa 240

attccagtgt tttagtttgg atcagttctg ccttgtgcag tgatggtgtt gactatgttg 300

ggagggtttc ttgcaaggtg ttgcagtttt gtaacacaac aacaacatgc tacaggagat 360

ttccatcaac ttccctgcca caggcgtttg ggtaaaaaca aaatgttaag tcaactaata 420

gccaggaaat tccattacac tttcacatgc acacagtaaa aagaaacaag ttatatattc 480

agagggtgat tagaatcaat gaattttata tcccttctaa attcgtacca aacaatttaa 540

ttgtaagaaa ataaggaatc caaaatatgt acttgactag acttatgata tagtggaata 600

aatgatat 608

<210> 2363
<211> 628
<212> DNA
<213> Glycine max

<400> 2363

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aaagttatga ccatttgaat ttctcgagag cttccgttgt tcaattacaa gcgtctctat 120

atattatgcg cctgaatcgg acctccgagt gaaacgttat gaccatttga attgctcaag 180

agcttccatt gttctatttc gagcgtctcg atatattatg cgcctgaatc ggacatgcga 240

gtgaaaagct atgaccattt gaatttctcg agagcttccg ttgttcaata tcgagcgtct 300

cgatatatta tgcgactgaa tctgacatct gaattaaaag ttatgaccat ttgaaattct 360

cgagagcttc cgttgttcaa tttcgagcgt ctcgatatat tatgcgcctg aatcggacct 420

ccgagttaaa agttatgacc atttgaattt ctcgagagct ttcggtgttc aattcgagcg 480

tctctatata ttatgcgcct gattcggaac ttcgagttaa aagtttgacc cttctaattt 540

ttcggagctt ccgttgttca attacaaccg tcttatttttt atgcgcctga atcggactct 600

ccagtgaaag gttttacctt tgaatttt 628

<210> 2364
<211> 605
<212> DNA
<213> Glycine max

<400> 2364

tgccagaata atgggttgga tacagatcat tctgggaggg ttggtcatct ttgtaagcct 60

tttgagtctc actagattct actcagcagg atttttcctc cacaatgaag atatatgcca 120

acacttctac aatctgaggg atgtttctga tggttttgat gtcaaatcat tctctgatag 180

agttggagaa gtgatagaca tgttggaagc tttgcaggcc aagcttgagt caaaagttca 240

agaaatggag aaaaacaaag gcaccatgtt ggacaagaag tttctagagg atcaaatagt 300

tagccctctt catagtgcta atgttgctct aaggcagatt cgggttccca aggttgatga 360

agggacgaac tccacagtga aggaggatca tttgatcaat tttttcatca ttgaggaaat 420

tagaaagtac ataaccccca aggagaatag ggttggtaag atcaacctat atggtgcaga 480

caaggtttac aacacaatag gccatgcttg tgttttgtac aagaaagagt tagagaagta 540

catggactat gacattggct cctattggga tgatgattgg aatttgctca gaagcctatg 600

ctaat 605

<210> 2365
<211> 373
<212> DNA
<213> Glycine max

<400> 2365

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acttccattt gcccatcggg tcgtgggtga caagtggctg aaaataacaa tttattgccc 120

aacttgctcc actaagtcct acaaaatagg cttatgaact taaagtccct atcactaaca 180

atgctccttg gcaaactatg gagtctcaca atctccctga aaaacaaatc agccacatgg 240

gaagcatcat ctatttatct acatggaata aaacgagcca ttttagaata cctttcagca 300

ccacaaatat ggaatctcta ccattggttg tgttcggcag ccccacaaca aaatccctgg 360

ttaaatcaaa tcc 373

<210> 2366
<211> 592

<212> DNA
<213> Glycine max

<400> 2366

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aattcttttt gcggctttta gatgaggaga ggtaggagcc tccataaagc gacacacaac 120

tcccaccgca tatagaatat cgggccttgt attggttaga taccttaaac tccccacaag 180

actcttgaag atcatggagt ctaccttctc tccttcatca aactttgata acttcaagcc 240

accttccata ggtgtgttca cgggattgca atcaagcata ttaaatttct tcaacacttc 300

ttttgtgtac ctttcttgtg agacaaagat accattctcc gtttgcttca cttccattcc 360

caagtaatat gacatgagtc ccatatctgt catatcaaat tcacgagaca tggactcctt 420

gaagtcttca aacaaatttg ggttattgcc ggtaaagata aggtcatcca cataaagaca 480

aataaataag acatcaccat tattaaaagt tttaacataa agagcataac tcatttgaca 540

acgaacaaac ccattgtctt ggaagtactt gtcaatgcga gtattccatg cc 592

<210> 2367
<211> 677
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2367

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caaaacctag actacctaaa ctgggagcag caggacaaac aattagtgtc tttggcttct 120

accatcaatg gcaccgagtc ttcacacaaa aggatggttg gaagatactt gaaacctaac 180

cttttagacc aaagccaaaa tcaaacaact aaaacagaaa ctaagtgtct aatagatagg 240

agcaatgaat gtatattttt gaaacataat catagtaaca cgaatgggta agaaaaacta 300

actggttttg aaacaaaatt aactataatg acttagtatc gtcttagtct aatttaaatc 360

tccaaattca cagtaacacg aatgggtaac aaaacctatt gttcagaaaa ataatcatat 420

tgactagtct catcttagtc aaatatcaat catattagtt agtctaacta tggtttcgaa 480

acatgagaat agagatagac cactgaacaa tggattttca tcattaacag agaatagaga 540

cataccttcg atggcttccc tggcagtctt aaagccaagc ccaatggact tccaaaatcg 600

attcccaccc ttttcgagac tttntccttt cctagttctc ttcgagctgc aaaagtgacc 660

aaatgttaaa atgagga 677

<210> 2368
<211> 618
<212> DNA
<213> Glycine max

<400> 2368

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ctgtatcctt ggaaagtaga aaaaggtcag cttctcaagg gcagggaaga ctcctaaagt 120

tgaaaggcta gaattggtgc acacaaatgt ttgggagcca accctagtga aatctattgg 180

aaactcacgc tattatgtca cctttatcga cgactctacc agaaaggtat gggtttattt 240

tcttaaaaat aaatctgatg tgttttctgt gtttaaaagg tgaaaaacag aagttgaaaa 300

tcagacaggt ctaaaagtct aaaatatgac aatggcgggg agtatgatag tcaggagttt 360

aaagactttt gttcaaaaca tgggatcaga ataatcaaga caatacctgg aacacctgag 420

caaaacggtg ttgcagaaaa gatgaataga accttgaacg agaaagtgag gtgtatgcag 480

atccaatttg gcttgcctaa agcattctgg gcaaaagcaa taaacacagc cacatatctc 540

atcaatagag gaccatcagt tcccttgaaa tatcacgtcg cccgaagaag tatggtctga 600

aaaagaggtt aaactttc 618

<210> 2369
<211> 663
<212> DNA
<213> Glycine max

<400> 2369

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aattcttttt gcggctttta gatgaggaga ggtacgagcc tccgtaaagc tacacacaac 120

tcccaccgca tatagaatat cgggccttgt attgattaga taccttaaac tccccacaag 180

aatcttgaag atcgtggagt ctaccttctc tccttcatca aactttgata acttcaagcc 240

accttccata ggtgtgttca cgggattgca atcaagcata ttaaatttct tcaacacttc 300

ttttgtgtag cttccttgtg agacaaagat accattctcc gtttgcttca cttccattcc 360

caagtaatat gacatgagtc ccatatctgt catatcaaat tcatgagata tggactcctc 420

gaagtcttca aacaaatttg ggttatggcc ggtaaagata aggtcatcca cataaagaca 480

aataaataag acatcaccat tattaaaagt tttaacatac agagcatact cattttgaca 540

acgaacaaac ccattgtctt ggaagtactt gtcaatgcga gtattccatg ccctcggtgc 600

ttgctttata ccatacaacg cccttgtcaa tttcaagact tttccttctt gacccttgat 660

gac 663

<210> 2370
<211> 641
<212> DNA
<213> Glycine max

<400> 2370

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gttggacctc ccagatgagt atggaatcaa caccactttt aacatttctt atttaattcc 120

ttttgcacgt ggagctgata ttgacgagga ggaactaaca gatttgaggt caaatcctct 180

tcaacgggaa gggaatgatg caatcctccc taggaaggga ccagtcacta gagccatgag 240

caagaggctc caacaggatt gggttagaac tgctgaagaa ggccttagga ttctcatgaa 300

cctcaaggta aatttcttag cccatgagct aaggttgggt ccaattatct ttgtacatat 360

tagactagga tgtcattata tttggtcctt gtatttaggg ctccataatg taggtagggt 420

accctagaag tataagattt ttcagccctt gtattttagg gtgattttag gcagtcttct 480

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cttaagcata aactaacttg acaacagtaa agggaatttg a 641

<210> 2371
<211> 587
<212> DNA
<213> Glycine max

<400> 2371

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acaagagtca tgtcttcaag ggctccacca ctagcatcat ctatcatact cctctccata 180

ttactgagtc cttcataaaa atattggaga agaagttgct cccaaatcgg atggtgaggg 240

caactggccc atagtttttt aaatctctcc cagtattcat ataagctccc tccactgagt 300

tgtataatac ctgagatatc cttcctgatg gccgcggtcc tggcaacatg aaaaaaaaaa 360

tgctaaaata ctctcttata gtcatcccaa ctcgtgatgg accttggagc aaggtaatac 420

agccactcct ttgccactcc ctctcaaaaa tgaggaaaag cccttacaaa tatgtgaccc 480

tcttggacat ctgggggttt catggtggaa ccgacaatat taaattcttt cacatgtttg 540

tgcgagcctt cacctgcaat gccctgaaac tttcggaacc acatgga 587

<210> 2372
<211> 506
<212> DNA
<213> Glycine max

<400> 2372

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tactcggatg tctgattgag tcccgtaaca tatcgagacg ctcgaaattg aatgttgaac 180

ctgtgagcca attcaaacga caataacttt tttctcggat gtctgattga gtcccgtaac 240

atatcgagac gctcaaaatt gaatgttgaa cctctgagcc aattcaaacg acaataactt 300

tttactcgga tgtctgattg agtcccgtaa catatcgaga cgctcgaaat tgaatgttga 360

acctctgagc caatccaaac gacaatagac tttttactcg gattgagtga tagcgtcccg 420

gaacatatcg agacgcttga aattgaatgt tgaacctgtg ggccaattaa accgacaata 480

actttcttct ccgatgtctg attgag 506

<210> 2373
<211> 636
<212> DNA
<213> Glycine max

<400> 2373

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tttctggcgc taaactgctg ggagttggaa gccatctcct caattaaatt tctggcttca 120

gcaagagtca tgtctccaaa ggctccacca ctagcagcat ctatcatact cctctccata 180

ttactgagtc cttcataaaa atattggaga agaagttgct ccgaaatcgg atggtgaagg 240

caactggcac atagtttttt aaatctctcc cagtattcat ataggctccc tccactgagt 300

tgtataatac ctgagatatc cttcctgatg gccgtggtcc tggaagcaag aaaaaaaaat 360

tgtaagaata ctctcttaag gtcatcccaa ctcgtgatgg accttggagc aaggtaatac 420

agccagtcct ttgccactcc ctctaaagaa tgaggaaaag ccttcagaaa tatgtgatcc 480

tcttggacat ctgggggttt catggtggag cagacaatat gaaattcttt cagatgtttg 540

tgcgagtctt cacctgccag gccatgaaac tttggaagca aatggattag tccagtttta 600

agaacatatg ggacatcctc atcagggtat tggatg 636

<210> 2374
<211> 607
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2374

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ctgagcaact ccttcttcag tatttctatg agagacttag caacatggag aggagtatga 120

ttgatgctga cagtggtgga gctcttggtg atatgaccct tgcagaggct aggaatttga 180

ttgagaagat ggcttccaac tcccaacaat ttagtgcaag aaatgatgct attgttctta 240

gaggattcca tgaggcagcc acggattgat catcatctat tgaaaataaa aagcttgaag 300

gaaaacttga tgccttggtc aacttggtaa ctcaacttgc catgaatcag aaatctacac 360

ctgttgcaag agtctatggt ctatgttctt ctgcaaatca ccatacagat ctttgtcctt 420

ctttgcagca atctggagtc aatgagcaac ctgaaactta tgatgtaaac atttataata 480

gacctcctca gtagcaaaac caacaacaac aaaataatta tgacctttca agcaatagat 540

acaatccagg ttggaggaat catccaaatc tgagatggac aagtcctnca caacaacaat 600

agcatgt 607

<210> 2375
<211> 488
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2375

tgatccaact caaccatgga tagacaaaat atctaccaga caccgcatat actaaaagct 60

ctnaccctta tcgcgattga actactttaa ggaagtaggg gaatgaaagc cccccataac 120

cattaactgg gaaccaagtt catgatcgcg tcaacgacat tgttaccgtg tttgggaagt 180

cccacaagaa gacatcatct tccaacaaca tgtggaagaa acgctcaata ttctttgatc 240

tttcatactg ggctgatcta tatgtgcgtc actgtctaca tgttatgcat gcggagaaaa 300

atgtgcggga tagcttaatt tgtactcttc ttaaccttaa agggaagaaa aacgatgggt 360

tgaaatttct tcacgacttg cgtgacatgg gaatacgaga gcatttgctt tccatatcac 420

aaggtccggg aacatattta ccccctacat gccacacact tgtctacatc agagaacaaa 480

aacttttg 488

<210> 2376
<211> 623
<212> DNA
<213> Glycine max

<400> 2376

tcatccaact caagcatgga aagaaaaaag tatataccag acaccgaaga tttctaaaag 60

cttttcaccc ttatcgacga ttgaaaaaag cttttaatgg aagtcagggg aatgaaggcc 120

ccccagaacc attaactgga aaccaagttc atgatcgcgt aaaggacatt gtaaccgtgt 180

ttgggaagtc ccagaagaag acatcatctc ccaacaacat gtggaagaaa cgctcaatat 240

tctttgatct tccatactgg tctgatctat atgtgcgtca ctgtctaaat gttatgcatg 300

tggagaaaaa tgtgtgtgat agtttaattt gtactcttct taacattaaa gggaagaaaa 360

aggatggttt gaaatttcgt caagacttgg ttgacatggg aatacgagag cagttgcatc 420

ccatatcaca aggtcggcga acatatttac ccccagcatg ccacacactg tcaacagcag 480

agaagaaaag tttttgtcaa tgtctgcgga atgtctaagt tccacaagga tactgttcaa 540

atatcaagag cctttgtgcc ctcaatgatc ttaagttggt tggcttgaag tctcatgatt 600

gccatgtctt tatgcgacaa tta 623

<210> 2377

<211> 536
<212> DNA
<213> Glycine max

<400> 2377

tgactgcgtg gagatacgaa ccatgtgcct ctccaagata cgagcagtca tatttacctc 60

ataacctaac acagctcata ctttgctgta cccttattta cgtgactata tatatggagg 120

aacgatggtt tcttgattta aacatacaca ctttgataaa ttctcacctt cggactttga 180

ctccagagga tgtcaagata atttatcggg aacaccgtgc accatatatc ttcaacattt 240

gaccgtcaat tcgattcata cttggtcacc tgcagcctat ttattgcata tggtaccttc 300

tatgatgccc acataaatac gtgtatcaga aaccatacgt attattctaa aatatatatg 360

atgcacatca gtgaaacctc caagagtaac tgtattggat acgtatccac tacggatgtg 420

tgaaacaaat tggactattg gcgtgcttca tataccttac cgggagttgc tgcactaaca 480

ctcttatgta tccaggtgga gatcgatgga gtccctatga tactgttgtc aagaaa 536

<210> 2378
<211> 419
<212> DNA
<213> Glycine max

<400> 2378

ccagaaacca tgggagttgg ctgagattta gaggacctac gtccttcaaa gaagacttgt 60

taagatgagc aataagagag gtgatttcaa aagaagaaga gttggtgaag attatatcat 120

caacatacac caacacatag gttttagagg taggtgtaaa tcacatgaaa agagaagtat 180

cactcttggc tgaattaaat cccaaggacc tcaaagtcaa actgagtttg tgaaaccaag 240

acctggaggc ctgtttcaag ccataaagag ctttgagcag tttgcatact ttgtgtttgt 300

cggatgaaac aaagcttggt ggttgagtca tatatacagt ttcttgaagg tctccatgca 360

aaaaggcatt gttgatatcc acttgatgaa taggccattg ttgagaaacc acaaaggac 419

<210> 2379
<211> 364
<212> DNA
<213> Glycine max

<400> 2379

gatgaagacg acagggacca ccgaggggt tccaatgagc cgcatgaggg cgcgttttag 60

gtccttgcct cttggatcct cgtccagctc gtgcacggtt gggttcacac ccatgccgca 120

gaagagcctc ttgatggcgt ggcacatgca gcacgtgctc acgctgaata tcaccaccgc 180

gctctccgac gccagcctct ctatgcgctc cagcgggtcc cccactaccg ccgccgccgc 240

gttccgaggg gccgccacgt agctcccccа ccacgccgcc gccgctgctt ggtaatgcat 300

tctcagaaga attttatgtg atgaaagaat gacacgcaca atgtatgaaa atgagagtga 360

gaat 364

<210> 2380
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2380

agctntgagc aaattcaaac gacaataact ntttatctcg gatgtgtgat tgagtcccgt 60

catatatcga gacgctcgaa attgaatgct gaacctatga gccaattcaa acgacaataa 120

ctttttactc ggatgtctga ttgagtcccg caatatatcg agacgctcga aattgaatgt 180

tcgacctgtg agccaattca agcgacaata acttgttact cggatgtcgg attgagtcct 240

gtaatatatc gagacgctcg aaattgagtg tttagactgt gagctatttc atacgacaat 300

aactgtctac tcggatgtct gatagagtcc cgtaatatat agagacgctg gaaattgaat 360

gttgaaactc tgagccaatt catacgacaa taacttttta ctcggatg 408

<210> 2381
<211> 337
<212> DNA
<213> Glycine max

<400> 2381

ccacaaacca tgggagtcgg ctgagattta caggacctat gtccttcact taaaacttgt 60

taagatgagc aataagagag gtgatctcac aaacaccaag agttggtgaa cattatatca 120

tcaacataca ccaacacata ggttttacag gtacgtgtaa atcacatgaa aagagaagta 180

tcactcttgg ctgaattaaa tcccaaggac cttaaagtca aactgagttt gtgaaaccaa 240

gacctgcagg cctgtttcaa gccataaaga gctttgagca cgttgcatac tttgtgtctg 300

tccgatgaaa cacagcttgg tggttgagtc atatata 337

<210> 2382
<211> 324
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2382

agcttgtaat cgattacaca tataatgtaa tctattgcca gagcagattt tcagaaaata 60

ttctcaacag tcacatcttt ttatgtggtt cttgaatggc tatcaaaggc ctatatatat 120

gtgacttgag acacgaattt gctaagagtt tttcagaaca aaaaagtctt atcctcttat 180

aaagaaaaat tgttttatcc tcttacaaat tccttggcca aattacttgt gattcaataa 240

ggaatttttg agtgctcaaa tngttcaatn tatctctttc aagagagatt tcttcttttc 300

ttcttcttca ttctgaaaag ggat 324

<210> 2383
<211> 399
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2383

tctccatctc tacaganaca aacgtaactt catcattcaa ctctgccatt ctgagctgat 60

ttagagtcct tttggcatag acagtgaatg caatagaggt aactattgcc ataatgaaag 120

aaataatgtt gtatacgata tccacaggag tcaagcggtg cttcccatac tgtgcgtctg 180

ccaatgtctc tattaaccga ccactgagag atggagaaaa agataaatct caagatgaga 240

tgttagttta tttaacagaa gtaaaaagat aacacgttct aagctgatcc acatctatat 300

gactatatcc atcagaagtc atatatgctt ctcaacttct caattctcat tttcatacat 360

gtggagctaa caaaaactcg ggtacggtag ggaactcat 399

<210> 2384
<211> 469
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 2384

agctnggttc gaatgacttt ntaatgaaaa attgttatca accgaactaa tattttatgg 60

tttggtttgg ttcgattttt gtaattttta caaaatatta tttcactaaa atttataatt 120

ttttttaata ttttgaatca aattacatta aaaaaattgt taataacaat ctatgaaact 180

tattaatatg ttaaacattc taaaataaaa attttcaaaa atctcatcta tttctaacat 240

atcttaaaaa aatcatatga aaaaaagtaa tatgcattat ataagtctta tatacatgac 300

aataaaaaac attgtgaaac tcaagtgata catgcataaa atacataaca ctaaagtaat 360

ataagtatta gtacaagtat tatggtttga tttgcgttca aaaacatata ccgcaaatcg 420

aactgaacca atcattttga gaaaaacatt caaacaattc aaaaaaagt 469

<210> 2385
<211> 465
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2385

agcttggtct ctntntcatt tctagtttag ttatgaaaca tgttcaagtt tgtctctgtt 60

aagaggatta taaaattccc acctatatat gatgtacata ttataaaatg cagtgtttac 120

taaaagatgc ataacaacta cacaatccct gtcactggcc taataataaa attttgaggg 180

gatgtctctt tgattaatct ggcataaatt aaaaaaaatt gaaagaaaag tataatacat 240

ttacagtgta aatgttttgg aagtatcata agcattttga ttttagagat cgagaaataa 300

aaaagatata tcagttataa aaatgtgtgt aaaagtaata tagtttacta atttgtcctg 360

tacttttttg ttctatgttt taaatagtga ttctgtaaaa cacaacataa cacttttaa 420

agaaagacta aaacaggaca gagacatgta tgtctgatgt ctata 465

<210> 2386
<211> 461
<212> DNA
<213> Glycine max

<400> 2386

gtaacaatct caaaacttct caacattgtc ttaatgaccc tcacattttg cattgatgct 60

tcaccaaaga atatggtatg atctgcatat cacaggatac taatttccac tgagcttctt 120

cccaccaaga ggcctttaaa ctgatttttt ttagagcttc tctcattaga cccgttaatc 180

cctcagccac aatattgaac aggagtgggg ctaacagatc cccttatcta agtcctcttt 240

gagggaaaaa ttctgctaaa ggactcttat tgatcaatat ggagacaaaa gctgatctaa 300

aacatcctgt gacccaagtt atccacttta gggtagaatc ccatcctcct acgcatatat 360

accagaatat cctcactaac tgaatcatgt gccttctcat agtcgacttt gaacaccaag 420

cagctcatat cacctctctt cacttcctcc acttcattgg c 461

<210> 2387
<211> 385
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2387

gcttgccgcc atggagtntt ccgactatgc tcttgtgtgg tggaacaagc tacaaaaaga 60

gagagcgaga aatgaagagc caatggttga tacatggacg gagatgaaaa agatcatgag 120

gaagcgatat gtgccagcta gttactcaag ggacttgaaa ttcaagctcc aaaaactaac 180

ccaaggcaac aaggggggttg aggagtattt caaggaaatg gatgtgctca tgattcaagc 240

aaagattgaa gaagatgagg aggtaactat ggctcgattt cttaatggtt tgactaatga 300

tatccgtgat attgttgagc tgcangagtt tgttgaaatg gatgaatttc ttcacaaagc 360

aatccaagta gagcaacaat taaaa 385

<210> 2388
<211> 392
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2388

tgaatgtgtt actntgacac tctctgatga ggaatacacc atagtccata gctctagaag 60

cgccacacaa atgtggaaca ccttagccat aacatacaaa gggtgctcac aggtaaaaag 120

gaacaatatt aaactaagac tcctaacaca taagtatgag atgtttagaa tggaggaagg 180

cgcagacata caatgtatgg ttgaatgctt ccaaaccatt ttaaacgagc ttacagcata 240

gtgtagaact cttgacaatt atgataatat tgataaaata ctaagaagtt tatcaagaaa 300

gtggagatcg tacgttacaa ctttaatagc tataaagaat cttgatactc tgtctctaga 360

agaatgtagt ggaaccttaa aggtcatgaa ca 392

<210> 2389
<211> 354
<212> DNA
<213> Glycine max

<400> 2389

tgtgcctctt caggtctgga atgtgaatgt agcatataga tctaaatacc cttatgcgct 60

ttgctgatgg cttctttccg ttgcaagctt caattggagt cttgtcgttt acagacttag 120

ttggacatct gttgagcatg tcaacagcat cagagactgc tatagtctag aatgcgttac 180

gtagattcgt tctcttgagc agtcatctag ccatctccat aactatgcca ttctttatat 240

cggacactcc atattgttga cgagaatatg ccactcgaag atggcgctca atgccttaat 300

cctcacaaaa tgtgtcaaac tcgcgagagg tgtactcttt gtccaatcac ttct 354

<210> 2390
<211> 315
<212> DNA
<213> Glycine max

<400> 2390

cttgcactat tatatttatt ttggtaacag tatatatttt gcctgaggtc tggttattac 60

gatgaagcaa gaaatgttgc ccaatcttca cgtgcttcac atcaatttgc tcctttggta 120

catactgtgg tcactactta tttactaatt tatgatttaa tctttcttaa taatttactt 180

atttctgaca gctgacagag tggattaata aaggagggat ggtaccagaa gagattgcag 240

ctgctgcatc tgatgaatgt gaaagaatgt tgagaactgg tgaccgggta ggtcgaactg 300

catatgacaa gaaaa 315

<210> 2391
<211> 361
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2391

tgcttctaaa ctttatacaa gaatgaagct ctgataccac ttgttagaca agtggcctca 60

gatatcttaa gaaggggggc attgaattaa gatatcacaa tcttttctaa attaaaaatt 120

ctattttgat tttaacccac atcccaagat ttctttcaaa aatgaactcc taaataatta 180

tgcaaattaa tcttactgaa tagaaacaat aagcaatata caatatacaa taaaagagtt 240

taagggaaga aagattgcan actcagaatt atactggttt ggcacaccct tgtgcctacg 300

tncagtcccc aagcaacccg cttgagagtt ccactatctt gcaaaagtcc ttacaagttc 360

t 361

<210> 2392
<211> 472
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2392

cgctgcatgc aagcttctac anaaatcctt attaaagaaa gacttcttga aagggaggac 60

cattatttac tgtgaacaat ttgctcaatt gacaacaagg ttagatcaaa tttgttacta 120

acaatcttta tattatgtca ttttcaatca atcaattata ttttttaatt ttctttaaca 180

caggtccatc gtctacaaat ttattctatt gggtggggtt ctataacaca taaactcaac 240

tttagaaaat gataaaaaga gaatgattat ctcaaatgat acaaaggtaa tatagtgaga 300

ttattttaaa atatttatgt actctaattt aataaatgca tatatttaat tttaaatttt 360

ctatcacttt catacaaaat aatttttcaa agacaagaca ctatgaatga tgtgtataaa 420

aaaaactaag aagactcatt ccaggttaat aattattcaa atttatatca tt 472

<210> 2393
<211> 386
<212> DNA
<213> Glycine max

<400> 2393

ctcagctata atatatcgaa tatgaacaac ggaagctctc gtgagattta tatggtcata 60

acttttcaca ctgacgtccg atacaggttt ataatgtatc gatacactcg aaattaaaca 120

tcggaaactc tctagaaatt caaatggtca taacttttca cacggatgtc cgattcgggc 180

gcataatatg tcgagaggct cgaaattgaa caacggaagc tctagagaaa ttcaaatggt 240

cataactttt cacacggatg tccgattcgg gcgaatcaca tttcgagacg ctcagaattg 300

aacaacggac gctctagaga aattcaaacg gtcgtaactt ttcacacgga tgggcgattc 360

aggctcatca tatatcgata cgctcg 386

<210> 2394
<211> 425
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2394

ttgaatttct caagagcttc cgttgttcaa tttcgagctt gtcgtcatat tatgcgcccg 60

aatcggacat ccgtgtgaaa agctatgacc atttgaattt ctagagagtt tccgatgttt 120

aatttcgagt gtatcgatat attataaacc tgaatcggac ctcagtggta aatgttatga 180

ccatttgtat ttctcaagac cttccgttgt tcaattctga gcgtctcaat atgtgatttg 240

ctcgaatcgg acatccgtgt gaaaagcaat gaccatttga atttctcaag agctctccgt 300

gttcaatttc gaccctctcg acatattatg cgcccgaatc ggacatccgc gtgaaaaggt 360

atggccattt gaatntctcg agagcttctg atgtttaatt tcgagcgcat tgatatatta 420

taagc 425

<210> 2395
<211> 315
<212> DNA
<213> Glycine max

<400> 2395

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gttcaatttc gtgcagctcg atatgtgata caccagaatc ggacatccga gtgaaaagtt 120

atgaccatat gaatttcttc atagcttccg ttgttcaatt tcgtgcatgt cgatatgtga 180

agcacctgaa tcggacatcc gagttaaaac ttatgaccat attaatttcc cgagagcctc 240

cgttgttcaa tttcgagcgt ctcgatatat taagcgcctg aatagcacct ccgtgtgaaa 300

agttatgacc atttg 315

<210> 2396

<211> 406
<212> DNA
<213> Glycine max

<400> 2396

agctctgctt taggggcaat gatacgacca ctgataagca atggaagcat gagaaaacat 60

gtgggcgtgc cctaggccta agatttgaca aagagagtgg agatctatac atagcagacg 120

catactatgg acttgttgtg gttggaccta atgggggact cgctacatcg ttggcaaccc 180

atgttgaaag aaagcccatt ctcttcgcaa atgagcttga cattcataag aacggatcca 240

tcttcttcac agacaccagc aaaagataca acagagtgta agcctttatt actcatatac 300

tatacatcat ttgagtatat tcatgcactc attattgctt tcaatggatt attattgttt 360

acaacgtact tattacttgt ttgcagcgcg cattctatta tattat 406

<210> 2397
<211> 387
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2397

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gaaaaagaaa tgttggcaat tgtctatgca cttgaaaagt ttaaatctta tttggtaggc 120

tcaagagtta tcatctacac tgatcatgca gctattaaat acttgctcaa caaggctaat 180

tccaaaccaa gattgataag atggattttt ttgttgcaag aatttgattt ggtgattcgc 240

gataaaaagg gatcaaagaa tgttgtagct gatcatctgt caagattagt gaatgaggaa 300

gttacagcaa aagaagtcga agtgagagat caattcccctg atgaatcanc tattttaata 360

agtgaaagac cctggtttgc tgatata 387

<210> 2398
<211> 478
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2398

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ctcatgttga ttcaatctca tcaattccat ttcatgttcg tgtaactttc caaacaaagc 120

agcaagagac atgttagata gatctcgtga ttcagtaatg gctgttacct tgggttgcca 180

ttctctgctt aagcatctca aaactttatt gataagatct tcatttggaa atgtttttcc 240

taaagatgca agatgattaa ttatgtgtgt aaacctcttt tgcatgtctt gtatggtttc 300

atttggattc attctaaata attcatattc atgagtcaaa atatttatcc tagatctttt 360

cacatttgtt gttccttcat gggttacctg taaggtatcc catatatnct tttgcatttt 420

acaatttgat acactaaagt attcattcat cgctaaagca gatgtaatta tatttttg 478

<210> 2399
<211> 438
<212> DNA
<213> Glycine max

<400> 2399

cttaagtcac ctgcggcatg caagcttggt tcccaacgct ttgttcagac tctcctaaaa 60

tctagaggtg aatctaggat ctctatcaga cactatgcta gatggcacac tatgtaatct 120

gacaatctca ctaatataca gggaggtcaa cttctccaag gaaaatctga tcttaatggg 180

aatatcctta gggaacactt caggaaactc tctgacaata gggaggtcac ccatggaaac 240

ctttgtctct acttctaggt tagacatgat catgtagact taagcatctt cttttaaaga 300

tgtcacaact tggttggcaa agataaacat cctatcctta ctcactccag aatcatcaaa 360

cactgcattt ttattaaaac aatttaacaa gacatggttg gaagataact agtccattcc 420

cagaataaca tcaatttg 438

<210> 2400
<211> 391
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2400

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cccacatcga gtagaagtgg aaaggttgag caccatataa gtgaggagaa gacccataaa 120

tctgagcctt aaggttttgg gttagagtgt gatgtcagat ctccttatgt ggtggctcgt 180

ggtccacagg tgtacccctc gaatctcccc aacaattggt atctgagctg atggttcaag 240

ttggtgaccg gctcagacga gtatgcaagt actgcaggtg gccaaaatgg ctagcggcac 300

agcgtgcccc gcaggtggag cggngtggcc agaatggcta gcgggcacgg caagtaccgc 360

aggtggccat ggctatactt gtggatgata a 391

<210> 2401
<211> 256
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2401

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gtggcggctc ctcagctggt ggttctcacg gaggcgacca ggctcccgag gcagaatacg 120

atgaggagaa gaagtaaggc gaggaggggt ttgtatccac ttctactgag ttattttggc 180

tagagttaga gatgaatcat ctttttttcat tcagcatatg atataaggta ttttgtacta 240

caaggctgga gttcat 256

<210> 2402
<211> 450
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2402

agcttccatc acanaatagc tactaaggtc ttgttgtcga gattnttctg gccaacactt 60

tttaaagatg cccatcacca tgtcttaaag tgtgatcaat gtcaaagaat ggtggatttc 120

ccgaaggaat gagacgcctc ttcaaaaaat tatggaggtt gaagtttttg attgttgggt 180

tattgacttc atgggtcctt tcccctcatc tgctagtaat aagtacatcg tggtagctgt 240

agattactgt gaatgtatgt atacatgatt ctgatgatgt caaaagaaga atcaaataag 300

gctcatttgc ttcaagatta atacaagatt gtntcaacaa ataaagcctt gattcaagat 360

gtcttcaaga tcaagtcttg cctcacaatg aaaggtttca agtcatccaa ggcatatgta 420

atcgattacc aatacatgtt gtcataccct 450

<210> 2403
<211> 424

<212> DNA
<213> Glycine max

<400> 2403

tttgtagata atgttaatgc ttcacctgta ccgttgaatg tgttgtcagt gccatggttg 60

ttcttaatgt ggggcataga tgtgattggg gctatcgagc ccatggcttc aaatgggcat 120

tgtttcatcc tagtccccat tgattacttc accaaatggg tggaagctgc ctcatatgct 180

aatgtgatta cgaatgtggt ggttagattc atcaacaagg agataatttg tagatatggg 240

ttgcctagaa aaataatcac cgataatact actaacttga aaaacaaaat gatgaaggag 300

atgtgtgggg atttcaagat ccaacaccat aattcgacac cttatcgacc caagatgaat 360

ggtgaagttg aggctgccaa taaaaatatc aagaagctca ttcacaatat gaggatgtca 420

taca 424

<210> 2404
<211> 393
<212> DNA
<213> Glycine max

<400> 2404

agcttacctt caattattgt gattcatggt atattgtcta attacacttc ttacttattc 60

atacaatact atgtttcaga tttatccata cacttgttat tatggataaa aataaatgaa 120

atacttttac actcaatctt attactataa aaatctctat tgaatctcac tattacattt 180

gattaccaca ttattataat taaaggatat ataagggagg aaatacttta taatgatcag 240

aggagggaat aaggtgaaag gaaagaagat atagggtcat aatgtcatgc acaaccagtg 300

tatctcttta taccatgtat aataatacat cagtctcttt ataccatgta caactagtac 360

atcaactatc ttatacattt gctcaggcct tta 393

<210> 2405
<211> 428
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2405

gtgatggtgt cgagaagaaa tcacatgttt gtcatcatca aaaaggggga gaatgtgaat 60

gtatgtatac atgattntga tgatgtcaaa aaagaatcta acaaggctgc ttcaaatgat 120

aagcatttgc ttcaagaata attcaagatt gcttcaacaa acaaagcctt gtttcaagat 180

tcactaaaga ccaagccttg ccttaaaaca aagtgatttc aagacatgca aggctctggt 240

aatcgattac caggaagtgt aatcgattac cacaagacgg cgttgagaaa tagctgttga 300

aaaaggtttt gaatttgaat tttcaacatg taatcgatta ccatatgtct gtaatcgatt 360

accagcaacg aaactttgga aactcanatt caaaagtcat aaccctctca aatataactg 420

tgtaatcg 428

<210> 2406
<211> 258
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2406

ntntagcaat tcagatggtc ataacgtttc actcggatgt ctgattcaag cgcataatat 60

atcgagacgc tcgagattga ataatggaag ctattgagca atcccaatgg atataacttt 120

taactctgaa gatcgataga tgcacatgat atattgagac gctcggaaat gaacaacgga 180

tgctctcgag acactcgaat ggtcataact tttaactcgg acgcctgctt gagacgcatt 240

atatatcgtg acgctcta 258

<210> 2407
<211> 334
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2407

agctttcaga aaatgtctat gccgagtgta taccattntt cttccatgtt tcagttgtac 60

gtagcttgtg ttttcttcat agatagggca atcacgatgt cctttaacac tatatccact 120

caaattccca tatgctcgaa agtcattaat ggtacaaaat agcattgcac gcaacttgaa 180

tgtctcattt cgatacccat caaatacaac aaccctctcg tcccacaact ttgtcaagtc 240

ttcaatcaag ggactgagat aaacatcaat gtcatttcct ggttgtctta ggcttgatat 300

catcatagaa cacataatgt attttctcta catg 334

<210> 2408
<211> 108
<212> DNA
<213> Glycine max

<400> 2408

attcttatga ttgcctatgc gtggaccctc aagtgcaatc ctccattctt ccctctattc 60

cgagccccat gaatgtcatt gcctactgct ggtcatgtgt cctccacc 108

<210> 2409
<211> 259
<212> DNA
<213> Glycine max

<400> 2409

tcgacactat gatacattgt gcctcctcat tgttgaatgg agtagcttca aaactgataa 60

tagacaagaa agatctcata cattgtgctc tatcacaact atgccagttg aacaacctct 120

tgatggcgtg gcacatgcag cacgtgctca cgctcaatat caccaccgcg ctgtccgacg 180

ccagcctctc tatgcgctcc agcgggtccc ccactaccgc cgccgccgcg ttcccagggg 240

ccgtcacgta tcttcccat 259

<210> 2410
<211> 304
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2410

tcatactatt tcaagaaact gaatncttgg tctccatgtt atcaaaaaca actctagcat 60

ctcttaacat ccctgacttt gaaagcatac taattagaga aggtgccaca agtctttctg 120

gctcaaaacc gagccttaca acccaagcat ggatttgcat tcctataacc accggaccct 180

tgatggccaa agctgcaatt acagtagaaa cagtataata gtcacgtctg tatcccctaa 240

cttggatcag acagaacaat tcccacacct gatcattaaa tctattccat gaataacccg 300

tgag 304

<210> 2411
<211> 463

<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2411

agcttcttct tcagactntg tgaacagtgt cttgttattt atcgaanaat catccattgc 60

atcaatgctt gaagaacctg ctatgtgttg gggaatattg gggggtttct tccaaaggtg 120

atttcatagg gggaaagtct ggtgcttgaa tgaattgata tgttatagga ccattcggtc 180

tatatcaaaa acttacccca ggacaacggg cgatggtgaa cggaggctcg taagtactgt 240

tcgacaactc gatttagcat tttcgtctgt ggatgatagg cagagctcat acaaaagttt 300

gtgtcgctga gttggaacaa ttcttgccaa aagtggctga tgaacaatgg gtctcgatag 360

tagaccaagc tatgaggcat tccatgaatt ttcccaacaa tgtccatgaa aaggattgca 420

atagtgtgag tcgtgaagtg tgacttgagc ttggccaggt gga 463

<210> 2412
<211> 278
<212> DNA
<213> Glycine max

<400> 2412

agcttaactc tattcgcatt cttatctctc ttgctgctac acatcattaa cctttatttc 60

gataggatgt acagaatgct atcttgcatg gtgacttaca tgaagaggtg tatatagagc 120

aatcacctgt gtttgttgct taaggggtgt ttggcaaggt gtgccgctta agggagttgt 180

taaatggctt gatgcaatca cctagatctt ggtttgggag atttagtggt gtggtccttg 240

catttggact gaagctgagt caaagtgatc atactgta 278

<210> 2413
<211> 400
<212> DNA
<213> Glycine max

<400> 2413

tcatcaaact acttggttcc cgagggaaat tctataaaca gaccttctat ctttaatgga 60

gtgggttacc actactggaa aacccgcatg ccaatcttta tagaggccat agatttaaat 120

atttaagaag ccctagaaca aggaccttat gttccctcta taatagctgc aagtgcaaca 180

atagaaaaac ctagagcaga ttggactgac gaagaaagaa gattagtacc atataattta 240

aaggccaaaa atattattac atctgcctta tgaatagatg aatactttac ggtttcaaat 300

cggtaaagtg ctaacgatat gtgggataca ctacaagtaa cacatgaagg cacaacatat 360

gttaaaagat ctagaataaa cactttaact cgtgaatatg 400

<210> 2414
<211> 386
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2414

agcttataag gtttgttgcc agcagcattg aatgattcaa tgaactccac attgtccttg 60

aatatctgga aacgttnttc cttctctgca gcatccttat atatttttcc atattctgcc 120

atccaatttt catgtctttc tcgcaaggct gtttgatgca gcttgcggng catcacttgg 180

gaaatcccaa ctgcaaggaa aaggaatagg gctaacatgt gttgctnttg gccagtgaaa 240

gccatttctt aattatcagc aatgatcagt tttgtaagaa aaggcttagt tggtatattt 300

gtgtaaagag agaaatgtga attggtatgc attgaaatga atgaatctgg agggttatat 360

agagatcata gtaccttatg ctatgg 386

<210> 2415
<211> 312
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2415

acacatattt tatccatagc aacataaaaa atctctgcac ggtaatgatg aagaataatg 60

atagtccttc cttctgctct tgaacgancc cgaactggta tttcgtcatc catatttggt 120

actagaatac ttttagcaac acaaanatct tggacatccg caaaaaaatt attccagcca 180

ctctctctca ttgtgcccaa ccgagctttg acaacatcaa ctaattncat ggcattcaca 240

atattaagaa tctttctttg caatatattt tgaaagctcg ttgtgatacc aaacaacttt 300

aacattaacc tc 312

<210> 2416

<211> 426
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2416

cttgcgtaag aaccagntta tncaatggaa cgatgactgt catttgtatt cggaangatc 60

aaatgatgcc ttatgaatcc tcctgtgctt acgccactag tgcctggaag gcccattatc 120

ctatacatga atatgttgga tgaatcaatg gggtgtatgc tggggcaaca tgacgagtct 180

ggaaagaagg aacatgccat ctattaccta agccagaagc tcacatcatg tgaaatgaac 240

tactctttgc ttgaaacgac atgttgtgcc ttggtatggg cagcccaccg tctaaggcag 300

tacatgttga gctacaccac tcttgtggtg tccaaaatgg acccagtcaa gtacatattt 360

gagaagcccg ctctttacat acggatcgct cggtgtaggt tctgctatat aatttgacat 420

cgttat 426

<210> 2417
<211> 402
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2417

ctgcaagctt gcttctacac taaagggttt ccttttacat ttaaatataa agactatccc 60

ataaaggtgt ctattttata tatcactaat gtccataaat tagggatgtt acactgcgga 120

caaaaaagta tattaataag aaaaaatgat tgataaatag ttatatgaaa tggtaaaaaa 180

attactatga atatattcac attaaagtat caaattcctt gaaaggaaaa ttcaagttat 240

ataaatgatt tcttttaata ttatagttaa aactcccgtg cattgcacgg gttttaatta 300

agttcttgaa catttttaa aaaaaatttt ccctgaacat aaaaattaat tcataatttc 360

ttaaaaatat ataacaaaat nttaagcaaa ccacaaatta ac 402

<210> 2418
<211> 405
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2418

agctttgacc acaaccccga tcttatctct acctattttt actcaaccat ttattgttga 60

aacagatgcc ttaggccaag gaattggtgt tgttttgtct cagaatggcc atccaattgc 120

ttttttcttt aagaagcttt cttctcgtat gcagaagcaa tcagcttatg ttcgtgagtt 180

gtatgcaatt actgaagcag tggctaagtt ttgtcattac ctttttggtc attattccat 240

tatctggaca gaccaacgta gtctcaagca cattacggac canatcattc aaacaccaga 300

gcaagagtcc ttgttaccta agcttcttga cttcaacttc tcgattgagt ataaacctgg 360

acccactaat ncaagtgctg atgctntatc atggtctttc tatat 405

<210> 2419
<211> 411
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2419

agctnttgcc tcanaacana gtgtttccaa gagatcaaga ctttggtaat tgtttaccag 60

acagtgtaat cgattaccag aagacaattt tgaaaaacag cttttaacaa gggttttaaa 120

tttgaatttt gaatcatgta atcgattacc agatgtttgt aatcgattac tagcaatgac 180

acttcataaa atactttgaa aagtcatgac ccttcaaaat ataactgtgt aattgattac 240

cagaaaccta taatcgatta ccagtgaaaa atttcagaaa aaagtttttg aaaagataca 300

tctcttcaaa tcattttgaa aagacacaat gggcctatat atanggtgtg ttgactntat 360

aaagtaaaga gagaattcta gagaacttaa ttgtcaattc tccaacaact c 411

<210> 2420
<211> 355
<212> DNA
<213> Glycine max

<400> 2420

agcttgaggg taaactttat cccttagtca acctattaac tcaacttgcc atgaatcaga 60

aatctacacc tgttgcaaga gtctgtggtc tatgttcttc tgcagatcac catacagatc 120

tctgtccttc tttgcagcaa tctagagtca atgagaaacc tgaagcttat gctgcaaaca 180

tttataatag acctcctcag tagcaaaacc aacaacagta gaataattat gaccttccaa 240

gcaacagata caatccaggt tggaggaatc atccaaatct gagatggaca agtcctccac 300

aacaacatca gtctgtcctt ttctttcaga atgttgctgg tccaagcaag cctta 355

<210> 2421
<211> 391
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2421

agtcacctgc ggcatgcaag ctttggtcca attcatacga ccataagttn tgtcatggtt 60

gtacgattta ggcccatggt atatggagac actcgaaatt gaaaaatgaa aggtctcaac 120

atattcaaat ggtcataact tttcactcaa atgtcagatg caggtatata atatatagag 180

atgctcgaaa ttgaacacgg aagctctgct ccaattcaaa ctgatatgaa ccctcatgga 240

acaagggctg acttaggatc gtctaggatt aaaccttgat ggaaaatgcg gaaattgatt 300

aacgtaagga tggaacataa ggtggttaat ttcgtgggtc ttaatcacgt ggctcttggc 360

ataaaatgga tgaatgggat gggtaaatgt a 391

<210> 2422
<211> 208
<212> DNA
<213> Glycine max

<400> 2422

ttcttcacag atggggcatg ctagatgacc cttaacactg taaccgctga gattctgata 60

tgctggaaag tcattaatgg tacaaaatat cagtgcacac atttgaaaag tctgcttgtg 120

aaacccatca aatactatta ccccctcatc ccacaacttt ctcacgtctg tcctcaacgg 180

acttagataa acatctatgt catatgct 208

<210> 2423
<211> 407
<212> DNA
<213> Glycine max

<400> 2423

tcgtctgcga tgggtgtagt tttatgatgt ggtggcttgc ggttgttgcg gcggacagtt 60

ttgatgatga gggtgaagaa gctgacgagg aaggcataga caacgagagt gcccagtgtc 120

tagatgaaga cctagcgact aacaatgatg cagcccagat atatgtacct tttcttcttc 180

tttttatggt ctcctttgcc caagagccac ctatgttggg tctcaccaaa gcaccttggt 240

ccagctcatg gagattcggt ggcggagtct atggtgtgaa tctcaagcag gcctccccac 300

agatccctac tgtgcatact atattttcga tcccttatga taaacaccag actcacatac 360

tgctagtaag tactacctag taactcgtat ttctctcgtt ctaaact 407

<210> 2424
<211> 372
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2424

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agtctacgtc tacgactcag cgcgtcaaat agttncagag cgaactcctt agagtccttc 120

atcccttcaa aaaattaaac aaagcataca aaactcttca aacaaggagt gaaaatgaca 180

aaccgattaa atgcacatgc caaacgcaag aatctgaact gaaatttgaa aaggaatcgt 240

acctatgcat tgcgcaaaat cagtgcgata aagataaccc gtcttggcaa gactatagaa 300

atggctttgc acctcgttcc aggcgtcagc gccattggat ntactgctaa taaatttcag 360

tccacggagc gc 372

<210> 2425
<211> 329
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2425

agctggcatt cgatcatcgg agccatagag agcatgatag cgctgaatac aacggtcctg 60

cattntgctc agagctttgg ccaaagggta gcttatggcg aaaccgcccc caccataggc 120

catgccgtag gagaagaata tgttctgcaa gtgactctcc gacaagctcc caatgtagta 180

catgtagttg tggtcgtact tgtttaaaat cctcagcaga ttgtccgtca cgaaaacggt 240

gtcgtcgtcg cccatcacga accaccgcac gttcttgtgc cccatacgca gcgtttccgt 300

cacgatgcgc gatattcgaa tcgcggagc 329

<210> 2426
<211> 448
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2426

tcacgatctc acacgtcgaa ctacatgtat ncttcattgg aagatcttag aggggacatg 60

cttaataaat aactctgaca ctcaaataag tacatgaatg agttgagtat gaaattgaaa 120

agggtgaaat aagatctgat ctttataacg tgagatagga gtttcgagtc cttgattgta 180

agagagttat tacagtgatg taacaactct agataattcc taacttggta ataatatata 240

gtagaaaaat catagcttgg taataatagt taatagataa ttcatcactt atagattatc 300

caatggatta tagataatcc atttattata gataattcat tactagtaga taagtaagta 360

cctgtaactt tgataagaaa taataacatt atcactaaga ttcaaatata tagatatttg 420

taacaacatg ttggccctat agctcgac 448

<210> 2427
<211> 341
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2427

gtacgattgt tgcccatggt atatggagac gctccgaaat gaaaaatgaa agttctcaag 60

aaattcaaat ggtcataact tttcactcaa atgtcagatt caggtatata atatatagag 120

atgctcgaaa ttgaacacgg aagctctgct ccaattcaaa ctgatatgaa ccctcatgga 180

acaagggctg acttangatc gtctangatt aaaccttgat ggaaaatgcg gaaattgatt 240

aacgtaagga tggaaaataa ggtggttaat ttcgtgggtc ttaatcacgt ggttcttggc 300

ataaaatgga tgaatgggat ggtaaaatgt acgttaagtg g 341

<210> 2428
<211> 442
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 2428

agctttaatt aatcgcgtac agaattccag gcatttctgt cgttcaatgt ctcttgttcc 60

caatcccaaa cacctcagaa gtttattagc aaaagccagt ctagcaaatg acatgtacat 120

gacataacct ttcaatttcg tgttcgtgta ttatatatgc aaactgtgat ggcatgtatt 180

caattcaccc tataaaaaac attccagttt ctattcatga aaatgaatta tcatttctat 240

acatattttt aatttaattt aatcaaaata catggacatt tacatcattt tttaatccta 300

taggaagagc attatatgtt atgcatgacc aaactatcga tatatgtatt ggaatgattt 360

taaaagatac aattgagata attntaatta gtttataatc taaaattctt tgcaccaata 420

atatatcaaa attattattt tt 442

<210> 2429
<211> 253
<212> DNA
<213> Glycine max

<400> 2429

ctggttcaac cttcttaaca ggtactttat agctgcatgg tctgtatgaa caataacacg 60

agtaccaagt gaatatgaac gaaatttctc acgagcacaa actatcgcta atcgctcatt 120

ctctgtgggc gtgtaattta cttgaacaac atccaaagtt ctggaagtgt gatagatcac 180

tcgaggtagc ttatcaatct ttctgagcaa ggacagcccc taatgcgtaa ttggatgcat 240

cgcacattat ctc 253

<210> 2430
<211> 246
<212> DNA
<213> Glycine max

<400> 2430

tatacacaca cacacacaca catatatata tatatatata tatatatata taatttgatc 60

ttaattaatt attaccggtg ggaagattaa tgacataaaa ataagaagtg tcatgatcat 120

gtattcatgt ggtacaagtt ttgatggaat agaactacat ggagcaaatg ggtacttgct 180

ggatcagttc ctaaaggaca aagtgaacga cgaagatgat gagtacggag gtactatata 240

aaatcg 246

<210> 2431
<211> 401
<212> DNA
<213> Glycine max

<400> 2431

gcttggaaaa aatcctcaca cagagagtca ttattagcat cgaatatgat atcgtccacg 60

tatatctgga tgattaagaa ttgactacca taatctttgt gaaacagagt agtatctacc 120

tttcctctta taaagccatt ttcaattaaa aatgaactta gcttttcata caaagctcaa 180

ggagctattt ttaaaatata caaagccttg ttaaatttga aaacatgata agggtatata 240

gaactctcaa accccagggg gctgttcaca tcaacttctt ccttgataag tccattgagg 300

aacacacttt ttatgttcat ttgatacaac atcataccgt gataagcaac acagttaaat 360

tggtttgtcc agcttgtttc taaacactca ctgagttcta c 401

<210> 2432
<211> 371
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2432

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taagtatatt caccaggaaa aaattgtagt ggaaggaaat tgtagtgttg tgattcaaaa 120

gatccttcca cccaagcata aagaccttgg gagtgtaact attccttgtt caattagaga 180

agtcactgtg ggaaaagctc tgattgactc gggagccaac attaatttaa tgtcattctc 240

catgtgcaga agggtgggag agatggagac catgcccact aagatgactt tacaactggt 300

tgaccgctcc attaccagac catatggagt aattaaagat gtgctggtca gagtgaaaca 360

ttntatcttc c 371

<210> 2433
<211> 376
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2433

agctntctat actaatgtca aaattcaaga aagctctttg atctctgagg tttatgggat 60

aaaaatggtc attgaccaat ccctttttcta tgacttgacc caattatcta gtgaaggtgt 120

accatttgaa ggtacactga atgatgattg gaaatttgat ttctctgtgc atgatgcccg 180

ccggttggtt tgaaccaacc aagaggatat gactggaagg cttcttgctg gatcattggc 240

ttttgaaagc catatccttc actatctcat tgtgtgtatt ttacttccaa gatcttcaaa 300

cctttgctca ggttctgaag acgatcttat agtcatgtgg gcttttcata ccggccgaca 360

aaatgatttg gcacac 376

<210> 2434
<211> 379
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2434

agctntgaat gcactattca atggagttga caatatcatc ttcagactga tcaacacttg 60

cacagtggcc aaagatgcat gggagatcct gaanatcact catgaaggaa cctccaaagt 120

gaagatgtcc agattgcaac tcttggctac aaaattcgaa aatctgaaga tgaaggagga 180

agagtgtatt catgacttcc acatgaacat tcttgaaatt gccaatgctt gcactgcctt 240

gggagagagg ataacagatg anaagctggt gagaaagatc ctcacatcct tgcctaagag 300

atttgacatg aaagtcactg gcatagagga ggcccaagac attngcaaca tgagagttga 360

tgaactcatt gggtctctt 379

<210> 2435
<211> 206
<212> DNA
<213> Glycine max

<400> 2435

agcttgaatc ggacatccgc gtgaatagtt atgatctttt gaatctctca agagcttccg 60

gtggtcaatc tcgatcctct tgacatatta tgcacccgca tcggacctct gtgtgaaaag 120

gcatgatcat tcgtatcttt cgagagcttc cgatgtttaa gtcccagcgt atccatatat 180

tattaactct gaatcggacc tcagtc 206

<210> 2436
<211> 163
<212> DNA
<213> Glycine max

<400> 2436

tttcgagtgt ctcaatatat tatgcgcctg aatcggacct ccgagtgaaa agttatgaac 60

attcgaatat ttcgagggct ctcgttgatt aaattccagc ttctgtatat attatgcgcc 120

tgaatcggac ctccgagtga taacgtatga ccattttaat atc 163

<210> 2437
<211> 413
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2437

ataatggaga cacatgaaca tcgctaggca atgactttca tggtgctccg aacaaaagtg 60

gagtatggag gattgccttg agggtccgca cttatgcaat catgaaactc aactccaaac 120

tcgaaagtga aggatatagg aacagcccta agcaataaca ttcatgtggc tccggaacgg 180

gatgagaatg gaggattgcc ttgagggtcc tctcttangc aatcatgaaa ctcaactcca 240

aactcgaaag tggagaacac atgaacagcc ctaagcaata acattcatgt ggctccggaa 300

caggatgaga atggaggatt gccttgaggg tcctctttta ngcaatcacg aaactcaact 360

ccaaacttga aaatggagaa cacatgaaca gccctaagca ataacattca tgt 413

<210> 2438
<211> 382
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2438

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tgtgttgttt gattctggtg ccacccattc ctttatatct tggttgtgtg tagaaaaact 120

taagcttttt gtgtcttctt taaataaaga tctagtagta gagaccccta ctagtggttc 180

tgtgttaact tctgatgtgt gtttgaattg ttctgtggag atttctggta ggatattctt 240

gattgatttg atttgtttgc ctttgagcta gaatgatgtt attcttagta tggactggtt 300

atcttccaac catgtcttgt tgaactgttt tgaaaaagtg tggtgtntga tgattctgga 360

gtgagtaagg atatgatgtt ta 382

<210> 2439
<211> 354
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2439

ctgatgcatc taccccgcag ggcattggat agaatagtcc aataacattg gaccaaagat 60

gcaagagaag gccctagggt tctcatgagt cttanggtag atntcgggcc catgggctaa 120

gtacgagccc acttatcttt gtaaatatta gattaaggtt tcattatttt tgggccttgt 180

agttagggct ccataatgta ggtagggtgc cttagaaata taggattttt cagcccttgt 240

attttagggc acctagacta gtttttgtat tatgggtagt tttgtaattt catatgcact 300

aagtgaatat ttgatcgtgt ggttggaaac taaattaatt gaattggtag aagc 354

<210> 2440
<211> 364
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2440

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tcaaatgatg ccttatgaat cctcctgtgc ttacgccact agtgcctgga aggcccatta 120

tcctatacat gactatgttg gatgagtcaa tggggtgtat gctggggcaa catgacgagt 180

ctggaaagag ggaacatgcc atctattacc taagcaagaa gttcacatca tgtgaaatga 240

actactctnt gcttgaaagg acatgttgtg ccttggtatg ggcagcccac cgtctaaggc 300

agtacatgtt gagctacacc actnntgtgg tgtccaaaat ggacccagtc aagtacatat 360

ttga 364

<210> 2441
<211> 399
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2441

agcttatccn cacaagagtg cataacaact ggtgagtctg cattgattat aggaggctga 60

accaggtaac ccgaaaagat catttccccc tgccattcat tgaccaaatg cttgagcgct 120

tggcaggtaa atctcattat ttttttcttg atggtttttc tagttattta caaattcata 180

ttgctcttga ggatcaagaa aagaccacat tcacctgtcc ctttggcact ttttcctata 240

ggaggatgcc ctttggccta tgcaacgccc ctggtacctt ctgtcgcaac ctacccttttt 300

gcgggcaagc gaggcgaggc tcacgggtgc cttttccaaa ggaggaaaat gcgcggagtc 360

gtcaccaacg tttatttgtg gaaaacgtcg aaaaaatcg 399

<210> 2442
<211> 396
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2442

agctnggatt tcctntgctc cggatacctc tcctttctca tgtgaaccca aacctaatct 60

ccgggttgga aaacaacctt nttgcgcccc ttgtttgctt gtttaacata gctctcattt 120

ctctttttaa ttatggcctt gactctttca tggagctttt tcacgtagtc cgctttggct 180

tgtccttcct tatgcttaaa aactgaaata ttaggcattg acaacaaatc aagaggagtt 240

agtggattga aaccatatac aaccttcaaa ggagaacaac tagtggtgct atgcacagtc 300

ctattataag aaaattcaat gtgaggtaag caaacttccc aatttttaag attcttttta 360

aaagggtcct tatcaaggta cccaatgtcc tattca 396

<210> 2443
<211> 473
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2443

tcaagctcgc ttctacaatg atgatggagt ntaaagaaga cattatgaag atctttgaga 60

tgaccgacct cggtttgatg agttacttcc atggcataga agtaagtcac agaaatgaag 120

ggatattcat ctcacaaaag aaatacacaa aaggcttact taagagattc aagatgtatg 180

gttgcaaacc tgctgctact ccactcaaaa caaatgagaa actacagaag aatgatggag 240

caccaaaagt ntatgcatcc caataccaaa gtctaattgg aagcctccta tatctgaccg 300

ctacacggcc tgatataatg tatgctacaa gtcttctatc aagattcatg cagagtccaa 360

gtcacataca ctttggagca ggaaaaagaa ttttaggtat ctacaacgaa caaaagagtt 420

ccgtatatgg gatactaccg ataccaactc acaattactt ggctacactg aca 473

<210> 2444
<211> 446
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2444

agcttaacct ctataccctt aatccanaac tctattaact aaaccctaaa ctctaaggct 60

tagacaccaa accctatatt tgaaaacccg aaacccttaa cccaaccttn taagcccttа 120

accctaaaat ataaaaaata aaccctaaac cctaatggtt tagacaccaa accccaaacc 180

tcaaaaccct aaaccataaa cccttaaccc taaattctaa tccctaaacc ctaaactcag 240

aattctaata cctaaaccca aaactatgca ttataaaccc taaaccctaa actctaaacc 300

acaagggtta gacaatacac catacatctt aaaccctaat cccttaaccc taaaatttaa 360

atactaaacc ctaaaccctt aaccctaacc tttaaaccct taatcctaaa atatcaaaaa 420

taaaccctga accctaaacc taaaca 446

<210> 2445
<211> 421
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2445

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ccatgttatc aaaaacaact ctagcatctc ttaacatccc tgactttgaa agcatactaa 120

ttagagagtt gcacacaagt ctttctgtct caaaaccgag ctttacaacc aaggcatgga 180

tttgcattcc tatagccacc gcaccctgat tggccaaagc tgcaattaca gtacaaacag 240

tataatagtc aggtctgtat ccctcaactt gcatcagaca gaacaattcc cacacctgat 300

cattaaatct attccatgaa taacccgtga gcaaggaatt ccacgacacc acgtctctgt 360

cacccatctc atcaaaaact ctcctcccat ctctaacatt ccccgttntc gtgtacatat 420

c 421

<210> 2446
<211> 418
<212> DNA
<213> Glycine max

<400> 2446

agcttgtctt ttctcttctg gtcaaaaatc atatttacga gaattattaa tttgaattct 60

gcgaaggaca tttgggacta cctcaaatca gagtattaag gtagtgtgca aactaaaggt 120

atgaaggcac ttaacttggc tacagaattt gagatgcaaa gcatgaagga gacaaaaact 180

atcaaaagtt atgctgacaa acagttgagc attgcaaaca aggtacgtct ccttggtaag 240

ggatttccta acgaaaggat agtgcacaaa atagttgtta ctatacctga aaaatatgaa 300

tccaaaatat cagcattaga ggagtcaaaa gaattgtcaa atatcaccct cggagaattg 360

gtaaatgctt tacaggcaca ggaacatagg agaatgatga gacatcgggt ggcaatac 418

<210> 2447
<211> 483
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2447

agcttacggc ccatgaaaat actccaaaac ttaactttta aaatatagca ngaaacaaac 60

cacaaataaa aatttcatcc tcatctctaa gaatgatccc acagtgtcaa cttacatagt 120

ataaaaaaat ctgtaagttt gttctagata gtgtttgaaa tttagtaaga tcaaattaca 180

tagttaaact caaaaaaatg cttttggtct cttagccccc tccccncgga tatttggtct 240

tagtttttta ttttcaaact gatgaattaa aaaccaaatt ttgaaatgac taatttatat 300

tttaacatta aatataaaaa aatatttaca aatcattatt caataatatt tcattaatta 360

aactnaattt gaagatattt ntaaactaaa aaagacaaat acatgtggtt ggtatattta 420

atttaatatt ttttaattat taacacaaca acctttcctt aaagagaaag tgattacaaa 480

ttt 483

<210> 2448
<211> 389
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2448

tctggtggga catcttgact ggctntccaa tctgactatt acctcatatt ctgccttctt 60

ctattttcag attgggaatg cctctaacag caccttttgtc aatgattttc ttcatgcctc 120

ttaagtgcag atgtccaaat ctttgatgcc atattctgac ttcatcttct ctggagaata 180

gacatgtgga ggagtaactg gtttcttgag gtgtccatag gtaacagttg tcctttgatc 240

tgctgccctt cattaggact tcactcttct catttgtcac caagcattct gactttgtga 300

agtttacatt gaatccttca tcacacagct gactgatgct gatcaagttt gcagtcagtc 360

ccttcaccag cagtactttt gtccagact 389

<210> 2449
<211> 457
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2449

ctaagcttac atcttcctga gtagctgcca ttggttgtat tgtagcactt ttataccttc 60

taaaggaaca agtatagctg gtaaattgtt tgtttgtctg tgatgaattc ctatggtatt 120

ctccttttat agagctagga atcaggacta gctagtattc agcagatacg taatcaatta 180

gaaaagatat acctatatac atatcatggg tatagtcaat agtggggacg ataacaaaaa 240

aatgggaaag tgctaccgtg tattaaattc attttgattg ctgcgtatga atgcggagac 300

attgcacatg agaaggatct aganaaaata tgaaaaaact nttccctatc aagaagaatc 360

ctcagagnta acaaatgtgg aaaaataaat gatgtaagag attgcgtaaa ccgtgtagag 420

aagattcctc taatatactc gatcctcaat caaatat 457

<210> 2450
<211> 227

<212> DNA
<213> Glycine max

<400> 2450

gctgtacatt caatttcgag cgttccgata tattacggga ctcaattgta catccgagta 60

attagttatc gtcgcttgaa tttgctcaga gcttcaacat tcaatttcga gattttcgat 120

atattacggg actcaatcag acatccgagt aaaaagttat tgtcgtttga atttgctcag 180

cgcttccgta ttcaatttcg agcgtctcga tatattacgg gactcaa 227

<210> 2451
<211> 262
<212> DNA
<213> Glycine max

<400> 2451

ccttcatctc ttcggtgtgg caagcttgtt ttcttttgtg ttaggatatc tacatcgtct 60

gcctcagtca ttgtggtgca gtttatatat ctgttggaca acttcactta atgccacatt 120

gatttaagat gaaatctaac atgatatcag agcttatagt ccggcttagt tctctctacc 180

atgttggttg taaaagcagc agtacctgag attctcattc agttgtttgc tcttagaaga 240

gccctacata ctactaatct ca 262

<210> 2452
<211> 288
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2452

agctctgaat gcactattca tgtttttgac aagattatct tcagactgat caacacttgc 60

acagtggcca aagatgcatg ggagatcctg aaaatcactc atgaaggaac ctccaaagtg 120

aagatgttca gattgcaact cttggctaca aaattcgaaa atctgaagat gaaggaggaa 180

gagtgtattc atgacttcca catgaacatt cttgaattgc caatgcttgc actgccttgn 240

gagagaggat aacagatgaa cagctggtga gaaagaatct tatatcct 288

<210> 2453
<211> 374
<212> DNA

<213> Glycine max

<400> 2453

ctgcataccc caaggatcca ttaggaaatt acttgtgaaa gagatccatg agggtgggct 60

catgggccac tttgggatag acaagaccct tgtcttcctc aaagaaaagt tttattggcc 120

ccatatgaag aaagatgtcc ataagcattg cactaggtgt gtggcttgtt tacaagccaa 180

gtctacggtg atgcctcatg ggctatacac acccttaccc atcccatctg caccttgggt 240

agacattagt atggactttg tccttgggct tcctagaacc caaagaggtg tagactctat 300

ctttgtggtg gtggataggg ttagcaagat ggcacactct ataccatgcc acaaggtgga 360

tgatgcttcc caca 374

<210> 2454
<211> 385
<212> DNA
<213> Glycine max

<400> 2454

ttcggagcgt cgcgatatat tacgggactc tattggacat tcgagaagaa cgttattgtc 60

gtttgaattt gatacgagct tccgttttca atatggagca tctcgatata ttacgggact 120

caatcggaca ttcgaataaa aagttatcgt cgcttaaatt tgcttagagc ttctattttc 180

aattcggagc gtctcgatat attacggcac tgaatcagac atccatgcta aaaagttaat 240

gtcgtttgaa tttgatacga gcttccaatt tcaatttgga gcgccgcgct atattacggg 300

actctattgg agatcccaga aaaaagttat gtctcgttga aattgatatg agctcccata 360

ttcaatttgg agcgtcttga tatat 385

<210> 2455
<211> 379
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2455

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cctgtngcaa gagtttgagg tctatgttct atagcagatc accatataga tctttgtcct 120

tctttgcaac aatctggagt caatgagcaa cctgaagctt atgctgcaaa catttataat 180

agacccccctg agcagcaaaa ccaacaacaa caaatacaat ctatggtgga ggaatcatcc 240

aaatatgaga tgggcaagtc ctctacaaca acaatagcct gtcccttatt tccaaaatgt 300

tgctggtcca agcaagccat atgttcctcc tgcaatgcat cagtagtagt aacaacaaca 360

acaaagacaa caagcaact 379

<210> 2456
<211> 422
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2456

agctatagaa gaccgnggaa ntatttattg ttgtgtggnc tggatcttct gttggactag 60

tttgacccct ttgcttgaca ccatgtggcc caagtactcc acctgngttt gggcgaagga 120

acatttcgag agcttaatga agaactggcc ctgcaacaaa accttgaaag ccaattccaa 180

atgaagtaaa tggtcattga aggagctact ataaattagt atgtcgtgat gtggacatca 240

aagcccaagc ccatgacaac caccagcccc aggcccatga ctagatggaa gcccaagacc 300

caatacaagg cataggaaga cccatgacaa gagcaagagc taaaaaggca caagatgctt 360

tggaacatat ggtgattatt ctgagggtag ttcaaatgca gggagaggcc caacacttgg 420

ag 422

<210> 2457
<211> 416
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2457

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ctatcagaca ctatgctaga tgacacacca tgtaatctaa caatcttact aatgtatagg 120

gaggccaact tctctaagga aaacctaata ttgatgggga taaagtgtgc agatttggtc 180

aatttgtcaa caataaccca aatagaatca aaacctttgg gggtcatagg tagtcctaaa 240

tcgaaatcca tggagatacc gtcccacttc cactgnggta tctctaaggg ttgtaactta 300

cctgaaggtc tctgatgttt atcttagcct tatgganact aaacatgaat acacaaactt 360

cctaaccact cttttatgtg ggccaccaaa acattatctt tagactctaa tacatc 416

<210> 2458
<211> 416
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2458

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gatcaaatgg agaatagaga ccatatgaat tgctcaagag cttccattgt tcaatttcga 120

gcgtctagat atataatgcg cctcaatcgg acctccgagt taaaagttat gaccatttga 180

aatgctcaag agcttccatt gttcaatttc gagcgtcacg atatattatg cacctgaatc 240

ggacctgcga gtgacaactt atgaccattt gaatngctca agagctctca ttgttcaatc 300

ttgagcgtct cgatatatta tgcgcctgaa tcggacctgc cagtgacaac ttatgaccac 360

ttgaattgct caagagctct cattgctcaa tttctagcgt ctcgatatat tatgcg 416

<210> 2459
<211> 377
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2459

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acggaagcta tcgagaaatt caaatggtca atacttcgaa ctcggaggtc ctattaaggt 120

gcataatata tctagacgct caaaatttta caatggaagc tctntggcta tacaaatggt 180

cataactttt cactcgaagg tccgattaag gcgcataata tatcgagacg ctcaaaattg 240

aacaatggaa gctcttgagc aattcaaatg gtcataactt gtcactcgga ggtccgattc 300

aggtgcataa tatatcgaga cgctcgaaat tgaacaatgg aagctcttga gcaattcaaa 360

tggtcataac ttgtcac 377

<210> 2460
<211> 421
<212> DNA
<213> Glycine max

<400> 2460

agcttaagca cgagtaaatt gctacatgct taagttgtgt ttaaggtgca tccttaaagt 60

gtatgcttaa gaaagttatg caaaatgctt ttttttttaa aaaaatggta ttccaagtgt 120

gataaaatga aaattggttc atgatatgag tatttatata tagtatggag ttaattgtat 180

gctaatatca tgcacttcac attcatatga ggattttgat gtggtgattg taaaaattca 240

tggtgttgga tgtcttacta tgcttaacaa actattgatg gattcataag tgtgatgaat 300

atatgaatgg ttaacttatg atatggtaat ttgatgaaat atcgttataa tgaaaagata 360

attatattga taagataatt atgtaaatta ttgaatgtct gagttatgtc gggttaattt 420

c 421

<210> 2461
<211> 374
<212> DNA
<213> Glycine max

<400> 2461

ccatgaatca gaaatctaca cctgttgcaa gagtctgtgg tctatgatcc tctgcagatc 60

accatacaga tctctgtcct tctttgcagc aatctagagt caatgagaaa cctgaagctt 120

atgctgcaaa catttataat agacctcctc agtagcaaaa ccaacaacag tagaataatt 180

atgacctttc aagcaacaga tacaatccag gttggaggaa tcatccaaat ctgagatgga 240

caagtcctcc acaacaacat cagtctgtcc tttctttcca gaatgttgct ggtccacgca 300

agccttatgt tcctctctca atgcagcaac aacaaagaca acaagcaggt gaggcctcct 360

tttcaacctt ctta 374

<210> 2462
<211> 340
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2462

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tccaaagcta tcgtatcaag attcattttg tgtagcttcc caaaaaggga agcaagttaa 120

aagttctttt aaagccaaaa aaaatctttc cacttctagg ccttttagag ctcctacacc 180

ttgacctttt tggaccaacc aagaatacac ccctctttgg atgcangtat ggtctggtca 240

tagtggacga ttacaccaga tggacatggg ttaggttcct aacccacaag gatgagtctt 300

ttgatacctt ttataaactt tgtaaatgat tcaaaatgaa 340

<210> 2463
<211> 185
<212> DNA
<213> Glycine max

<400> 2463

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ggtcactatg agtatctagt catgctcttt ggtgtggcta atgctccagg tgtgtttata 120

tacttcatga ataaagtctt tcacccttac ctagatagtt ttgtggtacg attcatagat 180

gatat 185

<210> 2464
<211> 409
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2464

gcttcanaaa gtcaagcaga acagcttaaa gaagaacaat gtggcgatct ctgatgtaac 60

caatcatgct cggaaagaag agttagaaac tggccgttaa taatttgcat ctgtaattac 120

agaacttgat gttgcaaagc aagaactgag taaaattcgt caggggtatg atttatcctt 180

ggaagcaaga gtttctgctc tcaagcaaac agcagaagct gaagatgcaa tgaaggcaaa 240

catggaaaga gcatgtgagg tatcctaaag aaatttggtt gtgcaggaat cagttgagaa 300

aatgaatgct gaatctgtcc aagcacatca actgcaagaa gagacattag ccggacaaaa 360

agttcttaga caatcatatg aagccatcct tgaagaatca aaaaagaag 409

<210> 2465
<211> 463
<212> DNA
<213> Glycine max

<223> unsure at all n locations

<400> 2465

gtcacctgcg gcatgcaagc ttgtccattg gcaaagttac agaaggccaa tttataaaaa 60

tgatctattc agtcaattat tcttcaccat catttttaat tatctaaagt tcattggttg 120

gatttaacat taacaattag tcagtcaagt tcaagaggac ttaattacat gggttaaaga 180

atatgtatct ttttttctcc aaaaaaaaaa taagtccctt gatgcatttc ataagttaat 240

ggaaaataaa aggtgtagaa gaaatgcnat taaaggtgat aagccatagc aagtgtttgc 300

agtttaccgc ttgaactcan gtgactgctt atattngtca aactcttgca accattcttc 360

atccgagaaa ggagggagag taccggtgaa ttccaatcag tcattgaaga ccagatcggt 420

gagtcttgta aactcccgag caccaccatg ctgaacaccc atg 463

<210> 2466
<211> 426
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2466

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tggagagtga gtcatcctcc acatcaagca gtgcaagaat tatatgcgac tgtagattac 120

taggtggaca cgcttcatcg tcaagcattt ctggtgcgtc caaagcatta acttgtaacc 180

tagcccgctt gattgcctcg gcgtcaccct gaaggagctn tgagatctgt ggtccaaatg 240

tccgagagaa tatccatgag attttcaata aaaaggacta atgtactgaa tgagaatatt 300

tctatggnga tcaaacaaga agataaagtt aacggctgca ctatagaggt cagataccac 360

attgattagg ataagcaaaa cgcagaaagt ccgtccattg tccaggatat acactcaata 420

tgcaac 426

<210> 2467
<211> 445
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2467

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gaacaattat gacctctnca gcaacagata caaccctgga tggaggaatc acnctaatct 120

cagatggtct agccctcaga aacatcagca gaagcctggc tccttcttcc aaaatgctgc 180

tggcccaagc agaccataca ttcctncacc aatccaacaa cagcaatagc cccagaaaca 240

gccaacagtt gaggctcctc ccgcaacctt cctcaaagaa cttgtgagac aaatgaccat 300

gcagaatatg cagtttcaac aagagaccag agcctncatt cagagcttga ccaatcagat 360

gggacaattg gctacacaat taaatcaaca acagtcccag aattctgaca agcttgcttc 420

tcaaatctgt ccaaaatcca aaaat 445

<210> 2468
<211> 437
<212> DNA
<213> Glycine max

<400> 2468

agcttcatct atggcagcca agttctcagc aacttttaaa tataatctcc tagatccgat 60

caattggttc agtgcgatcc tgcacagcaa tcccttctga gacatcggcg agtgatttga 120

gattgcactt aattaaggcc tcaacgaagt agcaggtttc atctttggtg ttgccctcag 180

gtacatccac cacaaaagat tcaattacca gtgtacctgg ccttccatca ataatttctg 240

ggtggaggga catgatagat gagtagttct gaaagataag agatacaact tatgttaaaa 300

aaaattattg tgtcaggtga cacggacaag atagcttaat catttagccc aacttcttag 360

acaggccggg aaaacaaaaa tctatataat tactcatggt ggacgtaatg cttggtgcgt 420

ctttaataca tgaatat 437

<210> 2469
<211> 335
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2469

agcttganat tgaataatgg aagctctcga gaaatataaa tggtcataac ttttcactcg 60

gattgccgat tcaggtgcat aacatatcga gacgctcaaa attgaacaac agaagctctc 120

gagaaattca aatggtcata agttttcaca tggatatccg attctgtgtt ataatatatc 180

gagacggtcg aaattgaaca acgactcgag aaattcaaat ggtcataact tttcactcgg 240

atgttcgatt caggcgcata acatattgag acactcggaa ttgaacaatg gacgctctcg 300

agaaatacaa atggtcataa cttttcactc ggatg 335

<210> 2470
<211> 477
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2470

tatcccaata acactatcaa catagtatga atnctacact atgagaatcc taattactga 60

tattctaatc atttaacacc ttgaagggca tacatgatat taagtaacaa aagcaagcag 120

aagcttcttt cccattacca agcaaatgtt ctattctaga cagaacaagg agataaaata 180

cacctgttaa tagcaattgt ccatttactg tctataaagt cagttgctgc aagtaatgca 240

gctggccaag ccaaagcagt taagagtgag ctcaaaacag tcatcattgc ccctcgtttc 300

atagctccat cgcaagtcct gatgcaagtc acagcaatac taacatcatt cacagcacta 360

ctaataaact gantacttag ttttataagc acccctaaac ctacaacaat tacttgaagt 420

aagccaatct tgaattcagt gctcacagaa tcagatcttg actccactga gtgatac 477

<210> 2471
<211> 492
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2471

agctntgata taacatgata tagttcttca cctatacana tatattaaaa tggagtgaaa 60

catatacttt ntatcttaga gaaataatgg atactaactt attttattca aaaaatttcc 120

aagtcgaatc taattgattg tgtggatgca tgtcatttgt gaagataatt atatgtaggt 180

tatttcatat gtgtacaaag aaacttgtgc tttatcttta gggaaaatgg catcaactat 240

catatgcatg tgaagacaat ttgcatatat tgctcagttg anagatggac acactaaaga 300

ggatagaaca aaacatatnt cttctaaagt cttctacact cgatctttga aggaatggtg 360

atataaacat tcaacaaatt tgttcaagtg agaatataac agatntctnt acaaagtctt 420

ttgctaagga gaactntnta gtaatcggta cacaagaatt gaacttcgtg tcttatagac 480

aatcatctac at 492

<210> 2472
<211> 427
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2472

tctaaactnt atacaagaat gaagctcaga taccacttgt tggacaagtg gcctcagata 60

tcttaagaag gggggggggt tgaattaaga tatcacaaac tattccccag ttaaaaattc 120

tacttttaat ttaacccaac tacccaagat tccttttaaa caagaactcc ttgataataa 180

tgcaaattta tcttactaaa taaaaataat aagcaataaa tagtaaagga gtttaaggga 240

agagaaaatg caaactcaga tttatactgg tttgaccaca cctttgtgcc tacgtccagt 300

ccccaagcaa cccgcttaag agttccacta tcttgcaaaa tccctttaca agatctgaac 360

cacaccagga caacccttcc tttgtgttca gaattcttta caacaagaga accttggtct 420

cttaatc 427

<210> 2473
<211> 414
<212> DNA
<213> Glycine max

<400> 2473

ctgagcagat tctatcgaca ataactgttt acttggatgt tcgatatagt cacgtaatat 60

atcgagtcgc tcgacataga atacacaagc tgtgagataa ttctgacgac aataactatc 120

tactcggatg tacgattgag tcacgtaata tatcgagacg cccgaaattc aatacagaaa 180

ctctgagcaa attctaacga caataatctt ttacttggat gtccaattga atcacagaat 240

atgtcgagac actcgccatt gagtacacaa gctctgagga gattcagata taaataccct 300

ttgactcgga tattcgattg agtgccgtaa tgtatcgata cattcgaaat agaatacaga 360

tgctgtgagc aaattctaat agaaataact ttatactcgg atgtgcgatt gagt 414

<210> 2474
<211> 225
<212> DNA

<213> Glycine max

<400> 2474

tatgctgtac acatgtatta taaacctcct cagccgcgaa acctacagca atagaataat 60

catgaccttt aaagcacttg atactatcct agttggagga atcatcctaa tatcagatgg 120

gctattcctt cacaaacaca acagtatata tctccttttc tgaatgctgc tggtccacgc 180

aagccatata gttcttcttc aatgcagcaa ttgcaggaac aacaa 225

<210> 2475
<211> 467
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2475

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ttatgataag taggccatta tgtcacaact aagccttcta atctgtcttt ctgaacaagg 120

tgctatttgt ataaatgtct ggcttgtttg tcacgtttag cttatgcatg tacttataca 180

ccaatttcta gagattctgc gaaaccatga ataataacta tgactgcata gctatgccat 240

gtaaatttac aatgtagttg ttggatttcc tttttaaagt tattagttta atttatgcat 300

ctattttgtt tattggaaga tgtgtatgta tgtcaaatcg ggttatgata tcatatacat 360

gatgtgtgga atacatntgt aatttcataa atctctcgtg atttcatctg atatatntgg 420

gatggaacat actagacttt taatgatgat catttttata tgataag 467

<210> 2476
<211> 396
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2476

atgcatgcta agctataagc tctacaactg aataacactt ggactcttac cattcttcct 60

cctcacaaaa ctgccattgg gtggtcgtgg gtatataaaa tcaaataaat aaatgatggg 120

tctatagaaa gatacaaggc acatttagtc acgaaaggat acacttaaac agaggggttt 180

ggattatctc gataccttct cgccagttgc aaacctcacc accattcatc tnctttttcta 240

gctntggttg ctttccatca atggcatctg cgacaactcg atgtgaataa cgccttcctt 300

cacggtgagc ttaatgaaga gggttacatg catgtnctct ctggacttct agtcacaagc 360

ccgaaccacg gttggtcgct tcaacgatct ctatat 396

<210> 2477
<211> 456
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2477

tatntaaaca atatataatt gatgttntgt agtctatgat caatgtacac atgtaacatg 60

ttataccttt catcattctt ccttcacttt attcttatat tactcttata aaatttatac 120

ataatgctta ttttttatca actttagtcg agtgatcagc ctctaatttt aaaaaatttc 180

cttacaaata tgttgataaa taaaaaatat tttaagttat acgaaatctt tttatcttct 240

ttaataaaaa atgatataaa atatcttttt gacaattata tttttaaact tagtttatga 300

aagaaataat ttatttaaat atttctttaa tgatttataa attggcgcaa cccgtgaatg 360

tgtgtctagt tagttttaac agtcaaatac acgttctgta gtattaccac ttaccagtgt 420

aaatggctag ttcctaaaaa ttctacaata cacttt 456

<210> 2478
<211> 381
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2478

agcttatcca ganatcgaag cactatgatc ttctgctgaa tattaggttg agaaacattc 60

tctaggaccc tgagaacaat catagggaaa aaaactccaa tttctgcctt caatccagct 120

ctaaatcttg acaccagact gatgaaaatg gagcatgaca gttgaaacac aatcaaaaga 180

gttgaagcac tgttcttcaa caaggataga cataagtact gcttgatggc gcctaaaaac 240

ctgctcatcc acaaccaaat ttaaccatca ggactatttt tgtcatctgg aaaaattatg 300

aagtanaaaa aaaatatagt gtcaagtggt gtatagaaca aagaaagaaa atgttaattt 360

gcattaatga tgagggacaa a 381

<210> 2479
<211> 390
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2479

ggagggagaa ctggatgcct tggtcaacct agtaactcag cttgccatga atcagaaatc 60

tgcatctgca cctgttgcaa gagtttgtgg tctatgttct atagcggatc accctgtgga 120

gcgggagcat ctttaatgaa ataatctgga gncaangagc aacctgaagc ttatgctgca 180

aacatttata atagaccccc tcagcagcaa aaccaacaac aacaaataca atctaggttg 240

gaggaatcat ccaaatttga gatgggcaag tcctctacaa caacaatagc ctgtcccttа 300

tttccaaaat gttgctggtc caagcaagcc atatgttcct ccctcaatgc atcagtagta 360

gtaacaacaa caacaaagac aacaagcaac 390

<210> 2480
<211> 419
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2480

agctntagaa gaccgtggaa ttagccattg gtgtgtggcc tgtgatcttc tgtggactag 60

ttngacccct ttgcttgaca ccatgtggcc caagtactcc acctgngttt gggcgaagga 120

acatttcgag agcttaatga agaactggcc ctgcaacaaa accttgaaag ccaattccaa 180

atgaagtaaa tggtcattga aggagctact ataaattagt atgtcgtgat gtggacatca 240

aagcccaagc ccatgacaac caccagcccc aggcccatga ctagatggaa gcccaagacc 300

caatacaagg cataggaaga cccatgacaa gagcaagagc taaaaaggca caagatgctt 360

tggacatatg gtgatattct gagggtagtc aaatgcangg agaggccaac acttggagt 419

<210> 2481
<211> 371
<212> DNA
<213> Glycine max

<400> 2481

gtctgcgccg ggttaaagtc ctacaacgat actcttcaaa tattaagagc cttgtgcagc 60

tgaagaagct taacctactg gggttaaaga ctcatgattg tcacatgttg atgcaacaat 120

tgttagccgt ggtcatacga gacatattgc ctaacaaagt caggttagcc ataactcgcc 180

tgtgcttttt cttcaatgcc atgtgtagca cagtccttga tcctgtcaag tttgatgacc 240

tggaaaacaa ggctacaatt atactgtgcc agctggagat gtattttcct cctgctttct 300

ttgacatcat ggtccactta attgtttaac tggtcagaga atcaaatgtt gtggtcctcg 360

ttatctgtgc t 371

<210> 2482
<211> 379
<212> DNA
<213> Glycine max

<400> 2482

tgcacaacgg aagcactcga gaaattcgaa tggtcataac ttttcactcg gatgtccgat 60

tcgcgggcat aactcatcta gatgctcgaa attgaacatc ggaagctctc gagaaattcg 120

aatggtcata acttttcaca cggatgtccg aatttaggac ataatatatc gagacactcg 180

aaattgcaca acggaagcac tcgagaaatt tgaatggtca taacttttca cacggatgtc 240

cgaatttggg acataatata tcgagacgct tgaaattgcg ctaccgaagc actcgagaaa 300

ttcgaatgat cataactttt cacacggatg tctgatttgc ggacataact catctagacg 360

ctcgaaattg aacaacgga 379

<210> 2483
<211> 395
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2483

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atcccaaggt tcagaatttc tacatctaga ccactccttg anacactcct tttttactct 120

aactttgctc tgaacatttt cattccacca ccacgattct ttacccctag gtccaaaacc 180

tctagattca cccaacgtct ctttagccac tttaataatc tcttatctac caaattgtga 240

catccgcgtg aaaagttatg accatgcgaa tttctcgagt acttccattg tgcaatatcg 300

agcctctcga tatattacgt cccacattct gacatccgtg tgaaaagata tgaccattcg 360

aatttctcta gagcttccgc tgttcagttt cgagc 395

<210> 2484
<211> 388
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2484

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aattgaaaac agaagctcat agcaattgca gacgacaata actgtgagcg gcggaagata 120

ataaatattt ccgcnanaca ccgagacgct cgaaattgaa tacaaaagct ctgagcaaat 180

tccaacgaca ataactttta actcggatgt ccaaataaaa cccgtaatat atcgagatgc 240

tcgaaattga aaacagaacc tcgtagcaat tgcaaaccac aataactttt aactcggatg 300

tacgattaag tcccgtaata tatcgagacg ctcgaaattg aaaacaaaag ctctgagcaa 360

attcaaacga caattacttt ttactcgg 388

<210> 2485
<211> 306
<212> DNA
<213> Glycine max

<400> 2485

agcttgagca aattcaaacg acaataactg ttaactcgga tgtccaaatg aaacccgtaa 60

tatatcgaga cgctcgaaat tgataataga agctcatagc atatgcaaac cacaataact 120

tcttactccg atatccgact gagtcccgaa ttatatcgag acgcttgaga ttgaaaacag 180

aagctctgag caaattcaaa cgacaataac ttttaactcg gatgtccgat tgagtcccat 240

aatatatcga gacgctcgta attgataacg aaagctcgtt ggaaagtcaa aagacaataa 300

atttta 306

<210> 2486
<211> 421
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2486

agctatgagc catactattc caaactaaaa cttctgtacc aaatcgacga aaggtgttgg 60

aacttggata catactgatg cttttggtat tgcaaaaaaa tggaacatct tagaatgtgg 120

attttggtct aactcaaccc caaaagctat ctcttatggt gagaggtgcc ctccacttat 180

atactctatc ttggtactat cgctagtcaa tgaaggactt ggattgtttt caatacaccc 240

cctcacgtcc aagcactttt gagcttggcg tgtggataac atggtgggtg acccttttgaa 300

tggatctagg ataggctcta ataccatctt agaatgtggg tttaggccta actcaaccgc 360

aacagctaac tcatanggtg agggtttcct ccacttatat actctatctt ccactatctc 420

t 421

<210> 2487
<211> 421
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2487

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ctgcaaaagt caaatgagat agctgaatac atgcacaatt gggatgaaat ttaaaattgg 120

catcatcctt aagactgctc atatctctgg aaaagtactc caaacaaagc acaaacagat 180

aagggaagag aggatcccct tgtctaagac cccgctaccc cttgaagtgg ccataaatgg 240

atccattgac tgtgacacta aaggaaaaag ggtcaacaaa aatacaccaa tgaaaacata 300

tttttgtggt gtaagtatat aatagaatca tgtttttttgt ttgttaaatg atagcgaaaa 360

agttatcgac ggaaacaaaa tttatntcat atatatacaa acatgtacaa cgagtgaaat 420

g 421

<210> 2488
<211> 485
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2488

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gccagttcta ctagtaattt acaatttgct tccttggttg tgcatgaagt gaaaatacat 120

gatgttgtct atgatgatat caggcccaac acagccagga aatgacattg atgtttatct 180

aagtccgttg attgaagact tgacaaagtt gtgggacgag gggattttag tgtttgatgg 240

gtttcagaat gagattctca aatgtgtgca atgctctttt gtaccattaa tatcattcta 300

gcatatanga atttaagcag ttacagtgtt aagggtcatc atgcatgccc catctgtgaa 360

gaagacacaa gctacataca actgatacat ggtagaaaaa cagtctacac tatgcatcga 420

cgttttctaa aacctcatca cccttacagg gcgatgaaaa agcattaatg gaagtcagac 480

atgaa 485

<210> 2489
<211> 464
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2489

agcttatcca tgcctcctta gtggatgttg catcanaaat cttctcgaac gcaccatcat 60

ctaatccttg atagatgagg aagagagctt tcttgtctct ctttcttgaa tccttanaag 120

tctattnttg tgcttggggt agtgaagtca ctactagaaa ataaggtttt aacattggtt 180

atttaggact ttcaagatcg gttattaaca aatgttgaaa gtaccgacgt tgaaagtatt 240

aacgttaaca tcagtttttg aaaactgatg ttaacgtaaa ataacaacat cagttattta 300

aataaccaat gttatataat aagaattaca aaaaanaggt atatatgttc ataccaacgt 360

tgacagttaa catcgattnt tcattcaaaa ccgatgtaac ttccanacgt taacacgttt 420

aacatcggtt ttttaaaaaa ctgatgttag ttacaaacgt taac 464

<210> 2490
<211> 502
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2490

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gatcaaacac tactcattac tagactaaaa gatgtagctg atggtaaaaa taaaattctg 120

ttaatttcct caaagaattt tagagttaca actaacttaa gagtatggaa attaaattca 180

tcatggagta ctgtgagatg ttaaattcat caaattcttg ttggaatcgc gttaaccaaa 240

ttaaataaaa tcaacacatc ttataaagtt ttaaagtcaa tatatagttg aaagtaaaaa 300

ttaactgttg atcatattaa gaattgcaaa gggagaaagc atagccctta aaagtctttn 360

tttttacata aaataaatag taagtttagc attactactt tctatacgta cattntacgg 420

ataatttcat ttgaaaaata atgctactca naataaatgc atatatatta ccattngcta 480

taaactatta caataattat gg 502

<210> 2491
<211> 423
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2491

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actatggcgt catttctggc gctaaactgt tgggagttgg aagccatctt ctcaattaaa 120

tntttggctt cagcaggagt catgtctcca agggctccac cactggcaac atctatcata 180

cttctctcca tatttctgag tccttcataa aaatattgga gatgaagctg ctccgaaatc 240

tgatggtgag ggcaactggc acatagtttc ttaaatcgct cccagtactc atacaggctc 300

tctccactaa gttgtctaat acctgagata tctttcctga tggttgtggt cctcggaagc 360

agggaaattt tttctaagaa tactctctta aggtcatccc agctcgtgat ggaccttgga 420

gca 423

<210> 2492
<211> 331
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2492

agcttgtatg gtctanaaca naccccaaga caatggtaca agaagtttga aagctttatg 60

cacaacgaaa gtttctagaa gtgcaacgcc gatcanttgt gtttctttaa gagatataaa 120

tctagttata ttattttgct actttatgtc gatgttatat tagtagttgg atcagacatg 180

gatgaaatta anaacttaaa gatgcggcta taaaaaaaaa ttgacatgaa gcacttagat 240

ctagcaaaga agatccttgg tatgcaaatc acgaaagata agtaaatagg gattttgcag 300

ttatctcagg taaagtacat caatcgtgtt t 331

<210> 2493
<211> 228
<212> DNA
<213> Glycine max

<400> 2493

gcgtctcgag atctgatgcg cctgagtcga acgtccgagt gagaagaggt gaccatccaa 60

atttgtcgag agagtacggt gctcaatgtc aagcgtactg atatattatg tgcctgaatc 120

ggacatgccc gcgaagaggc atgaccattt gaagttctcg agagcctacg ctgtccaatg 180

aacaacgtcc gcacctgtga ttgacctgaa tcggtcctcg agcgcgtg 228

<210> 2494
<211> 428
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2494

agctnggctt cattcctgcc ccacttctaa tacttttatc attntctaaa ggtttaattg 60

cattttaaga aaattatgtg acaatttaaa agtaggagac aaaaaattgc ggataagaat 120

agattagatc atccgttagg tatctatggt ctcaccaata ataagcttat gttatatcat 180

acttctttag aaaataaata ggttaagacc ttttaaaagt ctatttagtt aaaaaaaatt 240

ggactctatc acttaaaaaa tcttttagac ataatagatc aatcttagtg ttattattat 300

attaaatttg ttatgatata ttgaatactt gtttatcgga aacatttgtt tcaagacatc 360

ttttanttgc gaaaatgtaa gagtgagaat tattattntc atatctttta gaaggttatg 420

acaatata 428

<210> 2495
<211> 440
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2495

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agtataaaga tattgtcggt tgaattntct cagagcttca acattcaatt tcgagcgtct 120

caatatatga cgggactcaa tcagacatcc gagtgaaaag atattgtcgt cttaattggc 180

tcagagcttc tacattcaat ttctagcgtn tcgatatatg accggactca atcaggcatc 240

cgtgtaaaaa gatattgtcg tttgagttgg ctcagagctt caacattcaa tttcaagcgt 300

ctcgatatat tacgggactc aatcaggcat ccgatgtaaa agttattgtc gtttgaattg 360

gctgagagct tcaacattca atttcgagcg tctcgatata tgaccggact caatcagaca 420

tccgagtana aagatattgt 440

<210> 2496
<211> 406
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2496

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atatatggag acgctcgaaa ttgaatgttg aagctctgag caaattcaaa cgacaataac 120

tctttactcg gatgtctaat tgagtcctat aatataacga gacgctcgaa gttgaatgtt 180

gaagctttga gcaaattcaa acgacaataa ctttttactc ggatgtctga ttgagtcccg 240

caatatatca acacgctcga aattgaatgt tgaagctctg agcaaatnca aacgaacata 300

tatctntaat cggatgtctg attgagtcct ataatatatc gagacgctag aggttgaatg 360

ttgaagctct gagcaaattc anacgacaat aactttcact cggatg 406

<210> 2497
<211> 412
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2497

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aggaaattat agtgctgtga ttcaaaagat ccttccaccc aagcataaag accttgggag 120

tgtaaccatt ccttgcttaa ttggagaagt cactatggga aaggctctta ttgacctagg 180

agccagtatt aatttaatgc cattcttcat gtgcagaang gtgggagaag tggagatcat 240

gcccactacg atgactttac aacttgctga ccgctccatt accagaccat atggagtaat 300

tgaagatgtg ctggtcagag taaaacattt tatcttgccg acagactttg tggtaatgga 360

tatatgtgaa gataatgaca ttcctgtaat ttgggaaggc catcatgtaa ct 412

<210> 2498
<211> 305
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2498

agcttgtagc atttgtcctt tatgtgtccc aacatgtcac agtgagcaca nttgggtctt 60

tctttcttga tgtatttccc tttattgata tcacattggt tctttgatgc agaattaaca 120

gaaaatacta tattttctaa agtattggtg ggtgggtgag taaacaacaa tctcctttga 180

gcttcttctt gaaggattag ggagaaaaca ttaccaattg aaggcaaagg atcagagatc 240

aggatctgac ctcgtatttg agagaaagaa tcattcaaac ccatcaagaa tgacattaca 300

tactc 305

<210> 2499
<211> 413
<212> DNA
<213> Glycine max

<400> 2499

ttatctaatc attccaatcc actcaaatca tacaattgct tattcaaatc attctcaaac 60

attcatttca tgcaaaacaa tccactgcat atcattttca atcaattcac tattcaaaca 120

cgctttatgt acaagcaaac aactcaaagt gctgaaattt aaataactga aattaaaata 180

actgaaatat gacaacgaaa tcagctggaa atataaggtg tttaaccttc accaaaacat 240

cttcaatgac tccatatggc cttgtgatgg agcggtcaac taactggagg gtcatgcgtg 300

tgggcattat ctctatctct ccaagtcgct ggcacatgga aagaggcatt aaatcgatac 360

tagcttccaa gtctatgaga gctttgccta caacaacctc accaatataa cac 413

<210> 2500
<211> 445
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2500

ttgagcatan tcaaacgaca ataactctct actcggatgt ctgattgagt cctgtaatat 60

atcgagacgc tcgacatgga ataccgaagc tctgagcaaa tttaaacgac aataaccttt 120

ttactcggat gtctgatcga gtcccgaaat atatcgagat gctagaaatc gaatgtcgaa 180

gctctgatca aattcaaacg acaataactt tttactcgga tgtccgattg actctcgtaa 240

tatatccaga cgctcgaaat gcaatatcga acctccgacc gattccaaca ataataactt 300

tttactcgga tgtccgattg agtcccgcaa taatccgaac gctcgatatt gaatgttgaa 360

gctttgagca aatccatacg acaataactt tctactcgga tgcctgatcg agtcccgaat 420

atatcgagac gctcgaaatg gaata 445

<210> 2501
<211> 288
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2501

agcttctaca ttcaatttcg agctcttcga tatattactg tactcaatcg gacatccgag 60

taaaaagtta ttgtagttcg aatctgctca nggcttcggt attccatttc gagcgtctcg 120

atatattacg ggactcaatc ggacatcaga gtataaaggt attgttgttt gaatctgctc 180

agagcttcgg tattccattt ctagcatctc gatatattac ggcactcaat cagacatccg 240

agtaaaaagt tattgcagtt tcaatatgct cacggcttcg gtattcca 288

<210> 2502
<211> 373
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2502

acctttagaa atttgaatct aaatttcaca gtctataatc gactacagag tgtatataat 60

tgattaccag agttaaaatt caaatctcaa atatgaagag tcacaactct ttagaaaaca 120

actgtgtaat cgattacacc attctggtaa tcgattacta gtgaggaatt ttcgaaaata 180

actcccaaca gtcacatatt ntcaaatgtt tttgaatggc catcaaaggc ctatatatat 240

gtgacttgtg acacgaattt ctagagagag tttttctgaa ctgagatgtc ttatcctctc 300

aaagagattc ctaggtcaaa cacttgcata ttcaataagg aatcttgatt gattttaatt 360

gaatatcctt ctc 373

<210> 2503
<211> 423
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2503

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tttgcccttc tatgcaacaa tctggagcaa ttaagcagcc tgaagcttat gctacaaaca 120

tttacaatag acctnctcaa cctcagctgc aaaatcaacc acagcagaac aattatgacc 180

tctccagcaa cagatacaat cccggatgga ggaatcaccc aaatttcaga tggtctagcc 240

ctcaacaaca acaacagcct gctctttcct ttcaaaatgg tgctggtcca agtaggccat 300

acgttcctnc tccaatgcaa caacaacaac cacagtagca acaacaatag agacaacaat 360

caactgagac ccttctcaac cttncttaga ggaagtagta aggcaaatga caatacagaa 420

tat 423

<210> 2504
<211> 496
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2504

ttatcaatat atgggtctaa cacanataat taaagggttt aaattgatta tttctagaga 60

agtagatgat ttccctgaac acaattttta tttgataggt aatatgataa aattactgcg 120

aaagttacga acttagaaat gaagagtaat ttgaagaaat aactttatat ctttgtgtac 180

tgactccaac tgaattgttt ggatgaaaga aatcatttta tctactaatc atagacaaat 240

tggagtatta ccaaatgatg cacgtattgc caatgtcgta gatataggta ctttgagaat 300

gtcttcttaa acaccaatgg ctctgatggg cagttttact agagaatttt gtaaagttca 360

aacctttgaa actgattgaa gaaggtaaga gttcccagaa ggtggagaat gcaagatctt 420

gaagacaatt agaatcgtta tttacgaaca aatgtgggag ctttgaggtg tgtgactgtg 480

aatgacttgc acacat 496

<210> 2505
<211> 438
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2505

agcttctaaa ctntgtacaa gaatgaagct ctgataccac ttgttagaca agtggcctca 60

gatatcttaa gaaggggggg ttgaattaag atattccaaa ctgtttcccc taattaaaaa 120

tctatttcac tntntactca agttatgaat tcccttaatg acaatcttct taaatattaa 180

ttcaaatgaa gcaacttgaa tatgaatata aagcaataat aaataaagga gattaaggga 240

agagaaaatg caaactcagt tttatactgg ttcggccaca cccttgtgcc tacgtccagt 300

ccccaagcaa cccgcttgag agttccacta tcttgtaaat tccttttaca agttctaaac 360

acacaaggac attccttcct ttgtgntaga gatcctttac aacaagagac tcacagtctc 420

ttaatccctt agagaatg 438

<210> 2506
<211> 382
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2506

agctnntggc tttntcccag tcattgattc ataacttgtc cctgatgtaa gctccattgg 60

agcttgtagg cctatgatct tcttcatcaa tggattcctt tgcttctcgg aagatgaatg 120

gaagcggatg agtctagaag atgctcacca ccataggtgg ccatggataa gagcttggag 180

gaagaatgag atgaatgaag ggagaggaag agaagagcat gannatttgt gctctaaaag 240

agctctgaaa tctgaagttt aatattcaaa tgatcatagt ttaaaaaatg cacacacatg 300

acctctattt atagcctaag tgtcacacaa aattggaggg aaattcgaat atcaattcan 360

atttcacttg aatttgaaat tg 382

<210> 2507
<211> 472
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2507

ntattcaaga canagcaatt aaagatattc aagatggatg atcaagacag tctatagagt 60

cttagaaagg gtatattaaa taggaaggga attccaattg aagtagcaaa aggtttggcc 120

aagaatttta agttaaaaag tcttttacaa gaaatttact ctctggtaat cgattaccag 180

aggatgtaat cgattaccag tagccaaaac tgatttacaa acagctatta aaatttgaat 240

tcaaaatttg ccctgtgtaa tcgattacca tatatggtaa ttcanattnt aaagcttgta 300

atcgattaca catatactgt aatcgattac cagagcagat tttcagaana tattctcaac 360

tgtcacatct ttttatgtgg ttcttgaatg gctatcanag gcctatatat atgtgacttg 420

agacacgaat ttgctaagag tttttcagaa caaaaaggtc ttatcctctt at 472

<210> 2508
<211> 511
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2508

ngctntanga ataagcttaa gagacatcat tattntgata gaattcaaat tcacatgtcc 60

aagcctagca tgccacacat canaacattc aacatttgca acaagagaag aaatgctaga 120

tattctatta atagaaagag gcataagact taacttaaac aaaccatcac aaatgtagcc 180

tttaccaata aaaacaccat gtctagtaat aacaactcta ttggactaaa aaacaacctt 240

gtatccttgt tagactaaca aagaagtact tattaaaant ttcctaatat cagaaacatg 300

atagacttca tctaaaacaa gaaaattccc tagagatagc tctagcttca cttgaccttc 360

tcctaacaca tgtgtcatac tcttattccc catgttcaca gtacgcgtgc ttgattctng 420

atataaagaa aaatattttt tttatcaaca cacatatgat aattagcccc gagatctata 480

aaccaatcat ttgagttaaa acacaattaa c 511

<210> 2509
<211> 437
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2509

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gtcgacgacc cgccggaana ttgccttcac ttctcggtgc tctcggaggc gaacgagagc 120

gacgcgccgg aggttgatat ccaacccgac gacgcggtgg cgatgccgtt ctcttncggc 180

acgacgggtt tacctaaagg agtggttctc acgcacaaga gtttaacaac cagtgtggcg 240

caacaagttg acggagagaa ccctaacctc tacctcacca ccgaggacgt gctcctatgc 300

gtgcttncgt tgtttcacat attctccctc aacagtgtgc tnttgtgcgc gcttanggcc 360

gggagtgcgg ttttgttgat gcagaagttc gagattggga cgctgttgga gctcatacag 420

cggcaccgcg tgtcggt 437

<210> 2510
<211> 349
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2510

tatgttcacc tgctgcattt agatcaaaat tcanaatctt caatgctcaa taggctttgt 60

gccccaactc aataggtaag tgacaagntt tgccatagat aaattggaag ggagtcagtc 120

ctataggagt attgtatgca cacgtagctt tatctaattt ttgagactag tccttccttg 180

actgagcaac tattttctcc agaatcttct tgacttccct attagaaact ttagctcgcc 240

caatggtcta aggatggtaa ggtgaggcta ccttgtgtct aacactatag tgttggagaa 300

ctttcttgag ttggaatgta tagatatgag atcctctatc acttataaa 349

<210> 2511
<211> 427
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2511

agctnntgaa gtagatatta tttattatta taatacatgc ttatctattn gttaagtatg 60

tnttgtagtt agttaattga gacttgnggg tgtatatcag tgttttatac ttactacttt 120

gatttggtta gtgtgtgtat attacataga gtttatattt tattaattaa ttgacactaa 180

agatgttata gttttgctat gatatgaatt tgaaaattat tcgagtcgat gtatatgtat 240

atgggttggg tcttgtaaac attgctacga atgtataata tgatatatga gaataagtga 300

agtatgcgat gaattgtgag ctatgaactg tgtagtcaca caactataat actctttaag 360

ggcgacgagt tcatgcgcaa tgagttttgt gatgggcttc actatgggaa ctcgacgagt 420

taatcac 427

<210> 2512
<211> 395
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2512

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gctgaatatg caacagcaat ccaaggacgc atacccaaac gaaaactaag ttcccactca 120

cgcgccatgt agcaagctac accaagtaag aagtgtagaa caattagttc ataaggaccg 180

ccgttgtata accattcatc aacagatgcc gccttccaaa taggataaaa gtgcaaacct 240

atagccgcag aagtaggaat aatggcacca gagatgatat tgtntccata aagtagagat 300

ccagagacac gctcacgaat accatcaata tctactggag gggcagcaat aaaagcgata 360

ataaatacag aagttgcggc caataaagta tgaat 395

<210> 2513
<211> 289
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2513

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cctcattaag aactagctct tttcttcctc tattgccttt agttgaatac acctttgtt 120

ggctctctat ttgggtctta accctctcat gcatcttctt tacaaattct gacctaagat 180

tcccttcttt atgtataaaa aaagtgtcca gtgggagggg aatgaggtct aacggtgtga 240

ggtgatngaa cccatagacc aacctcaaag gggacttgtt ggtggtttc 289

<210> 2514
<211> 332
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2514

agctntacgg gtatacagaa caacatataa agccctcata tgacttatct ctttnccagn 60

nggcctatgg aaaatcttgt cacctaccta ttgagttgga acataaagct ctttgggctt 120

taaaatttac gaacttcaac tcagatacaa ctggtgaaca taggaagctc caactctatg 180

aattggagga actgatggtt caagcttctg agaattccaa gctttataag caaaaattaa 240

aaatctatca tgacaaaaag ctatcaaaaa gaaattttca gcctagtcaa caactattgt 300

tatttaattc tcgattaaga ttgtttccag gt 332

<210> 2515
<211> 408
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2515

caagcttgaa tgctctattc aatggagttg actagataat cttcagactg atcaacacat 60

gcacagtggc caaggatgca tgggagatcc tganaaccac tcatgaagga acctccaaag 120

tgaagatgtc cagattgcaa ctattggcca caaaattcga aaatctgaag atgaaggagg 180

aagaatgtat tcatgacttc cacatgaaca ttcttgaaat tgccaatgct tgcactgcct 240

tgngagagag gatgacagat gaaaagctgg tgagaaagat cctcagatcc ttgcctaaga 300

gatttgacat gaaagtcact gcaatagagg aggcccaaga catttgcaac ttgagagtgg 360

atgaactcat tggttccctt canacctttg agctaggact ctcggata 408

<210> 2516

<211> 135
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2516

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attcatcagt gggctttcct tctgtgtcca gcatcttggg atgatcccag cctttgatga 120

caggtttcca tgttc 135

<210> 2517
<211> 409
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2517

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tacgagacat cttgccaaac aaagtcaggt taacgataac tcgcctgtgc tttttcttcc 120

attctatatg tagcacagtc attaatccag tcatgtttga tgagttggga aatgaggccg 180

caattatact gtgctagttg gagatgtatt ttccccctgc tttctttgac atcatgattc 240

acttggttgt gcatctggtc agagaaatca aatgttgtgg tcctgtttat ctacggtgga 300

tgtacccggt tgagcgatac atgaagatct taanagggta tacaaagaat ctatatcgtc 360

cagaagcatc tattgttgag aggtacattg cagaagaacc attgaattt 409

<210> 2518
<211> 430
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2518

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agagagcaag agatgaagag ccaatggttg atacatggac agagatgaaa aagatcatga 120

ggaagcggta tgtgccggct agttactcaa gggacttgaa atttaagctc caaaaactaa 180

cccaaggcaa caaggggttt gaggagtatt tcaaggaaat ggatgtgctc atgattcaag 240

caaatattga agaagatgag gaggtaacta tggctcgatt tcttaatggt ttgactaatg 300

atatccgtga tattgttgag ctgcaggagt ttgttgaaat ggatgatttg cttcacaaag 360

caatccaagt ggagcaacaa ttaanaagga agggagtggc taagaggagt tttaccaact 420

ttgattcttt 430

<210> 2519
<211> 317
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2519

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agaagaccgt gctcacagcg ataaaaaatg agaaggagga gctgattact actcgggtgg 120

agaacagttg gagagtctgc attgactata ggaggctgaa ccaggttacc aaaaaggacc 180

atntcccctt gccattcatt gaccagatgc ttgaacgcct gggcaggcaa atctcactac 240

tgtttccttg atggtncttc tggttatatg ccaaatacta ttgctcttga ggatcaggaa 300

aagaccacat tcacctg 317

<210> 2520
<211> 388
<212> DNA
<213> Glycine max

<223> unsure at all n locations
<400> 2520

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gccaaacaaa gtcaggttag cgataactcg cctatngctt ttcttccatg ctatatgtag 120

caaagtcatt gatccagcca agtttgatga cgtggaaaat gagggcgtaa ttatattgtg 180

cctgttggag atgtatttcc cctcctgctt tctttgacat catgattcac tcgattgtgc 240

atctggtcag agaaatcaaa tgttgtggtc ttgttatcta cggcggatgt acccagtaga 300

gcgatacata aagatcttca aggggtctac aaagaatata tatcgtctag aagcatctat 360

tatagagagg tacattgcag aagaagcc 388

<210> 2521
<211> 382